

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 31.1423 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-1
Perfect score: 234
Sequence: 1 ELKRLRLPLVLFSEER.....QGALNABREDELSGESS 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	100.0	47	5	ABB80769 A. salmon
2	153	65.4	97	7	ABO81308 Pseudomon
3	68.5	29.3	4558	6	ABU04362 Protein e
4	68	29.1	365	3	AB14131 Bordetell
5	68	29.1	386	6	ABU22986 Protein e
6	68	29.1	395	9	ABE43018 Lawsonia
7	66.5	28.4	5206	9	AEA29369 Vibrio vu
8	66	28.2	445	9	AEB39774 L. pneumo
9	66	28.2	451	9	AEB36357 L. pneumo
10	65	27.8	2000	9	ADY15562 PRO polyp
11	65	27.8	5032	7	ADJ68220 Human hea
12	65	27.8	5038	8	ADQ18491 Human sof
13	65	27.8	5038	8	ADY19486 PRO polyp
14	65	27.8	5072	2	AAR11510 Rvancodine
15	65	27.8	5081	4	ABB11480 Human rya
16	65	27.8	5081	4	ABG04969 Novel hum
17	61.5	26.3	61	4	ABU43730 Propionib
18	61.5	26.3	61	6	ABM40249 Propionib
19	61	26.1	840	10	AEG11146 Human tra
20	60.5	25.9	385	7	ADM25471 Hyperther
21	59.5	25.4	993	9	AEB08385 c-Jun inh
22	59.5	25.4	1225	6	ABU04466 Human exp
23	59.5	25.4	1225	6	ABU04463 Human exp

ALIGNMENTS

RESULT 1
ABB80769
ID ABB80769 standard; protein; 47 AA.
XX
AC ABB80769;
XX
DT 23-SEP-2002 (first entry)
XX
DE A. salmonicida type III secretion protein acrI sequence.
XX
KW Type III secretion protein; acrI; acr2; acr3; acr4; acrD; acrR; acrG;
KW acrv; acrH; antibiotic; vaccine; fish.
XX
OS Aeromonas salmonicida.
XX
PN WO200240514-A2.
XX
PD 23-MAY-2002.
XX
PF 15-NOV-2001; 2001WO-CA001589.
XX
PR 15-NOV-2000; 2000US-0248864P.
XX
(FREY/) FREY J.
(STUB/) STUBER K.
(THOR/) THORNTON J C.
(KUZ/) KUZIK M A.
(BURI/) BURIAN J.
Frey J; Stuber K, Thornton JC, Kuzik MA, Burian J;
WPI: 2002-537338/57.
N-PSDB; ABB86172.
Novel protein from Aeromonas salmonicida and nucleic acid encoding the protein, useful for reducing susceptibility of fish to infection by a virulent strain of Aeromonas salmonicida.
Claim 13; Page 26; 39pp; English.
The invention relates to A. salmonicida type III secretion genes and encoded proteins AcrI, Acr2, Acr3, Acr4, AcrD, AcrR, AcrV or AcrH. A. salmonicida type III secretion apparatus is useful for producing selected products, especially Aext. AcrV in vaccine, epitope or epitopic region of AcrV or any other protein of A. salmonicida type III secretion apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of *A. salmonicida*. The proteins and encoding DNA are
CC useful for manufacturing a diagnostic agent. Detecting the presence of
CC the genes of AcrD, AcrV or any other components of the *A. salmonicida* type
CC III secretion apparatus is useful for the production or quality control
CC or efficacy of vaccines made from *A. salmonicida* or its genes. The present
CC sequence represents the *A. salmonicida* type III secretion protein acrl
XX
SQ Sequence 47 AA;

Query Match 100.0%; Score 234; DB 5; Length 47;
Best Local Similarity 100.0%; Pred. No. 5.8e-24;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELKRLIRLLPVLFSEEEQRNLQCCGALDIAEREEDELSGSS 47
DB 1 ELKRLIRLLPVLFSEEEQRNLQCCGALDIAEREEDELSGSS 47

RESULT 2
ABO81308
ID ABO81308 standard; protein; 97 AA.
XX
AC ABO81308;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #13483.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
XX
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.

XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
XX
DR N-PSDB; ABD14879.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.
XX
XX Disclosure; SEQ ID NO 30054; 455pp; English.

XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
SQ Sequence 97 AA;

Query Match 65.4%; Score 153; DB 7; Length 97;
Best Local Similarity 70.5%; Pred. No. 1.3e-12;
Matches 31; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELKRLIRLLPVLFSEEEQRNLQCCGALDIAEREEDELSG 44
DB 52 ELKRLYLLPVEVFGDEQRNLNACQMALDLAIEEEQHQH 95

RESULT 3
ABU49362
ID ABU49362 standard; protein; 4558 AA.
XX
AC ABU49362;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #34889.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Vibrio cholerae.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX
PR 06-SEP-2001; 2001US-00948993.
XX
PR 25-OCT-2001; 2001US-0342923P.
XX
PR 08-FEB-2002; 2002US-00072851.
XX
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
DR N-PSDB; ACA53232.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 77286; 1766pp; English.

XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC on a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational

CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 386 AA;

Query Match 29.1%; Score 68; DB 6; Length 386;
Best Local Similarity 32.4%; Pred. No. 2.2;
Matches 12; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 2 LKRLIRLLPVELFSEEEQRQNLQCCGALDIAIERE 38
Db 348 VQIILKULPTQIYADMDVRATVLAQAQALDIAIAME 384

RESULT 6
AEB43018
ID AEB43018 standard; protein; 395 AA.

XX
AC AEB43018;

XX
DT 06-OCT-2005 (first entry)

XX
DE Lawsonia intracellularis protein #6.

XX
KW Vaccine; antigen; bacterial infection; infection; antibacterial.

XX
OS Lawsonia intracellularis.

XX
PN WO2005070958-A2.

XX
PD 04-AUG-2005.

XX
PF 18-JAN-2005; 2005WO-EP000562.

XX
PR 22-JAN-2004; 2004EP-00100202.

XX
PR 22-JAN-2004; 2004EP-00100203.

XX
PR 22-JAN-2004; 2004EP-00100205.

XX
PR 22-JAN-2004; 2004EP-00100206.

XX
PR 22-JAN-2004; 2004EP-00100208.

XX
PR 22-JAN-2004; 2004EP-00100209.

XX
PR 22-JAN-2004; 2004EP-00100210.

XX
PR 22-JAN-2004; 2004EP-00100211.

XX
PA (ALKU) AKZO NOBEL NV.

XX
PI Vermeij P;

XX
DR WPI; 2005-533996/54.

XX
DR N-PSDB; AEB43017.

XX
PT New Lawsonia intracellularis nucleic acids and proteins, useful as

XX
PT vaccines or for manufacturing vaccines for combating Lawsonia

XX
PT intracellularis infections.

XX
PS Claim 19; SEQ ID NO 12; 99pp; English.

XX
CC The invention relates to a nucleic acid encoding a Lawsonia
CC intracellularis protein or a part of the nucleic acid that encodes an
CC immunogenic fragment of the protein. The invention also relates to a DNA
CC fragment comprising the nucleic acid, a recombinant DNA molecule
CC comprising the nucleic acid or the DNA fragment under the control of a
CC functionally linked promoter, a vaccine for combating L. intracellularis
CC infections comprising the nucleic acid, the DNA fragment, recombinant DNA
CC molecule, live recombinant carrier, host cell, or protein and a
CC pharmaceutical carrier, a vaccine for combating L. intracellularis
CC infections comprising antibodies against the protein above, a method of
CC preparing the vaccine and a diagnostic test for the detection of
CC antibodies against L. intracellularis comprising the protein or its
CC fragment or comprising antibodies against the protein or its fragment.
CC The L. intracellularis nucleic acid and protein can be used in a vaccine
CC or in the manufacture of a vaccine for combating L. intracellularis
CC infections. They can also be used for detecting antibodies against L.

CC intracellularis. This sequence represents an L. intracellularis protein
CC of the invention.
XX
SQ Sequence 395 AA;

Query Match 29.1%; Score 68; DB 9; Length 395;
Best Local Similarity 31.0%; Pred. No. 2.3;
Matches 13; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 ELKRLIRLLPVELFSEEEQRQNLQCCGALDIAIEREDEL 42
Db 336 EMLAAVRKFPITMVDNVRVGVQDAVDDAVRREDEFL 377

RESULT 7
AEA29369
ID AEA29369 standard; protein; 5206 AA.

XX
AC AEA29369;

XX
DT 28-JUL-2005 (first entry)

XX
DE Vibrio vulnificus RTX toxin rtxA protein SEQ ID NO:2.

XX
KW vaccine; toxin; rtxA.

XX
OS Vibrio vulnificus.

XX
PN KR2004098202-A.

XX
PD 20-NOV-2004.

XX
PF 14-MAY-2003; 2003KR-00030495.

XX
PR 14-MAY-2003; 2003KR-00030495.

XX
PA (UYCH-) UNIV CHONNAM NAT.

XX
PI Kim SY, Kim YR, Lee JH, Lee SE;

XX
DR WPI; 2005-239015/25.

XX
DR N-PSDB; AEA29368.

XX
PT RTX toxin and related genes of vibrio vulnificus responsible for the

XX
PT contact-cytotoxicity and lethality to animals.

XX
PS Example 4; SEQ ID NO 2; 62pp; Korean.

XX
CC The invention relates to the Vibrio vulnificus RTX toxin and related
CC genes responsible for the contact-cytotoxicity and lethality to animals.
CC Also described is a method for producing a mutant Vibrio vulnificus
CC strain with attenuated cytotoxicity by deletion of the cytotoxicity
CC related genes. The mutant strain with attenuated cytotoxicity is produced
CC by deletion of one or more genes in the RTX operon of Vibrio vulnificus,
CC selected from the rtxB2 gene of AEA29372, the rtxD gene of AEA29374, the
CC rtxB1 gene of AEA29370, the ORF (open reading frame) between the rtxB1
CC gene and rtxC gene of AEA29378, the rtxC gene of AEA29376 and the rtxA
CC gene of AEA29368. An alive vaccine against Vibrio vulnificus is produced
CC by using the RTX toxin production of the deficient mutant strain. The
CC present sequence represents the Vibrio vulnificus rtxA protein, which is
CC used in the exemplification of the present invention.

XX
SQ Sequence 5206 AA;

Query Match 28.4%; Score 66.5; DB 9; Length 5206;
Best Local Similarity 35.4%; Pred. No. 76;
Matches 17; Conservative 10; Mismatches 18; Indels 3; Gaps 1;

QY 2 LKRLIRLLPVELFSEEEQRQNLQCCGALDIAIEREDEL--LSGES 46
Db 2926 LSPETRFNNELGYEKDARRKIGETITQLLDHAVENGESQKVLKGEA 2973

```
RESULT 8
AEB39774
ID AEB39774 standard; protein; 445 AA.
XX AC AEB39774;
XX
XX 08-SEP-2005 (first entry)
DT
XX L. pneumophila protein SEQ ID NO 4106.
DE
XX detection; infection; Antibacterial; Vaccine.
XX Legionella pneumophila.
OS
XX WO2005049642-A2.
XX
XX 02-JUN-2005.
XX
XX 23-SEP-2004; 2004WO-IB003578.
XX
XX 21-NOV-2003; 2003FR-00013687.
XX
XX (INSP ) INST PASTEUR.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
XX Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
XX Jarraud S;
XX WPI; 2005-388305/40.
XX
XX New genome of Legionella pneumophila Paris strain and derived
XX polypeptides, useful for detection or identification of the strain and
XX for treatment and prevention of infections.
XX Claim 3; SEQ ID NO 4106; 660pp; English.
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
XX from Legionella pneumophila Paris strain. (I), and their related
XX sequences or fragments, are useful as primers and probes for detection
XX and amplification, including differentiation between the Paris and
XX Philadelphia strains of Legionella pneumophila and to prepare recombinant
XX (hybrid) polypeptides (II). (II) are also useful for preparation of
XX specific antibodies (Ab), also used for detection/identification of
XX Legionella, and some (I), specifically those involved in synthesis of
XX surface proteins, are targets for identification of inhibitors. (II), or
XX vectors that contain (I), are useful as vaccines and immunogenic
XX compositions, for treatment and prevention of infections by L.
XX pneumophila. The present sequence represents the amino acid sequence of a
XX L. pneumophila protein.
XX Sequence 445 AA;
SQ
Query Match 28.2%; Score 66; DB 9; Length 445;
Best Local Similarity 26.8%; Pred. No. 4.9;
Matches 22; Conservative 7; Mismatches 13; Indels 40; Gaps 2;

QY 2 LKRLIRLLPVELFSEEEORQ-----NLQCCQ----- 28
DB 17 LKDLIRMTAEQFLSEKREKQVLLQKMRAPSGLEASRYESLCSVLVENLVNYCONLPETAN 76
QY 29 -----GALDNAIEREDEL 43
DB 77 SYYSQFGLVDHALNTEAALS 98

RESULT 9
AEB36357
ID AEB36357 standard; protein; 451 AA.
XX AC AEB36357;
XX
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XX 08-SEP-2005 (first entry)
XX L. pneumophila protein SEQ ID NO 689.
XX detection; infection; Antibacterial; Vaccine.
XX Legionella pneumophila.
XX WO2005049642-A2.
XX
XX 02-JUN-2005.
XX
XX 23-SEP-2004; 2004WO-IB003578.
XX
XX 21-NOV-2003; 2003FR-00013687.
XX
XX (INSP ) INST PASTEUR.
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
XX Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
XX Jarraud S;
XX WPI; 2005-388305/40.
XX
XX New genome of Legionella pneumophila Paris strain and derived
XX polypeptides, useful for detection or identification of the strain and
XX for treatment and prevention of infections.
XX Claim 3; SEQ ID NO 689; 660pp; English.
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
XX from Legionella pneumophila Paris strain. (I), and their related
XX sequences or fragments, are useful as primers and probes for detection
XX and amplification, including differentiation between the Paris and
XX Philadelphia strains of Legionella pneumophila and to prepare recombinant
XX (hybrid) polypeptides (II). (II) are also useful for preparation of
XX specific antibodies (Ab), also used for detection/identification of
XX Legionella, and some (I), specifically those involved in synthesis of
XX surface proteins, are targets for identification of inhibitors. (II), or
XX vectors that contain (I), are useful as vaccines and immunogenic
XX compositions, for treatment and prevention of infections by L.
XX pneumophila. The present sequence represents the amino acid sequence of a
XX L. pneumophila protein.
XX Sequence 451 AA;
SQ
Query Match 28.2%; Score 66; DB 9; Length 451;
Best Local Similarity 26.8%; Pred. No. 5;
Matches 22; Conservative 7; Mismatches 13; Indels 40; Gaps 2;

QY 2 LKRLIRLLPVELFSEEEORQ-----NLQCCQ----- 28
DB 23 LKDLIRMTAEQFLSEKREKQVLLQKMRAPSGLEASRYESLCSVLVENLVNYCONLPETAN 82
QY 29 -----GALDNAIEREDEL 43
DB 83 SYYSQFGLVDHALNTEAALS 104

RESULT 10
ADY15562
ID ADY15562 standard; protein; 2000 AA.
XX AC ADY15562;
XX
XX 05-MAY-2005 (first entry)
XX DE PRO polypeptide SEQ ID NO 1368.
XX
```


CC receptors. The peptides in the feature table were determined from the
CC purified receptor protein. (Updated on 25-MAR-2003 to correct PR field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 5072 AA;
SQ Sequence 5072 AA;
Query Match 27.8%; Score 65; DB 2; Length 5072;
Best Local Similarity 29.3%; Pred. No. 1.2e+02;
Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;
QY 1 ELKRLIRLLPVLEFSEEEQRNLLQCCGALDNAIERDEDE 41
DB 1857 DVKQILKMIPEVFTSEEEDEEE--EGEEDDEBEKEDE 1895
RESULT 15
ABB11480
ID ABB11480 standard; peptide; 5081 AA.
XX ABB11480;
AC ABB11480;
DT 11-JAN-2002 (first entry)
XX Human ryanodine receptor homologue, SEQ ID NO:1850.
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antitachycardic; antiarrhythmic; haemostatic; antiarteriosclerotic;
KW cytoskeletal; osteopathic; vasorropic; cardiac; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.
XX Homo sapiens.
OS Homo sapiens.
XX WO200157188-A2.
FN WO200157188-A2.
XX 09-AUG-2001.
PD 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US003800.
PF 05-FEB-2001; 2001WO-US003800.
XX 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457740/49.
DR N-PSDB; ABA08724.
XX Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX Claim 20; Page 197-200; 1963pp; English.
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides,
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may

CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention
XX Sequence 5081 AA;
SQ Sequence 5081 AA;
Query Match 27.8%; Score 65; DB 4; Length 5081;
Best Local Similarity 29.3%; Pred. No. 1.2e+02;
Matches 12; Conservative 18; Mismatches 9; Indels 2; Gaps 1;
QY 1 ELKRLIRLLPVLEFSEEEQRNLLQCCGALDNAIERDEDE 41
DB 1901 DVKQILKMIPEVFTSEEEDEEE--EGEEDDEBEKEDE 1939
Search completed: June 16, 2006, 19:06:42
Job time : 33.1423 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 4.77642 Seconds
(without alignments)
946.773 Million cell updates/sec

Title: US-10-813-908A-1
 Perfect score: 234
 Sequence: 1 ELKRLIRLLPVLEFSEEEQR.....QGALDNAIEREDELSSGSS 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10
                  Listing first 45

```

```
Database : PIR_80:*
1:  _pir1:*
2:  _pir2:*
3:  _pir3:*
4:  _pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	153	65.4	92	2	H83431		conserved hypothet
2	150	64.1	92	2	B35392		hypothetical prote
3	150	64.1	92	2	T43587		yop secretion and
4	150	64.1	92	2	S15321		hypothetical prote
5	68.5	29.3	4558	2	C81219		RTX toxin RtxA VC1
6	65	27.8	5032	1	A35041		ryanodine receptor
7	63	26.9	358	1	H88921		protein F56E10.1 [
8	61	26.1	539	2	T18430		hypothetical prote
9	60.5	25.9	1208	2	T34469		hypothetical prote
10	60	25.6	289	2	H69645		myo-inositol catab
11	59.5	25.4	1233	2	I54383		chromosome segrega
12	58	24.8	203	2	T18653		hypothetical prote
13	58	24.8	293	1	EDBEF7		immediate-early pr
14	58	24.8	507	1	FWCNBA		beta-globulin A pr
15	57.5	24.6	5035	1	I46646		ryanodine receptor
16	57	24.4	518	2	S53804		protein kinase NPK
17	56.5	24.1	190	2	E82614		protein F24B9.1 [i
18	56.5	24.1	495	2	T48372		ATB/alpha regulato
19	56.5	24.1	567	2	E84658		hypothetical prote
20	56	23.9	340	2	A36988		replication factor
21	56	23.9	405	2	T01218		hypothetical prote
22	55.5	23.7	168	2	B71486		hypothetical prote
23	55.5	23.7	423	2	AH0522		conserved hypothet
24	55	23.5	5037	2	B35041		ryanodine receptor
25	54.5	23.3	121	2	G90550		hypothetical prote
26	54	23.1	469	2	AE1234		ATP-dependent Clp
27	54	23.1	469	2	AE1597		ATP-dependent Clp
28	54	23.1	680	2	S71489		sulfinolalanine dec
29	54	23.1	493	2	T43077		probable relaxase

ALIGNMENTS

RESULT 1

H83431
C:Specified hypothetical protein in type III secretion PA1699 [imported] - Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83431
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liman, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen
A:Reference number: AB2950; UID:20437337; PMID:10984043
A:Accession: H83431
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-92 <STO>
A:Cross-references: UNIPROT:Q30532; UNIPARC:UPI000000B4211; GB:AEO04597; GB:AEO04091; NID:110984043
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA1699

```
Query Match      65.4%; Score 153; DB 2; Length 92;
Best Local Similarity 70.5%; Pred. No. 1e-11;
Matches 31; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
```

QY 1 ELKRLIRLLPVELFSEEEQRNLLQCCQCALDNAIEREEDELSG 44
 ||||| ||||| : : ||||| || ||||| ||||| : : ||||| |||||
 47 ELKRLYRLLPVEVFGDDEORNLNACOMALDLAIEEEEEOOHG 90
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RESULT 2

B35392
hypothetical protein 1 - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: B35392
R;Viitainen, A.M.; Toivanen, P.; Skurnik, M.
J. Bacteriol 172, 3152-3162, 1990
A;Title: The lcrE gene is part of an operon in the lcr region of Yersinia enterocolitica.
A;Reference number: A35392; PMID:90264308; PMID:2160939
A;Accession: B35392
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-92 <VIL>
N_Genes_refseq:CBM23097, NID_C15E454, BIDN

Query Match 64.1%; Score 150; DB 2; Length 92;
Best Local Similarity 67.4%; Pred. No. 2.4e-11;
Matches 20; Conservative 7; Mismatches 7; Indels 0; Gaps 0.

QY 1 ELKRLIRLLPVELFSEEEQRQNLLQCCQGALDNAIEREEDELS 43

A:Accession: I54383
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1233 <RES>
A:Cross-references: UNIPARC:UPI0000161C5B; GB:S78271; NID:g999379; PIDN:AAB34405.1; PID:
C:Genetics:
A:Gene: GDB:K1AA0178; SMC1; SB1.8/DXS423E
A:Cross-references: GDB:9785049
A:Map position: Xpter-Xqter
C:Superfamily: chromosome segregation protein SMC1

Query Match 25.4%; Score 59.5; DB 2; Length 1233;
Best Local Similarity 28.6%; Pred. No. 40;
Matches 16; Conservative 10; Mismatches 19; Indels 11; Gaps 2;

QY 2 LKRLRLPVELFSFEERQNLQCC-----QGALDNAIEREDELSGESS 47
Db 908 LQKEVTAETKLEQRSDRHNLQACKMQDIKLPLSGTMDP-ISQEEGSSQGEDS 962

RESULT 12
T18653
hypothetical protein B0035.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18653
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19002
A:Accession: T18653
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-203 <WIL>
A:Cross-references: UNIPROT:Q17432; UNIPARC:UPI00000829A8; EMBL:Z73102; PIDN:CAA97408.1;
A:Experimental source: clone B0035

A:Gene: CESP:B0035.3
A:Map position: 4
A:Introns: 16/1; 96/1; 136/3
C:Superfamily: Pyrococcus abyssi hypothetical protein PAB0445

Query Match 24.8%; Score 58; DB 2; Length 203;
Best Local Similarity 32.4%; Pred. No. 9.9;
Matches 12; Conservative 13; Mismatches 10; Indels 2; Gaps 1;

QY 2 LKRLRLPVELFSB--EEORNLQCCGALDNAIE 36
Db 94 IKKIHTVGPQVYGNVTDERENLVACYRTSLDIAIE 130

RESULT 13
EBBEF7
immediate-early protein IE68 - equine herpesvirus 1 (strain Ab4p)
N:Alternate names: in vitro host-range factor
C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: B36802
R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36805
A:Accession: B36802
A:Molecule type: DNA
A:Residues: 1-293 <TEL>
A:Cross-references: UNIPROT:P28940; UNIPARC:UPI000012D221; GB:M86664; NID:g330791; PIDN:
R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A:Reference number: A41831; MUID:92295566; PMID:1318606
A:Title: The DNA sequence of equine herpesvirus-1.
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Genetics:

A:Gene: 65
C:Superfamily: herpesvirus immediate-early protein IE68
C:Keywords: early protein

Query Match 24.8%; Score 58; DB 1; Length 293;
Best Local Similarity 31.3%; Pred. No. 14;
Matches 21; Conservative 6; Mismatches 16; Indels 24; Gaps 3;

QY 5 LIRLLPVELF-----SEEQRONLL-----QC-COGALDNAIERED 40
Db 148 LLQLPEOSFPIRATLRALNSEDRYEQRFLEPPDPPTLFGECDSVSGDSPSEEBED 207

QY 41 ELSGESS 47
Db 208 EASGESS 214

RESULT 14
FWCNBA
beta-globulin A precursor (clone 94) - upland cotton (fragment)
N:Alternate names: legumin precursor
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Oct-2004
C:Accession: B30838
R:Chlan, C.A.; Pytle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII cd
A:Reference number: A30838
A:Accession: B30838
A:Molecule type: mRNA
A:Residues: 1-507 <CHL>
A:Cross-references: UNIPROT:P09802; UNIPARC:UPI000016DD7A
A:Experimental source: var. Coker 201
C:Complex: homohexamer of heterodimer disulfide linked acidic and basic chains
C:Keywords: homohexamer; seed; storage protein
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-322,323-507/Product: beta-globulin A #status predicted <MAT>
F:20-322/Domain: acidic chain #status predicted <ACD>
F:323-507/Domain: basic chain #status predicted <BAS>
F:108-329/disulfide bonds: #status predicted

Query Match 24.8%; Score 58; DB 1; Length 507;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 16; Conservative 2; Mismatches 12; Indels 2; Gaps 1;

QY 16 EEEQRQ--NLQCCGALDNAIEREDELSCGE 45
Db 189 EEEQRRLRLAQMQGRSERGESEEEGE 220

RESULT 15
146646
ryanodine receptor, skeletal muscle - pig
N:Alternate names: calcium release channel protein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: I46646; I46645; S31395; I47133; S26624; A37105; I47212; S18135
R:Fujii, J.; Otsu, K.; Zorzato, F.; De Leon, S.; Khanna, V.K.; Weiler, J.E.; O'Brien, P.
Science 253, 448-451, 1991
A:Title: Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia susceptibility
A:Reference number: I46645; MUID:91320118; PMID:1862346
A:Accession: I46646
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5035 <FUJ>
A:Cross-references: UNIPROT:Q29105; UNIPARC:UPI00001101C2; GB:M91452; NID:gl64647; PIDN:
A:Accession: I46645
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-614, 'C', 616-5035 <FU2>
A:Cross-references: UNIPARC:UPI00001101C1; GB:M91451; NID:gl64645; PIDN:AAA311118.1; PID:
R:Leeb, T.; Brem, G.; Brenig, B.
submitted to the EMBL Data Library, November 1992

A;Description: Genomic organization of porcine skeletal muscle ryanodine receptor gene d
 A;Reference number: S31395
 A;Accession: S31395
 A;Molecule type: DNA
 A;Residues: 1542-2643 <LEE>
 A;Cross-references: UNIPARC:UPI00001741C8; EMBL:X69465
 R;Leeb, T.; Schmoelzl, S.; Brem, G.; Brenig, B.
 Genomics 18, 349-354, 1993
 A;Title: Genomic organization of the porcine skeletal muscle ryanodine receptor (RYR1) g
 A;Reference number: A48915; MUID:94117003; PMID:8288238
 A;Contents: annotation
 R;Harbitz, I.; Kristensen, T.; Bosnes, M.; Kran, S.; Davies, W.
 Anim. Genet. 23, 395-402, 1992
 A;Title: DNA sequence of the skeletal muscle calcium release channel cDNA and verificati
 A;Reference number: I47133; MUID:93036581; PMID:1329581
 A;Accession: I47133
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 2-2091, 'A', 2093-3494, 'L', 3496-4163, 'S', 4165-4182, 'R', 4184-4411, 'W', 4413-4971
 A;Cross-references: UNIPARC:UPI000016B7C5; EMBL:X62880; NID:g1936; PIDN:CAA44674.1; PID:
 R;Harbitz, I.; Kristensen, T.; Kran, T.; Davies, W.
 submitted to the EMBL Data Library, August 1992
 A;Reference number: S26624
 A;Accession: S26624
 A;Molecule type: DNA
 A;Residues: 482-706 <HAW>
 A;Cross-references: UNIPARC:UPI00001741C9; EMBL:X68247
 R;Harbitz, I.; Chowdhary, B.; Thomsen, P.D.; Davies, W.; Kaufmann, U.; Kran, S.; Gustave
 Genomics 8, 243-248, 1990
 A;Title: Assignment of the porcine calcium release channel gene, a candidate for the mal
 A;Reference number: A37105; MUID:91065640; PMID:2174405
 A;Accession: A37105
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 4785-4971, 'R', 4973-5035 <HA2>
 A;Cross-references: UNIPARC:UPI000016C6A7; GB:M32501; NID:g164428; PIDN:AAA31022.1; PID:
 R;Ledbetter, M.W.; Preiner, J.K.; Louis, C.F.; Mickelson, J.R.
 J. Biol. Chem. 269, 31544-31551, 1994
 A;Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by re
 A;Reference number: A55660; MUID:95081095; PMID:7989322
 A;Accession: I47212
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 516-676 <LED>
 A;Cross-references: UNIPARC:UPI0000000551; EMBL:U15965; NID:g562095; PIDN:AAA60467.1; PI
 C;Genetics:
 A;Gene: RYR1
 A;Introns: 527/1; 559/1; 598/3; 643/2; 1570/3; 1646/2; 1850/3; 1939/3; 2006/3; 2044/1; 2
 A;Note: the list of introns may be incomplete
 C;Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homolo
 C;Keywords: calcium channel
 Query Match 24.6%; Score 57.5; DB 1; Length 5035;
 Best Local Similarity 26.8%; Pred. No. 2.9e+02;
 Matches 11; Conservative 13; Mismatches 8; Indels 9; Gaps 1;
 QY 1 ELKRLIRLPVLFSEEQRLNLLCCGALDNAIEREDE 41
 ::::: ||::: : ||||
 Db 1859 DVKILKMTPEVFTTEEE-EE-----EEEEEEDE 1890

Search completed: June 16, 2006, 19:25:03
 Job time : 5.77642 secs

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OM protein - protein search, using sw model

Title: US-10-813-908A-1

Scoring table: BLOSUM62

[illegible]

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

CONFIDENTIAL

Maximum Match 100%

Database : UniProt_7.2:*

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2: uniprot_trembl:*
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SUMMARIES

Description

RP	[2]	NUCLEOTIDE SEQUENCE.
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RA Burr S.E., Puq

Microbiol. 151:2111-2118(2005)

CC

DR EMBL; AJ616218; CAE83101.1; -; Genomic DNA.

Best Local Similarity 100.0%; Pred. No. 1.3e-20;

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47 ET VBT T BT I DVET EEEBEBT ONY T OCOOCT ONA T EEEBEBT
48 ET VBT T BT I DVET EEEBEBT ONY T OCOOCT ONA T EEEBEBT

RESUL 2 AERHY
05X1.11

AC 05XL11: FREELIMINARY; FRI; 93 HA.

DT 23-NOV-2004, sequence version 1.

DE Acr1.

```

GN Name=acrl;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RL virulence of Aeromonas hydrophila.";
RI Infect. Immun. 73:6446-6457(2005).
CC -----
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CC -----
DR EMBL; AY763611; AAV30226.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10560 MW; EB215E253BB31A39 CRC64;

Query Match          96.2%; Score 225; DB 2; Length 93;
Best Local Similarity 93.6%; Pred. No. 1.6e-19;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELKRLIRLLPVLPFSEEQRNLLQCCOGALDNAIEREDELSGESS 47
Db 47 ELKRLVRLLPVLPFSEEQRNLLQCCOGALDNAIEREDELSGDPS 93

RESULT 3
Q6TLM9_AERHY
I.Q. Q6TLM9_AERHY PRELIMINARY; PRT; 93 AA.
AC Q6TLM9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Acrl.
GN Aeromonas hydrophila.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
RT pathogenesis.";
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
DR EMBL; AY394563; AAR26332.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10590 MW; CD3D11726471CB52 CRC64;

Query Match          96.2%; Score 225; DB 2; Length 93;
Best Local Similarity 93.6%; Pred. No. 1.6e-19;
Matches 44; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELKRLIRLLPVLPFSEEQRNLLQCCOGALDNAIEREDELSGESS 47
Db 47 ELKRLVRLLPVLPFSEEQRNLLQCCOGALDNAIEREDELSGDPS 93

RESULT 4
Q699R7_AERHY
ID Q699R7_AERHY PRELIMINARY; PRT; 93 AA.
AC Q699R7;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.

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DT 07-FEB-2006, entry version 8.
DE Acrl.
GN Aeromonas hydrophila.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
DR EMBL; AY528667; AAS91812.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10522 MW; 8BEFF64A3D71A CRC64;

Query Match          95.7%; Score 224; DB 2; Length 93;
Best Local Similarity 95.7%; Pred. No. 2.1e-19;
Matches 45; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ELKRLIRLLPVLPFSEEQRNLLQCCOGALDNAIEREDELSGESS 47
Db 47 ELKRLIRLLPVLPFSEEQRNLLQCCOGALDNAIEREDELSGESS 93

RESULT 5
Q84GZ2_PHOLU
ID Q84GZ2_PHOLU PRELIMINARY; PRT; 95 AA.
AC Q84GZ2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE LsaA.
GN Name=LsaA;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
CC -----
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CC -----
DR EMBL; AY144116; AAO18046.1; -; Genomic DNA.
SQ SEQUENCE 95 AA; 10859 MW; F12B5D44A35E808F CRC64;

Query Match          76.3%; Score 178.5; DB 2; Length 95;
Best Local Similarity 79.2%; Pred. No. 8.2e-14;
Matches 38; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 ELKRLIRLLPVLPFSEEQRNLLQCCOGALDNAIEREDEL-SGESS 47
Db 47 ELKRLIRLPVLPFSEEQRNLLNACQLALDAIEREDELWSGGA 94

RESULT 6
Q7NOW4_PHOLL
ID Q7NOW4_PHOLL PRELIMINARY; PRT; 95 AA.
AC Q7NOW4;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.

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[3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
[4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC -|- FUNCTION: Involved in the control of Yop release (By similarity).
CC -|- SUBUNIT: Interacts with the translocator YopD and with residues 242-293 of YopN (By similarity).
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DR EMBL: AF074612; AAC69793.1; -; Genomic_DNA.
DR EMBL: AF053946; AAC62566.1; -; Genomic_DNA.
DR EMBL: AL117189; CAB54315.1; -; Genomic_DNA.
DR EMBL: AE017043; AAS85864.1; -; Genomic_DNA.
DR PIR: T43587; T43587.
DR DRB: 1XL3; X-ray; C/D=1-92.
DR SMK: P69968; 2-86.
DR GenomeReviews; AE017043 GR; pCD45.
DR GenomeReviews; AL117189 GR; YPCD1_38C.
KW 3D-structure, Complete proteome, Plasmid.
FT CHAIN 1 92
FT Protein tyEA.
FT /FTrid=PRO_0000065703.
SQ SEQUENCE 92 AA; 10753 MW; E5046EDD93D92F9 CRC64;
Query Match 64.1%; Score 150; DB 1; Length 92;
Best Local Similarity 67.4%; Pred.No.2.4e-10;
Matches 29; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELKRLRLPLVLFSEEEQRNLQCCGALDNAIEREDEL 43
Db 47 DLKRMFLPFLGVFSDEEQRNLQMCNAIDMAIESEEELS 89
RESULT 11
TYEA VERPS
ID TYEA VERPS STANDARD; PRS; 92 AA.
AC P69969; P16161; Q663K2;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 04-JAN-2005, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Protein tyEA.
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OC NCBI_TaxID=633;
RN [1]
NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RX MEDLINE=91312137; PubMed=1857212;
RA Forsberg A., Viitanen A.-M., Skurnik M., Wolf-Watz H.
```

RT "The surface-located YopN protein is involved in calcium signal
transduction in Yersinia pseudotuberculosis.";
RL Mol. Microbiol. 5:977-986(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I; PLASMID=pYV;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lemerlin J., Stoutland P.O.,
Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
Rabaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
Simonet A., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
Derbise A., Hauser L.J., Garcia E.;
RA "Insights into the evolution of Yersinia pestis through whole-genome
comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Involved in the control of Yop release.
CC -!- SUBUNIT: Interacts with the translocator YopD and with residues
242-293 of YopN.
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CC -----
DR EMBL; X51833; CAA36130.1; -; Genomic DNA.
DR EMBL; BX936399; CAF25407.1; -; Genomic DNA.
DR PIR; S15321; S15321
DR GenomeReviews; BX936399 GR; pYV0064.
KW Complete proteome; Plasmid.
FT CHAIN 1 92 Protein tyeA.
FT FTID=PRO 0000065704.
FT SEQUENCE 92 AA; 10753 MW; E5046EDD9E3D92F9 CRC64;
Query Match 64.1%; Score 150; DB 1; Length 92;
Best Local Similarity 67.4%; Pred. No. 2.4e-10;
Matches 29; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 1 ELKRLIRLLPVLFSEEEQRQLLQCCGALDNAIEREDEL 43
Db 47 DLKRMFLPLGVFSDEEQRQLLQMCQNAIDMAIESEEEELS 89

RESULT 12
ID Q79NG7_YEREN PRELIMINARY; PRT; 92 AA.
AC Q79NG7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE TyeA.
GN Name-tyeA;
OS Yersinia enterocolitica.
OG Plasmid pYVal27/90, and Plasmid pYVe8081.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A127/90; PLASMID=pYVal27/90;
RA Foultier B.G.F., Bernard A., Purnelle B., Cornelis G.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8081; PLASMID=pYVe8081;
RX MEDLINE=21295118; PubMed=11402007;
RA DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Snellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype 0:8 low-
calcium-response plasmid reveals a new virulence plasmid-associated
replicon.";
RL Infect. Immun. 69:4627-4638(2001).
CC -----
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DR EMBL; AY150843; AAO39024.1; -; Genomic DNA.
DR EMBL; AF336309; AAK69221.1; -; Genomic DNA.
DR SMR; Q79NG7; 2-86.
KW Plasmid.
SQ SEQUENCE 92 AA; 10753 MW; E5046EDD9E3D92F9 CRC64;
Query Match 64.1%; Score 150; DB 2; Length 92;
Best Local Similarity 67.4%; Pred. No. 2.4e-10;
Matches 29; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 1 ELKRLIRLLPVLFSEEEQRQLLQCCGALDNAIEREDEL 43
Db 47 DLKRMFLPLGVFSDEEQRQLLQMCQNAIDMAIESEEEELS 89

RESULT 13
ID Q84GT3_YEREN PRELIMINARY; PRT; 108 AA.
AC Q84GT3;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE TyeA.
GN Name-tyeA;
OS Yersinia enterocolitica.
OG Plasmid pYVal27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A127/90;
RA Foultier B.G.F., Bernard A., Purnelle B., Cornelis G.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY150843; AAN37519.1; -; Genomic DNA.
DR SMR; Q84GT3; 18-102.
KW Plasmid.
SQ SEQUENCE 108 AA; 12736 MW; B690EBE113D0206 CRC64;
Query Match 64.1%; Score 150; DB 2; Length 108;
Best Local Similarity 67.4%; Pred. No. 2.9e-10;
Matches 29; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

OY 1 ELKRLIRLLPVLFSEEEQRQLLQCCGALDNAIEREDEL 43
Db 63 DLKRMFLPLGVFSDEEQRQLLQMCQNAIDMAIESEEEELS 105

RESULT 14
ID Q66PU2_PASPI PRELIMINARY; PRT; 94 AA.
AC Q66PU2;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative TTSS secretion and targeting control protein.
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
RT "Photobacterium damsela subsp. piscicida encodes a functional type
three secretion system (TTSS) that is involved in pathogenesis.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY647223; AAU11474.1; -; Genomic DNA.
SQ SEQUENCE   94 AA;  11133 MW;  F22D6F4CE0G9D69FB CRC64;

Query Match          55.1%; Score 129; DB 2; Length 94;
Best Local Similarity 57.1%; Pred No. 9.3e-08;
Matches 24; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY      1 ELKRLIRLLPVELFSFEERQNLIQCQGALDNAIEREDEL 42
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Db      47 ELHKLIRHIDVFNDSEQRNLIQAQVKALDEAIDLEEEEM 88

RESULT 15
Q6QVR5_VIBHA
ID ID Q6QVR5_VIBHA PRELIMINARY; PRT; 94 AA.
AC Q6QVR5;
DT 05-JUL-2004, integrated into UniProtKB/TREMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE VcrI.
GN Name=vcrI;
OS Vibrio Harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY524044; AAG13316.1; -; Genomic DNA.
SQ SEQUENCE   94 AA;  11120 MW;  E3B546FD7BB66BBD CRC64;

Query Match          55.1%; Score 129; DB 2; Length 94;
Best Local Similarity 57.1%; Pred. No. 9.3e-08;
Matches 24; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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Db      47 ELHKLIRHIDVFNDSEQRNLIQAQVKALDEAIDLEEEEM 88

Search completed: June 16, 2006, 19:22:53
Job time : 38.9122 secs
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 8.67398 Seconds
(without alignments)
474.285 Million cell updates/sec

Title: US-10-813-908A-1
Perfect score: 234
Sequence: 1 ELKRLIRLLPVLFSEERQ.....QCALDNIAREDELSGSS 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/pCTUS_COMB.pcp:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pcp:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	153	65.4	97	2	US-09-252-991A-30054
2	65	27.8	240	1	US-08-114-555A-6
3	65	27.8	240	2	US-08-559-397A-12
4	65	27.8	5032	2	US-09-538-092-979
5	59.5	25.4	1244	2	US-09-949-016-11702
6	58.5	25.0	155	2	US-09-902-540-11918
7	57	24.4	221	2	US-09-384-162-4
8	56.5	24.1	517	2	US-09-107-532A-6058
9	55.5	23.7	423	2	US-09-248-796A-16012
10	55.5	23.7	515	2	US-09-107-532A-5603
11	55	23.5	99	2	US-09-543-681A-6306
12	55	23.5	181	2	US-09-902-540-14043
13	55	23.5	240	1	US-08-114-555A-8
14	55	23.5	240	2	US-08-559-397A-14
15	55	23.5	616	2	US-09-690-185A-2
16	55	23.5	1231	2	US-09-595-684B-23
17	55	23.5	5037	2	US-09-424-783-4
18	54	23.1	506	2	US-09-117-250-1
19	54	23.1	665	2	US-09-949-016-10993
20	54	23.1	781	1	US-08-675-631-3
21	54	23.1	781	2	US-08-359-316A-3
22	54	23.1	781	2	US-09-248-776-3
23	52.5	22.4	376	2	US-10-094-749-2760
24	52.5	22.4	1040	2	US-09-564-805-238
25	52	22.2	136	2	US-10-104-047-3252
26	52	22.2	719	2	US-10-094-749-2001

27	52	22.2	1551	2	US-09-437-568A-46	Sequence 46, Appl
28	52	22.2	1551	2	US-10-418-036-12	Sequence 12, Appl
29	51.5	22.0	302	2	US-09-854-122-19	Sequence 19, Appl
30	51.5	22.0	496	2	US-08-881-784-1	Sequence 1, Appl
31	51.5	22.0	496	2	US-09-292-768-2	Sequence 2, Appl
32	51.5	22.0	496	2	US-09-292-768-64	Sequence 64, Appl
33	51.5	22.0	496	2	US-09-292-768-66	Sequence 66, Appl
34	51.5	22.0	496	2	US-09-172-339-6	Sequence 6, Appl
35	51.5	22.0	629	2	US-10-104-047-3226	Sequence 3226, Ap
36	51.5	22.0	720	2	US-10-094-749-2417	Sequence 2417, Ap
37	51.5	22.0	767	2	US-09-949-016-6167	Sequence 6167, Ap
38	51.5	22.0	789	2	US-09-949-016-9432	Sequence 9432, Ap
39	51.5	22.0	1286	2	US-09-964-956-38	Sequence 38, Appl
40	51.5	22.0	1286	2	US-10-017-216-7	Sequence 7, Appl
41	51.5	22.0	1597	2	US-09-964-956-41	Sequence 41, Appl
42	51.5	22.0	1597	2	US-10-017-216-6	Sequence 6, Appl
43	51.5	22.0	1641	2	US-09-964-956-40	Sequence 40, Appl
44	51.5	22.0	1641	2	US-10-017-216-5	Sequence 5, Appl
45	51.5	22.0	1958	2	US-10-028-946-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-252-991A-30054
; Sequence 30054, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30054
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30054

Query Match 65.4%; Score 153; DB 2; Length 97;
Best Local Similarity 70.5%; Pred. No. 1.6e-13;
Matches 31; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELKRLIRLLPVLFSEERQNLQCCGALDNIAREDELSG 44
Db 52 ELKRLIRLLPVLFSEERQNLQCCGALDNIAREDELSG 95

RESULT 2
US-08-114-555A-6
; Sequence 6, Application US/08114555A
; Patent No. 5854392
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF beta-APP-C100
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; CITY: 1155 Avenue of the Americas
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711


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; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF BETA-APP-C100
; TITLE OF INVENTION: RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,555A
; FILING DATE: 30-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6013-115
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-114-555A-8

Query Match 23.5%; Score 55; DB 1; Length 240;
Best Local Similarity 26.8%; Pred. No. 14;
Matches 11; Conservative 14; Mismatches 10; Indels 6; Gaps 1;

QY 1 ELKRLIRLLPVLFSEERQNLQCCGALDINAIEREDE 41
Db 95 DVKQILKMTPEVFTTEEE-----EEEEEEEEDE 129

RESULT 14
US-08-559-397A-14
; Sequence 14, Application US/08559397A
; Patent No. 6083713
; GENERAL INFORMATION:
; APPLICANT: Manly, Susan P.
; APPLICANT: Kozlowski, Michael R.
; APPLICANT: Neve, Rachael L.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF
; TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/559,397A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6013-135
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-559-397A-14

Query Match 23.5%; Score 55; DB 2; Length 240;
Best Local Similarity 26.8%; Pred. No. 14;
Matches 11; Conservative 14; Mismatches 10; Indels 6; Gaps 1;

QY 1 ELKRLIRLLPVLFSEERQNLQCCGALDINAIEREDE 41
Db 95 DVKQILKMTPEVFTTEEE-----EEEEEEEEDE 129

RESULT 15
US-09-690-185A-2
; Sequence 2, Application US/09690185A
; Patent No. 6471964
; GENERAL INFORMATION:
; APPLICANT: BIERING, EIRIK
; APPLICANT: KROSSOY, BJORN
; TITLE OF INVENTION: DNA ENCODING STRUCTURAL PROTEIN-1 OF INFECTIOUS SALMON
; FILE REFERENCE: BIERING
; CURRENT APPLICATION NUMBER: US/09/690,185A
; CURRENT FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: EP99203401.7
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 616
; TYPE: PRP
; ORGANISM: Infectious salmon anemia virus
US-09-690-185A-2

Query Match 23.5%; Score 55; DB 2; Length 616;
Best Local Similarity 35.9%; Pred. No. 44;
Matches 14; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 11 VLFSEERQNLQCCGALDINAIER--EEDELSGESS 47
Db 67 IRKFLKEEKMDMSPRCSGVAALAIERSVEFDNFSKEAA 105

Search completed: June 16, 2006, 19:28:55
Job time : 9.67398 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 26.2894 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-1
Perfect score: 234
Sequence: 1 ELKRLIRLPVELFSEEEOR.....QCALDNAIEREDELSSGESS 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	234	100.0	47	US-10-813-908-1	Sequence 1, Appli
2	68.5	29.3	4558	US-10-282-122A-77286	Sequence 77286, A
3	68	29.1	386	US-10-282-122A-50910	Sequence 50910, A
4	68	29.1	398	US-11-098-686-11398	Sequence 11398, A
5	65	27.8	5032	US-10-408-765A-26	Sequence 26, Appl
6	65	27.8	5038	US-10-723-860-1310	Sequence 1310, Ap
7	65	27.8	5038	US-10-756-149-5039	Sequence 5039, Ap
8	65	27.8	5081	US-10-276-774-1850	Sequence 1850, Ap
9	65	27.8	5081	US-10-450-763-35328	Sequence 35328, A
10	61	26.1	840	US-11-177-894-11	Sequence 11, Appl
11	60.5	25.9	385	US-10-506-454-77	Sequence 77, Appl
12	60.5	25.9	437	US-11-188-298-11708	Sequence 11708, A
13	59.5	25.4	804	US-10-437-963-183489	Sequence 183489,
14	59.5	25.4	1225	US-10-408-765A-166	Sequence 166, App
15	59.5	25.4	1225	US-10-473-127-1139	Sequence 1129, Ap
16	59.5	25.4	1225	US-10-473-127-1132	Sequence 1132, Ap
17	59.5	25.4	1233	US-10-473-127-1130	Sequence 1130, Ap
18	59.5	25.4	1233	US-10-473-127-1131	Sequence 1131, Ap
19	59.5	25.4	1233	US-10-473-127-1133	Sequence 1133, Ap
20	59	25.2	104	US-10-424-599-208094	Sequence 208094,
21	59	25.2	528	US-10-425-115-353333	Sequence 353333,
22	59	25.2	609	US-09-815-242-10740	Sequence 10740, A
23	59	25.2	609	US-10-282-122A-56965	Sequence 56965, A
24	58.5	25.0	467	US-10-437-963-187213	Sequence 187213,
25	58	24.8	293	US-10-626-832-79	Sequence 79, Appl
26	58	24.8	293	US-10-626-832-98	Sequence 98, Appl
27	57.5	24.6	481	US-10-282-122A-74407	Sequence 74407, A

ALIGNMENTS

RESULT 1

US-10-813-908-1

; Sequence 1, Application US/10813908

; Publication No. US20050058662A1

; GENERAL INFORMATION:

; APPLICANT: Frey, Joachim Stuber

; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and U

; FILE REFERENCE: MIC01/2315/WO

; CURRENT APPLICATION NUMBER: US/10/813,908

; PRIOR FILING DATE: 2004-03-26

; PRIOR APPLICATION NUMBER: US/10/416,902

; PRIOR FILING DATE: 2003-05-15

; PRIOR APPLICATION NUMBER: PCT/CA01/01589

; PRIOR FILING DATE: 2001-11-15

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 47

; TYPE: PRT

; ORGANISM: Aeromonas

US-10-813-908-1

Query Match 100.0%; Score 234; DB 5; Length 47;

Best Local Similarity 100.0%; Pred No. 1.5e-22;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELKRLIRLPVELFSEEEORQLLCCQCALDNAIEREDELSSGESS 47

DB 1 ELKRLIRLPVELFSEEEORQLLCCQCALDNAIEREDELSSGESS 47

RESULT 2

US-10-282-122A-77286

; Sequence 77286, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77286
; LENGTH: 4558
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; NAME/KEY: MISC FEATURE
; LOCATION: (3773)..(3773)
; OTHER INFORMATION: X-any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3940)..(3940)
; OTHER INFORMATION: X-any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3945)..(3948)
; OTHER INFORMATION: X-any amino acid
US-10-282-122A-77286

Query Match      29.3%; Score 68.5; DB 4; Length 4558;
Best Local Similarity 35.4%; Pred. No. 52;
Matches 17; Conservative 11; Mismatches 17; Indels 3; Gaps 1;

Qy      2 LKRLRLPVELFSEEEQRQNLQCCGALDNAIEREDE---LSGES 46
Db      3123 LSLPTRLFNLLYGDKEARRKIGETITQLLDHAVEKGSQKITLQGEA 3170

RESULT 3
US-10-282-122A-50910
; Sequence 50910, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
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; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50910
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-10-282-122A-50910

Query Match      29.1%; Score 68; DB 4; Length 386;
Best Local Similarity 32.4%; Pred. No. 3.8;
Matches 12; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy      2 LKRLRLPVELFSEEEQRQNLQCCGALDNAIERE 38
Db      348 VRQIKDLPTQIYADMDVRATVLAQAQDALDNIAME 384

RESULT 4
US-11-098-686-11398
; Sequence 11398, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11398
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11398

Query Match      29.1%; Score 68; DB 6; Length 398;
Best Local Similarity 31.0%; Pred. No. 3.9;
Matches 13; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy      1 ELKRLRLPVELFSEEEQRQNLQCCGALDNAIEREDE 42
Db      339 EMLAAVRKFTIMVFDNVNVRVGVQDAVDDAVRREDEFL 380

RESULT 5
US-10-408-765A-26
; Sequence 26, Application US/10408765A
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Result No.	Score	Query		Length	DB	ID	Description
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1	63	26.9	370	6	US-10-449-902-46118		Sequence 46118, A
2	63	26.9	661	6	US-10-449-902-55195		Sequence 55195, A
3	56	23.9	453	6	US-10-449-903-35701		Sequence 35701, A
4	56	23.9	783	6	US-10-449-903-55443		Sequence 55443, A
5	54	23.1	198	6	US-10-449-903-39618		Sequence 39618, A
6	53	22.6	440	6	US-10-449-902-49167		Sequence 49167, A
7	53	22.6	797	6	US-10-449-902-50327		Sequence 50327, A
8	53	22.6	940	6	US-10-449-902-55166		Sequence 55166, A
9	52	22.2	379	6	US-10-953-349-19483		Sequence 19483, A
10	52	22.2	392	6	US-10-953-349-19482		Sequence 19482, A
11	52	22.2	401	6	US-10-953-349-19481		Sequence 19481, A
12	52	22.2	719	7	US-11-293-697-3841		Sequence 3841, A
13	52	22.2	914	6	US-10-527-411-60		Sequence 60, Appl
14	51.5	22.0	249	6	US-10-449-903-38739		Sequence 38739, A
15	51	21.8	952	7	US-11-221-332-86		Sequence 86, Appl
16	50.5	21.6	856	6	US-10-449-902-46567		Sequence 46567, A
17	50.5	21.6	926	6	US-10-449-903-43578		Sequence 43578, A
18	50.5	21.6	991	6	US-10-449-903-46978		Sequence 46978, A
19	50	21.4	286	7	US-11-134-228A-27		Sequence 27, Appl
20	50	21.4	551	7	US-11-293-697-3946		Sequence 3946, Appl
21	50	21.4	667	7	US-11-311-555-16		Sequence 16, Appl
22	50	21.4	667	7	US-11-311-561-16		Sequence 16, Appl
23	50	21.4	700	6	US-10-449-903-50309		Sequence 50309, A
24	50	21.4	895	7	US-11-293-697-3081		Sequence 3081, Appl
25	50	21.4	971	6	US-10-449-903-53924		Sequence 53924, A

Query Match 22.6%; Score 53; DB 6; Length 440;
Best Local Similarity 37.8%; Pred. No. 34;
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELKRLIRLLPVELFSEEQRLNLLQCCQGALDINAIER 37
DB 315 ELRRKIRLLEEEIHKEKAQSSELGVQCQLKEQFTSR 351

RESULT 7
US-10-449-902-50327
; Sequence 50327, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50327
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50327

Query Match 22.6%; Score 53; DB 6; Length 797;
Best Local Similarity 37.8%; Pred. No. 66;
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ELKRLIRLLPVELFSEEQRLNLLQCCQGALDINAIER 37
DB 672 ELRRKIRLLEEEIHKEKAQSSELGVQCQLKEQFTSR 708

RESULT 8
US-10-449-902-54166
; Sequence 54166, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54166
; LENGTH: 940
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54166

Query Match 22.6%; Score 53; DB 6; Length 940;
Best Local Similarity 33.3%; Pred. No. 80;
Matches 11; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 12 ELFSEEQRLNLLQCCQGALDINAIEREDELSG 44
DB 693 QLFIEEQEKRLKETFEADLDSAMDHKYQKDG 725

RESULT 9
US-10-953-349-19483
; Sequence 19483, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19483
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19483

Query Match 22.2%; Score 52; DB 6; Length 379;
Best Local Similarity 36.4%; Pred. No. 38;
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 17 BEQRQNLQCCQGALDINAIERE 38
DB 154 KENREKLYNCCDGPLNSSFKNE 175

RESULT 10
US-10-953-349-19482
; Sequence 19482, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19482
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19482

Query Match 22.2%; Score 52; DB 6; Length 392;
Best Local Similarity 36.4%; Pred. No. 40;
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 17 BEQRQNLQCCQGALDINAIERE 38
DB 167 KENREKLYNCCDGPLNSSFKNE 188

RESULT 11
US-10-953-349-19481
; Sequence 19481, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19481
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-19481

Query Match 22.2%; Score 52; DB 6; Length 401;
Best Local Similarity 36.4%; Pred. No. 41;
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 17 EQRONLLOCCGALDINAIERE 38
DB 176 KENREKLYNCCDPLNSFKNE 197

RESULT 12
US-11-293-697-3841
; Sequence 3841, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3841
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3841

Query Match 22.2%; Score 52; DB 7; Length 719;
Best Local Similarity 30.8%; Pred. No. 78;
Matches 12; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 9 LPVLFSEEQRONLLOCCGALDINAIEREDELSSGSS 47
DB 585 LPQSVSKQAVGHEENAQCCKATSDNVIOSETCSQDSS 623

RESULT 13
US-10-527-411-60
; Sequence 60, Application US/10527411
; Publication No. US20060110410A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130005
; CURRENT APPLICATION NUMBER: US/10/527,411
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/GB2003/003824
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 10/241,596
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-527-411-60

Query Match 22.2%; Score 52; DB 6; Length 914;
Best Local Similarity 35.9%; Pred. No. 1e+02;
Matches 14; Conservative 7; Mismatches 16; Indels 2; Gaps 2;

QY 9 LPVLFSEEQRONLLOCCGALDINAIEREDELSSGSS 47
DB 852 IPFQL-SKYVDNQRLSLTC-GGLTDTTLQAETDQLEDEKS 888

RESULT 14
US-10-449-902-38739
; Sequence 38739, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38739
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38739

Query Match 22.0%; Score 51.5; DB 6; Length 249;
Best Local Similarity 31.0%; Pred. No. 28;
Matches 13; Conservative 11; Mismatches 13; Indels 5; Gaps 1;

QY 1 ELKELIRLLPVLFSEEQRONLLOCCGALDINAIEREDEL 42
DB 157 DVQOLVRSLAVENDSLREEMRTLQRACA-----ALSKENDKL 193

RESULT 15
US-11-221-332-86
; Sequence 86, Application US/11221332
; Publication No. US20060121498A1
; GENERAL INFORMATION:
; APPLICANT: Elix Therapeutics
; TITLE OF INVENTION: Enzymes invovled in apoptosis
; FILE REFERENCE: 8912/2042
; CURRENT APPLICATION NUMBER: US/11/221,332
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/00957
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: GB0305267.7
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 952
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-221-332-86

Query Match 21.8%; Score 51; DB 7; Length 952;
Best Local Similarity 32.8%; Pred. No. 1.4e+02;
Matches 19; Conservative 7; Mismatches 18; Indels 14; Gaps 3;

QY 2 LKRLIRLLPVLFSEEQRONLLOCCQ-----GALDNAI-----EREDELSSGSS 47
DB 582 LLRWCRY--VKISTETEETEGSLHCKDQNINGNGPNCIHEGSPSEMETDEPDDESS 637

Search completed: June 16, 2006, 20:25:52
Job time : 4.0252 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 81.5 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-2
Perfect score: 630
Sequence: 1 MNWIEPLLVOFQCDLGITIG.....POLHQAVTTLRLQREVLAAS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	123	5 ABB80770	Abb80770 A. salmon
2	180	28.6	262	7 ABO81423	Abo81423 Pseudomon
3	118	18.7	106	7 ABO81215	Abo81215 Pseudomon
4	84	13.3	167	7 ABO79119	Abo79119 Pseudomon
5	82.5	13.1	235	2 AAY59756	Aay59756 Human nor
6	82	13.0	176	7 ADM26981	Adm26981 Hyperther
7	80	12.7	253	2 AAR13507	Aar13507 P.denitri
8	79.5	12.6	96	5 ABP01518	Abp01518 Human ORF
9	77	12.2	652	8 ADN25464	Adn25464 Bacterial
10	75	11.9	314	9 ADZ75794	Adz75794 Mouse pho
11	75	11.9	318	8 ADR27701	Adr27701 Mouse PAC
12	74.5	11.8	420	6 ABUS0529	Abus0529 Protein e
13	74.5	11.8	742	5 ABP65368	Abp65368 Bifidobac
14	74	11.7	354	8 ADP30112	Adp30112 Human sec
15	74	11.7	1224	6 ABU39626	Abu39626 Protein e
16	73	11.6	421	2 AAR95055	Aar95055 IL-2-DETA
17	73	11.6	450	6 ABU39628	Abu39628 Protein e
18	73	11.6	565	7 ADB64142	Adb64142 Human pro
19	73	11.6	852	5 ABP69443	Abp69443 Human pol
20	72.5	11.5	496	2 AAR04934	Aar04934 Immunotox
21	72.5	11.5	3084	2 AAWS0891	AAWS0891 Mouse lam
22	72.5	11.5	3084	4 AAEL1215	AAel1215 Mouse lam
23	72	11.4	117	9 ADX40246	Adx40246 HIV Rev p

24	71.5	11.3	243	4 AAE03548	Aae03548 Human mit
25	71.5	11.3	243	5 AAE21799	Aae21799 Human pep
26	71.5	11.3	243	6 ABO00588	Abo00588 Novel hum
27	71.5	11.3	289	4 ABG11298	Abg11298 Novel hum
28	71.5	11.3	289	6 ABO00850	Abo00850 Polypepti
29	71.5	11.3	455	3 AAG59392	Aag59392 Arabidops
30	71.5	11.3	486	3 AAG59391	Aag59391 Arabidops
31	71.5	11.3	530	3 AAG59390	Aag59390 Arabidops
32	71.5	11.3	939	7 ADC87071	Adc87071 Human GPC
33	71	11.3	332	7 ABO72413	Abo72413 Pseudomon
34	71	11.3	361	6 ABU01324	Abu01324 S. pneumo
35	71	11.3	361	8 ADK48614	Adk48614 Streptoco
36	71	11.3	365	8 ADR95921	Adr95921 Novel S.
37	71	11.3	365	9 AEA59791	Aea59791 Streptoco
38	71	11.3	408	3 AAG57790	Aag57790 Arabidops
39	71	11.3	413	3 AAG57789	Aag57789 Arabidops
40	71	11.3	482	8 ADN26175	Adn26175 Bacterial
41	71	11.3	560	4 ABB64311	Abb64311 Drosophill
42	71	11.3	1162	6 ABU41801	Abu41801 Protein e
43	70.5	11.2	434	7 ABO78655	Abo78655 Pseudomon
44	70	11.1	402	8 ADS44505	Ads44505 Bacterial
45	70	11.1	618	7 ABO76713	Abo76713 Pseudomon

ALIGNMENTS

RESULT 1
ABB80770
ID ABB80770 standard; protein; 123 AA.
XX
AC ABB80770;
XX
DT 23-SEP-2002 (first entry)
XX
DE A. salmonicida type III secretion protein acr2 sequence.
XX
KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;
KW acrV; acrH; antibiotic; vaccine; fish.
XX
OS Aeromonas salmonicida.
XX
PN WO200240514-A2.
XX
PD 23-MAY-2002.
XX
PF 15-NOV-2001; 2001WO-CA001589.
XX
PR 15-NOV-2000; 2000US-0248864P.
XX
(FREY/) FREY J.
(STUB/) STUBER K.
(THOR/) THORNTON J C.
(KUZU/) KUZYSK M A.
(BURI/) BURIAN J.
Frey J, Stuber K, Thornton JC, Kuzysk MA, Burian J;
WPI: 2002-537338/57.
DR N-PSDB; ABN86172.
XX
PT Novel protein from Aeromonas salmonicida and nucleic acid encoding the
PT protein, useful for reducing susceptibility of fish to infection by a
PT virulent strain of Aeromonas salmonicida.
PS Claim 13; Page 26; 39pp; English.
XX
CC The invention relates to A. salmonicida type III secretion genes and
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.
CC A.salmonicida type III secretion apparatus is useful for producing
CC selected products, especially Aext. Acrv in vaccine, epitope or epitopic
CC region of Acrv or any other protein of A. salmonicida type III secretion
CC apparatus is useful for reducing the susceptibility of fish to infection

XX SQ Sequence 106 AA;
Query Match 18.7%; Score 118; DB 7; Length 106;
Best Local Similarity 32.3%; Pred. No. 1.5e-05;
Matches 31; Conservative 16; Mismatches 27; Indels 22; Gaps 4;
QY 49 WLAR-AVP--WHOSGEAIRRAMVLT-----AAQGPALPVRSGWLGE 87
DB 12 WISRTAAPCSNANAMSCSGWPTWPTGTRPIAAPCGRCALCHARAAG-SLPLRCAWSGE 70
QY 88 EQLILFVSLDERAVTLPOLHOAVTTLRLQREVLAS 123
DB 71 SRLLCITLBARQVGIPTLHQALRSARSEVILAA 106
RESULT 4
ABO79119
ID ABO79119 standard; protein; 167 AA.
XX
AC ABO79119;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #11294.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
XX 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD12690.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 27865; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biotech technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 167 AA;
Query Match 13.3%; Score 84; DB 7; Length 167;
Best Local Similarity 32.4%; Pred. No. 0.28;

Matches 24; Conservative 10; Mismatches 24; Indels 16; Gaps 3;
QY 30 ELEQSGTLQERHQGLTLWLARAVPWH-----QSGEAIRRAMVLTAAQGPALP--- 79
DB 14 EIDTGDLSHTTHPGDLALWLTEAVRLREEQAGPLEDSEAVRQAL-----AQGSIPRRI 68
QY 80 -VRSGWLGEQIL 92
DB 69 LTRAHWLGRREGIL 82
RESULT 5
AAY59756
ID AAY59756 standard; protein; 235 AA.
XX
AC AAY59756;
XX
DT 18-JAN-2000 (first entry)
XX
DE Human normal ovarian tissue derived protein 33.
XX
KW Human; ovary; screening; ovarian cancer; treatment.
XX
OS Homo sapiens.
XX
PN DE19816395-A1.
XX
PD 07-OCT-1999.
XX
PF 03-APR-1998; 98DE-01016395.
XX
PR 03-APR-1998; 98DE-01016395.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl B;
XX
DR WPI; 1999-552352/47.
DR N-PSDB; AA241237.
XX
PT Nucleic acid sequences potentially useful in diagnosis or therapy of
PT ovarian cancer.
XX
PS Claim 23; Page 229; 274pp; German.
XX
XX This invention describes novel nucleic acid sequences that are highly
CC expressed in normal ovary tissue. Artificial chromosomes and cosmid
CC clones containing the sequences can be used as gene transfer vehicles.
CC The sequences can be used to produce DNA fragments containing full-length
CC genes. Host cells transfected with the sequences can be used to produce
CC polypeptides or polypeptide fragments, which can be used to screen phage
CC displays for polypeptides that bind to them, or as tools for identifying
CC agents active against ovarian cancer, or to prepare medicaments for
CC treating ovarian cancer. The cDNA sequences can be used to obtain genomic
CC genes, their promoters, enhancers, silencers, exon structures, intron
CC structures and their splice variants. AAY59724-Y59837 represent protein
CC fragments encoded by the cDNA sequences represented in AA241222-241324
CC which are derived from normal human ovarian tissue
XX
SQ Sequence 235 AA;
Query Match 13.1%; Score 82.5; DB 2; Length 235;
Best Local Similarity 24.6%; Pred. No. 0.67;
Matches 32; Conservative 16; Mismatches 67; Indels 15; Gaps 5;
QY 5 EPLIVQFQDGLGITGDNPHSLIQLELQSGT---LQLERHQGLTLWLARAVPW----- 56
DB 49 EPLVLKVSQAQHGCTNLSGEPEGIQHWQEKGVAGVTEFGDGDGIVVMAPVSPMGVIQD 108
QY 57 HQSGEAI---RRAMVLTAAQGPALPVRSGWLGEQILFVSLDERAVTLP---OLHQAV 110
DB 109 HNAGEVTVDHREVLDVAALQQLQSAVLSPKLNASAIQVFI-CHSRIDLHACCKHHQLV 167

CC to treat immunosuppression. The method is useful for screening compounds
CC that treats and inhibits the signs and symptoms of inflammatory disorders
CC such as rheumatoid arthritis and asthma, and particularly reduces the
CC pain, inflammation, joint swelling, and lesions associated with the
CC diseases. Other disease which can be treated are allergy, atherogenesis,
CC anaphylaxis, malignancy, chronic and acute inflammation, histamine and
CC immunoglobulin E-mediated allergic reactions, shock, atherosclerosis,
CC multiple sclerosis, allograft rejection, fibrotic disease, inflammatory
CC glomerulopathies, respiratory allergic diseases such as allergic
CC rhinitis, hypersensitivity lung diseases, interstitial lung diseases,
CC anaphylaxis or hypersensitivity responses, drug allergies, insect sting
CC allergies, inflammatory bowel diseases such as Crohn's disease and
CC ulcerative colitis, spondyloarthropathies, scleroderma, psoriasis and
CC inflammatory dermatoses such as dermatitis, eczema, atopic dermatitis,
CC allergic contact dermatitis, urticaria, vasculitis, other autoimmune
CC diseases, cancers with leukocyte infiltration of the skin or organs and
CC other diseases or conditions which can be treated with promoters of PAC-1
CC function such as immunodeficiency syndromes such as AIDS. The present
CC sequence represents mouse PAC-1, which is used in the exemplification of
CC the present invention.

XX Sequence 318 AA;

Query Match 11.9%; Score 75; DB 8; Length 318;

Best Local Similarity 32.2%; Pred. No. 7.7;

Matches 37; Conservative 10; Mismatches 42; Indels 26; Gaps 5;

QY 28 QLEQSGTQLQERHOGQLTML-----ARAVPWQSGEAI--RRAMTLT 70

DB 12 ELECAALGALLPREAETLLDDCPFLACFESHVRAAPVFNW----ALLRRARGTF 67

QY 71 AAAQGALPVR--GWLGEQILFVSLDERAVT---LPOLHQAVTTLRLQREV 120

DB 68 AAALACLLPDRLARLGRGELARAVVLDESSASVAELPPDGPAPHLLAALQHEM 122

RESULT 12

ABU50529

ID ABU50529 standard; protein; 420 AA.

AC ABU50529;

XX 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #36056.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Yersinia pestis.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002NO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA54399.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX

PS

XX

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Claim 25; SEQ ID NO 78453; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

XX Sequence 420 AA;

Query Match 11.8%; Score 74.5; DB 6; Length 420;

Best Local Similarity 24.3%; Pred. No. 13;

Matches 33; Conservative 16; Mismatches 44; Indels 43; Gaps 4;

QY 24 HSLIQLELEQSGTL-----QLERHQQLTLWLA-----RAVPWHQ 58

DB 33 NSLLQQPLVQGGWILSTCNRTELYLSVQQENLHEQLTAWLCNHYKLPDDVRQSLYWHH 92

QY 59 SCEALRRAMTLTAAAGPALPVRSGWLGBEQILFV-----SLDERAVTLPOLH 107

DB 93 GNDVRLHMRVASG-----LDSQVLGEPQLIGQVKAFABESQSGSLSELERLFXS 145

QY 108 QAVTTLTLRLQREVLAS 123

DB 146 FSVAKRVRTETEIGAS 161

RESULT 13

ABP65368

ID ABP65368 standard; protein; 742 AA.

AC ABP65368;

XX 19-NOV-2002 (first entry)

XX Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:112.

XX Bifidobacterium longum NCC2705; Bifidobacterium; bacterial;

XX antidiarrheic; antibacterial; inhibitor of Salmonella; detection;

XX identification; lactic acid bacterium; diarrhoea; pathogenic bacteria;

XX rotavirus; food composition; pharmaceutical composition.

XX Bifidobacterium longum.

XX EP1227152-A1.

XX

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XX


```
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493373P.
PR 08-AUG-2003; 2003US-0493377P.
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 2110; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic.
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPWEB and is not in the specification.
CC
CC Revised record issued on 01-DEC-2005 : Sequence description line
CC corrected
XX
XX Sequence 354 AA;
SQ
Query Match 11.7%; Score 74; DB 8; Length 354;
Best Local Similarity 24.5%; Pred. No. 12;
Matches 27; Conservative 14; Mismatches 57; Indels 12; Gaps 4;
QY 5 EPLLVQFCQDLGITIGDNPHSLIQLEEQSGT---LQLERHQQLTLWLARAVPW----- 56
Db 162 EPLVVKVAHQHTNISGEPEGIQHREQVEKCVGTGTEFGDGLVWVAPVNPWRVSQD 221
QY 57 HOSGEAI---RRAMTUTAAQGPALPVRSGWLGEEQLILFVSLDERAVTL 103
Db 222 HNAGEVTVDQREVLDAALQSAVLWSRLKNASAIVQFI-CHSRAIDL 270
RESULT 15
ABU39626
ID ABU39626 standard; protein; 1224 AA.
XX
AC ABU39626;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #25153.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Pseudomonas putida.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US0009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
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XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
DR N-PSDB; ACA43496.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 67550; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1224 AA;
SQ
Query Match 11.7%; Score 74; DB 6; Length 1224;
Best Local Similarity 26.4%; Pred. No. 64;
Matches 34; Conservative 13; Mismatches 42; Indels 40; Gaps 6;
QY 20 GDNPHSLIQLEEQSGTQLERHQQLTLWLARAVPWHQSGEAIIRAMTLTAAQ---GP 76
Db 211 GPEPAALIQASLQQRGA-QLARIK-----APWAQWABELROI CRDALAAKQVDGR 259
QY 77 ALPVR-----SGWLGEEQLILFVSILD-----ERAVTLPOLHQAVTTL 113
Db 260 KMQARYFPFPWFKLCWASDEQL---VELDLGTGTRLTTPAGMAEAWKEPPEHPALNMM 316
QY 114 TRLQREVLA 122
Db 317 QHLQOQLQA 325
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Search completed: June 16, 2006, 19:06:57
Job time : 83.5 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 12.5 Seconds
(without alignments)
946.773 Million cell updates/sec

Title: US-10-813-908A-2
Perfect score: 630
Sequence: 1 MNWIEPLLVOFCQDLGITIG.....PQLHQAVTTTLRLQREVLAS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	392	62.2	123	2 C35392	hypothetical prote
2	392	62.2	123	2 T43588	hypothetical prote
3	392	62.2	123	2 S15322	hypothetical prote
4	279	44.3	123	2 A83432	conserved hypotet
5	83	13.2	518	2 AE3553	serine-type D-Ala-
6	80	12.7	253	2 H36145	cobM protein - Pse
7	78.5	12.5	268	2 A55511	2-hydroxypenta-2,4
8	77.5	12.3	292	2 T34997	lysR-type transcri
9	77	12.2	1707	2 AH2085	two-component hybr
10	74.5	11.8	420	2 AB0246	glutamyl-tRNA redu
11	74	11.7	314	2 B57126	dual specificity p
12	73.5	11.7	376	2 AG2227	DNA repair and gen
13	72.5	11.5	1047	2 G87398	AcBr/AcrD/AcrF fam
14	72.5	11.5	3084	1 MMMSA	laminin alpha-1 ch
15	72	11.4	461	2 G83602	hypothetical prote
16	71.5	11.3	486	2 B86411	protein F3M18.4 [i
17	71	11.3	234	2 F42696	thrombin (EC 3.4.2
18	71	11.3	361	2 D95106	conserved hypotet
19	70	11.1	283	2 T31122	probable transcrip
20	70	11.1	356	2 AC2319	hypothetical prote
21	70	11.1	361	2 F97974	conserved hypotet
22	70	11.1	402	2 B72502	probable ornithine
23	70	11.1	503	2 A28415	steroid llbeta-mon
24	70	11.1	503	2 JX0151	steroid llbeta-mon
25	70	11.1	503	2 JX0071	steroid llbeta-mon
26	70	11.1	580	1 S33743	aspartate-tRNA lig
27	69.5	11.0	361	2 B75444	probable phosphino
28	69.5	11.0	1644	2 AC0823	probable lipoprote
29	69	11.0	136	2 C72644	hypothetical prote

30 69 11.0 307 2 S51485 ribosomal protein
31 69 11.0 628 2 A10382 peptidylprolyl iso
32 69 11.0 749 2 H91170 hypothetical membr
33 69 11.0 772 2 H86016 hypothetical prote
34 69 11.0 952 2 S38653 transposase - kleb
35 69 11.0 961 2 A47055 transposase - Erwi
36 69 11.0 2241 2 T20971 hypothetical prote
37 69 11.0 2261 2 T20978 hypothetical prote
38 68.5 10.9 261 2 C95364 probable GntR-fami
39 68.5 10.9 613 2 F87390 TonB-dependent rec
40 68 10.8 260 2 AC0793 probable transcrip
41 68 10.8 335 2 T37044 hypothetical prote
42 68 10.8 450 2 S43914 hypothetical prote
43 68 10.8 4342 2 H83343 probable non-ribos
44 67.5 10.7 480 1 A70744 probable hexosyltr
45 67 10.6 241 2 B75628 DNA-binding stress

ALIGNMENTS

RESULT 1

C35392
hypothetical protein 2 - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: C35392
R;Viitainen, A.M.; Toivanen, P.; Skurnik, M.
J. Bacteriol. 172, 3152-3162, 1990
A;Title: The lcrE gene is part of an operon in the lcr region of Yersinia enterocolitica
A;Reference number: A35392; MUID:90284308; PMID:2160939
A;Accession: C35392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <VII>
A;Cross-references: UNIPROT:Q52095; UNIPARC:UPI0000179740; GB:M32097
C;Superfamily: Yersinia pestis hypothetical protein Y0044

Query Match 62.2%; Score 392; DB 2; Length 123;
Best Local Similarity 61.5%; Pred. No. 3.8e-33;
Matches 75; Conservative 20; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MNWIEPLLVOFCQDLGITIGDNPHSLIQLEBSQGLQLRHHQGLTLWLARAVPHWQSG 60
Db 1 VSWIEPIISHFCODLGVPTSPSLPLQLEMAQSGTLQLEHQGATLTLWLARSLAWHQCE 60
Qy 61 EATRRAMTLTAAAGPALPVRSQMLGSEQLILFVSLDERAVTLPOLHQAVTTTLRLQREV 120
Db 61 DAMVKALTLTAAOKSGALPLRAGLNGQLVLVFLVSLDERSLTLPLLHQAFELRLQOEV 120
Qy 121 LA 122
Db 121 LA 122

RESULT 2

T43588
hypothetical protein Y0044 - Yersinia pestis plasmid pCD1
C;Species: Yersinia pestis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43588; T42883
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubake
J. Bacteriol. 180, 5192-5202, 1998
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: Z22578; MUID:98422474; PMID:9748454
A;Accession: T43588
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-123 <HUP>
A;Cross-references: UNIPROT:P61380; UNIPARC:UPI0000139BF5; EMBL:AF053946; NID:g2996222;
A;Experimental source: strain KIM
R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
Infect. Immun. 66, 4611-4623, 1998

C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C;Accession: A31771; A30449; S00624; A30450; S02678; S01790; A30451; S14670
R;Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and he
A;Reference number: A31771; MUID:89034134; PMID:3182802
A;Accession: A31771
A;Molecule type: mRNA
A;Residues: 1-3084 <SAS>
A;Cross-references: UNIPROT:P19137; UNIPARC:UPI00000278CA; EMBL:J04064; NID:G309419; PID
A;Accession: A30449
A;Molecule type: protein
A;Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YPR
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SAS>
A;Cross-references: UNIPARC:UPI0000173C92; UNIPARC:UPI0000173C93; UNIPARC:UPI0000173C94;
C99; UNIPARC:UPI0000173C9A; UNIPARC:UPI0000173C9B; UNIPARC:UPI0000173C9C; UNIPARC:UPI000
10000173CA2
R;Hartl, L.; Oberbaumer, I.; Deutzmann, R.
Eur. J. Biochem. 173, 629-635, 1988
A;Title: The N terminus of laminin A chain is homologous to the B chains.
A;Reference number: S00624; MUID:88225080; PMID:3267223
A;Accession: S00624
A;Molecule type: mRNA
A;Residues: 1-208,'T',210-334 <HAR>
A;Cross-references: UNIPARC:UPI000016CE8F; EMBL:X07737; NID:G52857; PIDN:CAA30561.1; PID
A;Accession: A30450
A;Molecule type: protein
A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;
3-1389;1449-1459 <HAR>
A;Cross-references: UNIPARC:UPI0000173CA3; UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CA5;
CAA; UNIPARC:UPI0000173CAB; UNIPARC:UPI0000173CAC
A;Note: the sequence from Fig. 7 is inconsistent with that from Fig. 5 in having 209-Ile
R;Mann, K.; Deutzmann, R.; Timpl, R.
Eur. J. Biochem. 178, 71-80, 1988
A;Title: Characterization of proteolytic fragments of the laminin-nidogen complex and th
A;Reference number: S08895; MUID:89078415; PMID:2462498
A;Accession: S08895
A;Molecule type: protein
A;Residues: 153-169 <MAN>
A;Cross-references: UNIPARC:UPI0000173CAD
R;Fujiwara, S.; Shinkai, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
Biochem. J. 252, 453-461, 1988
A;Title: Structure and distribution of N-linked oligosaccharide chains on various domain
A;Reference number: S02678; MUID:88326259; PMID:2458101
A;Accession: S02678
A;Molecule type: protein
A;Residues: 630-642,'D',644;2690-2704 <FUJ>
A;Cross-references: UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CAE
R;Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbaumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A;Title: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A;Reference number: S01790; MUID:89030693; PMID:3181157
A;Accession: S01790
A;Molecule type: mRNA
A;Residues: 2338-3084 <DEU>
A;Cross-references: UNIPARC:UPI000016CE8E; EMBL:X13459; NID:G55499; PIDN:CAA31807.1; PID
A;Accession: A30451
A;Molecule type: protein
A;Residues: 1911-1929;1997-2006;2033-2045,'X',2047-2054,'X',2056-2066,'X',2068-2105;2120
470;2487-2498;2502-2525;2538-2557;2561-2591,'X',2593-2594;2600-2610;2616-2645;2648-2655;
93;2998-3005,'A',3007-3033,'V',3035;3068-3083 <DE2>
A;Cross-references: UNIPARC:UPI0000173CB6; UNIPARC:UPI0000173CB7; UNIPARC:UPI0000173CB8;
CBD; UNIPARC:UPI0000173CBE; UNIPARC:UPI0000173CBF; UNIPARC:UPI0000173CC0; UNIPARC:UPI000
10000173CC5; UNIPARC:UPI0000173CC7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CC9; UNIPAR
A;Note: 2256-Val was also found
R;Olson, D.; Nagayoshi, T.; Fazio, M.; Peltonen, J.; Jaakkola, S.; Sanborn, D.; Sasaki,
Lab. Invest. 60, 772-782, 1989
A;Title: Human laminin: cloning and sequence analysis of cDNAs encoding A, B1 and B2 cha
A;Reference number: A34961; MUID:89280632; PMID:2733383
A;Accession: S14670
A;Molecule type: protein
A;Residues: 2424-2436;2440-2451;2461-2467;2487-2525;2550-2557;2561-2593;2600-2610;2616-2
-2942,'T',2944-2964;2969-2976;2980-2993;2998-3000,'I',3002-3018,'V',3020-3034;3068-3083

A;Cross-references: UNIPARC:UPI0000173C9E; UNIPARC:UPI0000173CAE; UNIPARC:UPI0000173CB
C7; UNIPARC:UPI0000173CC8; UNIPARC:UPI0000173CCA; UNIPARC:UPI0000173CCB; UNIPARC:UPI00
1000173CD1; UNIPARC:UPI0000173CD2; UNIPARC:UPI0000173CD3; UNIPARC:UPI0000173CD4; UNIPAR
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-3084/Product: laminin alpha-1 chain #status predicted <MAT>
F;25-277/Domain: VI <DOM6>
F;277-331/Domain: laminin-type EGF-like homology <LE01>
F;278-519/Domain: V <DOM5>
F;334-401/Domain: laminin-type EGF-like homology <LE02>
F;404-458/Domain: laminin-type EGF-like homology <LE03>
F;461-507/Domain: laminin-type EGF-like homology <LE04>
F;510-519/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;520-715/Domain: IVb <DO4B>
F;716-1166/Domain: IIIB <DO3B>
F;716-746/Domain: laminin-type EGF-like homology #status atypical <LE06>
F;749-795/Domain: laminin-type EGF-like homology <LE07>
F;798-853/Domain: laminin-type EGF-like homology <LE08>
F;830-834/Region: cell adhesion #status predicted
F;856-906/Domain: laminin-type EGF-like homology <LE09>
F;909-955/Domain: laminin-type EGF-like homology <LE10>
F;958-1002/Domain: laminin-type EGF-like homology <LE11>
F;1005-1048/Domain: laminin-type EGF-like homology <LE12>
F;1051-1094/Domain: laminin-type EGF-like homology <LE13>
F;1097-1116/Domain: laminin-type EGF-like homology <LE14>
F;1118-1154/Domain: laminin-type EGF-like homology #status atypical <LE15>
F;1147-1149/Region: cell attachment (R-G-D) motif
F;1157-1166/Domain: laminin-type EGF-like homology #status atypical <LE16>
F;1167-1368/Domain: IIVa <DO4A>
F;1369-1561/Domain: IIA <DO3A>
F;1369-1407/Domain: laminin-type EGF-like homology #status atypical <LE17>
F;1410-1456/Domain: laminin-type EGF-like homology <LE18>
F;1459-1513/Domain: laminin-type EGF-like homology <LE19>
F;1516-1560/Domain: laminin-type EGF-like homology <LE20>
F;1562-2133/Domain: II/I <DOM2>
F;1562-2133/Region: heptad repeats
F;2134-3084/Domain: G <DOM2>
F;2150-2308/Domain: laminin G repeat homology <LG1>
F;2337-2492/Domain: laminin G repeat homology <LG2>
F;2518-2683/Domain: laminin G repeat homology <LG3>
F;2748-2897/Domain: laminin G repeat homology <LG4>
F;2925-3082/Domain: laminin G repeat homology <LG5>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
F;45,79,370,374,531,562,672,678,808,914,959,969,1052,1344,1414,1586,1603,1659,1706,171
e (Asn) (covalent) #status predicted
F;304-312/Disulfide bonds: #status experimental
F;770,857,1999,2055,2067,2835/Binding site: carbohydrate (Asn) (covalent) #status exper
F;845,2102/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 11.5%; Score 72.5; DB 1; Length 3084;
Best Local Similarity 32.7%; Pred. No. 1e+02;
Matches 32; Conservative 16; Mismatches 39; Indels 11; Gaps 6;

QY 33 QSGTLQLEHROGQTLTLARAVPHWQSGEAI-----RRAMTLTAAAGPA--LPVRSGLG 86
Db 1836 QDTLTQLEHRRDELLW-ARKTRSHVDDLVQMQRARDLVHRAEQHASSELQSRAGALD 1894

QY 87 EE-QILFVSLDERAVTLFQLHQAVTTLRLQREVLSA 123
Db 1895 RDLNVRNVSIN--ATSAAHVHSNIQTLTTE-EAEMLAA 1929

RESULT 15

G83602
hypoetical protein PA0345 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83602
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83602
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <STO>
A;Cross-references: UNIPROT:Q9I6E8; UNIPARC:UPI000000C5019; GB:AE004472; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0345
C;Superfamily: Neisseria meningitidis hypothetical protein NMB1645

Query Match 11.4%; Score 72; DB 2; Length 461;
Best Local Similarity 33.9%; Pred. No. 13;
Matches 21; Conservative 8; Mismatches 17; Indels 16; Gaps 3;

QY 42 HQGQLTLWLARAVPWH-----OSGEATRRAMTLTAAAGPALP----VRSGLGEEQL 90
Db 6 HPGLDALWLTEAVRLREQAGPLEDSEAVRQAL-----AQGSLPRILTRAHWLGRREG 60

QY 91 IL 92
Db 61 LL 62

Search completed: June 16, 2006, 19:25:13
Job time : 13.5 secs

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OM protein - protein search, using sw model
Run on: June 16, 2006, 18:53:15 ; Search time 96.6 Seconds
(without alignments)
1177.815 Million cell updates/sec
Title: US-10-813-908A-2
Perfect score: 630
Sequence: 1 MNWIEPLLVOFCQDLGITIG.....PQLHQA VTTTLRLQREVLAS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Uniprot_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	123	Q8GA94	AEROMONAS
2	591	93.8	123	Q699R6	AEROMONAS
3	556	88.3	123	Q5X1L0	AEROMONAS
4	524	83.2	123	Q6TLM8	AEROMONAS
5	419	66.5	123	Q7N0W5	PHOTORHABDUS
6	418	66.3	123	Q84G21	PHOTORHABDUS
7	396	62.9	123	SYCN	YERSENIA
8	392	62.2	123	SYCN	YERSENIA
9	392	62.2	123	SYCN	YERSENIA
10	279	44.3	123	Q9I329	PSEUDOMONAS
11	277	44.0	123	Q30533	PSEUDOMONAS
12	241.5	38.3	124	Q6QVR6	VIBRIO
13	239.5	38.0	123	Q87P53	VIBRIO
14	239.5	38.0	124	Q66PUI	PASPI
15	97	15.4	125	Q2SH41	HAHELIA
16	92.5	14.7	124	Q72M14	DESULFOVIBRIO
17	89.5	14.2	252	Q2JZV2	RHIZOBIVIBRIO
18	89	14.1	252	Q92LV3	RHIZOBIVIBRIO
19	88.5	14.0	989	Q3W8C4	FRANKIA
20	87	13.8	150	Q4BLG3	BURKHOLDERIA
21	87	13.8	518	Q579G4	BRUCELLA
22	87	13.8	518	Q8FV99	BRUCELLA
23	87	13.8	518	Q2YLB4	BRUCELLA
24	87	13.8	622	Q2JU70	CYANOBACTER
25	85.5	13.6	289	Q748U7	GEOPHILUM
26	83	13.2	518	Q8YD27	BRUCELLA
27	83	13.2	606	Q8RIU9	MUS MUSCULUS
28	83	13.2	654	Q8RI33	MUS MUSCULUS
29	83	13.2	675	Q8C816	MUS MUSCULUS
30	83	13.2	940	Q3U6C0	MUS MUSCULUS
31	83	13.2	960	Q8BSZ1	MUS MUSCULUS

32	83	13.2	960	2	Q8CIE4	MUS MUSCULUS
33	82	13.0	176	2	Q8TV14	METHANOPYRUS
34	81.5	12.9	98	2	Q5TY81	ANOPHELES
35	81	12.9	125	2	Q2SC38	HAHELIA
36	80	12.7	253	1	COBM	PSEUDOMONAS
37	80	12.7	960	2	Q3TLV7	MUS MUSCULUS
38	79.5	12.6	450	2	Q7SGI1	NEUROSPORA
39	79.5	12.6	459	2	Q7V8L4	PROCHLOROCOCCUS
40	79.5	12.6	984	2	Q6IEE7	HOMO SAPIENS
41	79	12.5	289	2	Q82M15	STREPTOMYCES
42	79	12.5	398	2	Q4BS00	BURKHOLDERIA
43	79	12.5	1224	2	Q2XDN4	PSEUDOMONAS
44	78.5	12.5	268	2	Q52433	PSEUDOMONAS
45	78	12.4	321	2	Q339I3	ORYZA SATIVA

ALIGNMENTS

RESULT 1
Q8GA94 AERSA
ID Q8GA94 AERSA PRELIMINARY; PRT; 123 AA.
AC Q8GA94
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Acr2 protein.
GN Name=acr2;
OS Aeromonas salmonicida subsp. salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RX MEDLINE=22826111; PubMed=12374830;
RX DOI=10.1128/JB.184.21.5966-5970.2002;
RA Burr S.E., Stuber K., Wahli T., Frey J.;
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida";
RL J. Bacteriol. 184:5966-5970(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type =III secretion mutant in a rainbow trout model";
RL Microbiol. 151:2111-2118(2005).
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CC -----
DR ENBL; A3458292; CAD30215.1; -; Genomic_DNA.
DR ENBL; A616218; CAB83102.1; -; Genomic_DNA.
DR SMR; Q8GA94; 2-122.
DR InterPro; IPR012673; TTSS SYN.
DR TIGRFAMs; TIGR02503; type III; 1.
SQ SEQUENCE 123 AA; 13738 MW; D80B2EC9F9AAD806 CRC64;

Query Match 100.0%; Score 630; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.5e-57;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWIEPLLVOFCQDLGITIGDNPHTLTQLESGTQLERHOGQLTLWLRVPHQSG 60
DB 1 MNWIEPLLVOFCQDLGITIGDNPHTLTQLESGTQLERHOGQLTLWLRVPHQSG 60

QY 61 EAIRRAMTLTAAAGQALPVRSGWLGEEQILFVSLDERAVTLPQLHQA VTTTLRLQREV 120
DB 61 EAIRRAMTLTAAAGQALPVRSGWLGEEQILFVSLDERAVTLPQLHQA VTTTLRLQREV 120

QY 121 LAS 123
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Db 121 LAS 123

RESULT 2
ID Q699R6_AERHY PRELIMINARY; PRT; 123 AA.
AC Q699R6;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ac22.
GN Name=acr2;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
DR EMBL; AY528667; AAS91813.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type III; 1.
SQ SEQUENCE 123 AA; 13741 MW; 01301E03BA6B7D8C CRC64;

Query Match 93.8%; Score 591; DB 2; Length 123;
Best Local Similarity 92.6%; Pred. No. 3.9e-53;
Matches 113; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNWIEPLLVOFCODLGTITGDNPHSLIQLELESGTQLERHOGQLTLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCODLGTITGDNPHSLIQLELESGTQLERHOGQLTLARAVPWHQSG 60
QY 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAHTLTTLRLQREV 120
Db 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAHTLTTLRLQREV 120
QY 121 LA 122
Db 121 VA 122

RESULT 3
ID Q5XL10_AERHY PRELIMINARY; PRT; 123 AA.
AC Q5XL10;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ac22.
GN Name=acr2;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Brova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
CC
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CC -----
DR EMBL; AY763611; AAV30227.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type III; 1.
SQ SEQUENCE 123 AA; 13995 MW; 5DB076AD0BD3FF42 CRC64;

Query Match 88.3%; Score 556; DB 2; Length 123;
Best Local Similarity 87.8%; Pred. No. 1.7e-49;
Matches 108; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNWIEPLLVOFCODLGTITGDNPHSLIQLELESGTQLERHOGQLTLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCODLGTITGDNPHSLIQLELESGTQLERHOGQLTLARAVPWHQSG 60
QY 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAHTLTTLRLQREV 120
Db 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAHTLTTLRLQREV 120
QY 121 LAS 123
Db 121 LVS 123

RESULT 4
Q6TLM8_AERHY PRELIMINARY; PRT; 123 AA.
AC Q6TLM8;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ac22.
GN Name=acr2;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
RT pathogenesis.";
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
DR EMBL; AY394563; AAR26333.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type III; 1.
SQ SEQUENCE 123 AA; 14008 MW; 8751D98C0FE97500 CRC64;

Query Match 83.2%; Score 524; DB 2; Length 123;
Best Local Similarity 82.0%; Pred. No. 3.5e-46;
Matches 100; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNWIEPLLVOFCODLGTITGDNPHSLIQLELESGTQLERHOGQLTLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCODLGTITGDNPHSLIQLELESGTQLERHOGQLTLARAVPWHQSG 60
QY 61 EAIRRAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAHTLTTLRLQREV 120
Db 61 DAIRHAMTLTAAAGQALPVRSGWLGEQILFVSLDERAVTLPQLHQAHTLTTLRLQREV 120
QY 121 LA 122
Db 121 LA 122
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RESULT 5
Q7N0W5 PHOLL
ID Q7N0W5 PHOLL PRELIMINARY; PRT; 123 AA.
AC Q7N0W5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Similar to YopN chaperone SynC.
GN OrderedLocusNames=plu3764;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt.886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Deroose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanolis A., Powell K., Signier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
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CC -----
DR EMBL; BX571871; CAE16136.1; -; Genomic_DNA.
DR Photolista; plu3764; -.
DR BioCyc; PLUM243265:PLU3764-MONOMER; -.
DR InterPro; IPR012673; TTSS_SynM.
DR TIGRFAMs; TIGR02503; type_III; 1.
KW Complete proteome.
SQ SEQUENCE 123 AA; 14111 MW; 6897750865FFDFE92 CRC64;

Query Match 66.5%; Score 419; DB 2; Length 123;
Best Local Similarity 63.4%; Pred. No. 2.8e-35;
Matches 78; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MNWIEPLLVOFCODLIGTIGNPHSLIQLELEQSGTLQLEHQQQLTLWLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCODLIGTIGNPHSLIQLELEQSGTLQLEHQQQLTLWLARAVPWHQSG 60
Qy 61 EAIRRAMTLTAAAGPALPVRSGLWGBEQLILFVSLDERAVTLTLPOLHOAVTTLTFLQREV 120
Db 61 EAMVKAMLLTFSGQGPPLRCGWLGEDRLLLFVTLDERDITLPLHQAQFSLRLVRQEV 120
Qy 121 LAS 123
Db 121 LAS 123

RESULT 6
Q84GZ1 PHOLU
ID Q84GZ1 PHOLU PRELIMINARY; PRT; 123 AA.
AC Q84GZ1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE LessN.
GN Name=LessN;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0956-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus.";

Query Match 66.5%; Score 419; DB 2; Length 123;
Best Local Similarity 63.4%; Pred. No. 2.8e-35;
Matches 78; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MNWIEPLLVOFCODLIGTIGNPHSLIQLELEQSGTLQLEHQQQLTLWLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCODLIGTIGNPHSLIQLELEQSGTLQLEHQQQLTLWLARAVPWHQSG 60
Qy 61 EAIRRAMTLTAAAGPALPVRSGLWGBEQLILFVSLDERAVTLTLPOLHOAVTTLTFLQREV 120
Db 61 EAMVKAMLLTFSGQGPPLRCGWLGEDRLLLFVTLDERDITLPLHQAQFSLRLVRQEV 120
Qy 121 LAS 123
Db 121 LAS 123

RESULT 7
SYCN YERN
ID SYCN YERN STANDARD; PRT; 123 AA.
AC Q52095; P16162; Q93KT9;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Chaperone protein synC.
GN Name=synC;
OS Yersinia enterocolitica.
OG Plasmid pYV, Plasmid pYVe227, Plasmid pYVe8081, and
OG Plasmid pYVal27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Serotype O:3; PLASMID=pYV;
RX MEDLINE=90264308; PubMed=2160939;
RA Vaitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrE gene is part of an operon in the lcr region of Yersinia
RT enterocolitica O:3.";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pYVe227;
RA Iriarte M., Lambrmont I., Kerbouch C., Cornells G.R.;
RT "Detailed genetic map of the pYVe227 plasmid of Yersinia
RT enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYVe8081;
RX MEDLINE=21295118; PubMed=11402007;
RY DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Snellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYVal27/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foultier B., Cornells G.R.;
RT "DNA sequence and analysis of the pYVal27/90 virulence plasmid of
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RL Trends Microbiol. 10:541-545(2002).
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CC -----
DR EMBL; AY144116; AA018047.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS_SynM.
DR TIGRFAMs; TIGR02503; type_III; 1.
SQ SEQUENCE 123 AA; 14174 MW; 0247D3A1D26A088A CRC64;

Query Match 66.3%; Score 418; DB 2; Length 123;
Best Local Similarity 63.4%; Pred. No. 3.5e-35;
Matches 78; Conservative 19; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MNWIEPLLVOFCODLIGTIGNPHSLIQLELEQSGTLQLEHQQQLTLWLARAVPWHQSG 60
Db 1 MNWIEPLLVOFCODLIGTIGNPHSLIQLELEQSGTLQLEHQQQLTLWLARAVPWHQSG 60
Qy 61 EAIRRAMTLTAAAGPALPVRSGLWGBEQLILFVSLDERAVTLTLPOLHOAVTTLTFLQREV 120
Db 61 EAMVKAMLLTFSGQGPPLRCGWLGEDRLLLFVTLDERDITLPLHQAQFSLRLVRQEV 120
Qy 121 LAS 123
Db 121 LAS 123

RESULT 7
SYCN YERN
ID SYCN YERN STANDARD; PRT; 123 AA.
AC Q52095; P16162; Q93KT9;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Chaperone protein synC.
GN Name=synC;
OS Yersinia enterocolitica.
OG Plasmid pYV, Plasmid pYVe227, Plasmid pYVe8081, and
OG Plasmid pYVal27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Serotype O:3; PLASMID=pYV;
RX MEDLINE=90264308; PubMed=2160939;
RA Vaitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrE gene is part of an operon in the lcr region of Yersinia
RT enterocolitica O:3.";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pYVe227;
RA Iriarte M., Lambrmont I., Kerbouch C., Cornells G.R.;
RT "Detailed genetic map of the pYVe227 plasmid of Yersinia
RT enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYVe8081;
RX MEDLINE=21295118; PubMed=11402007;
RY DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Snellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYVal27/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foultier B., Cornells G.R.;
RT "DNA sequence and analysis of the pYVal27/90 virulence plasmid of
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RT Yersinia enterocolitica strain A127/90.;
RL Res. Microbiol. 154:553-557(2003).
RN [5]
RP FUNCTION.
RC PLASMID=pyV;
RX MEDLINE=99102236; PubMed=9882687;
RA Iriarte M., Cornelis G.R.;
RT "Identification of SyncN, YscX, and YscY, three new elements of the
RL Yersinia Yop virulon.";
RN J. Bacteriol. 181:675-680(1999).
RN [6]
RP FUNCTION, AND SUBUNIT.
RC STRAIN=W22703 / Serotype O:9 / Biotype 2;
RX PubMed=11514512; DOI=10.1128/JB.183.18.5293-5301.2001;
RA Cheng L.W., Kay O., Schneewind O.;
RT "Regulated secretion of YopN by the type III machinery of Yersinia
RL enterocolitica.";
RN J. Bacteriol. 183:5293-5301(2001).
CC -!- FUNCTION: Functions as a specific chaperone for YopN. It could
CC facilitate the secretion and the subsequent translocation of YopN.
CC -!- SUBUNIT: Interacts with yscB to form a complex which specifically
CC binds to YopN.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic or peripheral membrane protein
CC that is not exported across the inner membrane (By similarity).
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CC -----
DR EMBL; M32097; AAA98431.1; -; Genomic DNA.
DR EMBL; AF102990; AAD16821.1; -; Genomic DNA.
DR EMBL; AF336309; AAK69220.1; -; Genomic DNA.
DR EMBL; AY150843; AAN37520.1; -; Genomic DNA.
DR PIR; C35392; C35392.
DR SNR; Q52095.2-122.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III_SynC; 1.
KW Chaperone; Plasmid.
FT CHAIN 1 123 Chaperone protein syncN.
FT FTId=PRO_0000072359.
FT VARIANT 58 58 Q -> R (in plasmid pYve8081 and plasmid
FT pYVal27/90).
FT VARIANT 77 77 A -> T (in plasmid pYve8081 and plasmid
FT pYVal27/90).
FT VARIANT 88 88 N -> S (in plasmid pYve8081 and plasmid
FT pYVal27/90).
FT SEQUENCE 123 AA; 13608 MW; 37732AA55A3FF9AD CRC64;
Query Match 62.9%; Score 396; DB 1; Length 123;
Best Local Similarity 62.3%; Pred. No. 6.8e-33;
Matches 76; Conservative 19; Mismatches 27; Indels 0; Gaps 0;
QY 1 MNWIEPLLQVFCODLGITTDGNPHSLIQLEQSGTLOLERHOGQTLWLARVPHQSG 60
Db 1 MSWIEPIIHFHCOPLGVPTSSPLIQLEMAQSGTLOLEHQAATLTLWLARSLAHQCE 60
QY 61 EAIRRAMTITAAAGPALVRSGWLGEOLILFVSLDERAVTLPOLHQAVTTTLRLQREV 120
Db 61 DANVKALTITAAQKSGALPLRAGLWLGENQLVLFVSLDERSLTLPLLHQAFEQLRLQREV 120
QY 121 LA 122
Db 121 LA 122
RESULT 8
SYCN_YERPE STANDARD; PRT; 123 AA.
AC P61380; P16162;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DT 07-MAR-2006, entry version 19.
DE Chaperone protein syncN.
GN Name=syncN; OrderedLocusNames=YPCD1.37c. y5041, y0044, pCD46;
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OS Yersinia pestis.
OG Plasmid pCD1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
ON NCBI_TaxID=632;
RX [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Ferry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RL Yersinia pestis KIM5.";
RN Infect. Immun. 66:4611-4623(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
RL pestis.";
RN J. Bacteriol. 180:5192-5202(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Farhikhi J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RN Nature 413:523-527(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Zhou Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Shou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RL avirulent to humans.";
RN DNA Res. 11:179-197(2004).
RN [5]
RP FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC STRAIN=KIM5 / Biovar Mediaevalis, and KIM8;
RX PubMed=10094626;
RA Day J.B., Plano G.V.;
RT "A complex composed of SyncN and YscB functions as a specific chaperone
RL for YopN in Yersinia pestis.";
RN Mol. Microbiol. 30:777-788(1998).
RN [6]
RP FUNCTION.
RC STRAIN=KIM5 / Biovar Mediaevalis, and KIM8;
RX PubMed=12535078; DOI=10.1046/j.1365-2958.2003.03343.x;
RA Day J.B., Ferracci F., Plano G.V.;
RT "Translocation of YopE and YopN into eukaryotic cells by Yersinia
RL pestis yopN, yscA, syncN, yscB and lcrG deletion mutants measured using
RT a phosphorylatable peptide tag and phosphospecific antibodies.";
RL Mol. Microbiol. 47:807-823(2003).
CC -!- FUNCTION: Functions as a specific chaperone for YopN. It could
CC facilitate the secretion and the subsequent translocation of YopN.
CC -!- SUBUNIT: Interacts with yscB to form a complex which specifically
CC binds to YopN.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic or peripheral membrane protein
CC that is not exported across the inner membrane.
CC -----
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CC -----
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CC EMBL; AF074612; AAC69794.1; -; Genomic DNA.
DR EMBL; AF053946; AAC62567.1; -; Genomic DNA.
DR EMBL; AL117189; CAB54914.1; -; Genomic DNA.
DR EMBL; AE017043; AAS58565.1; -; Genomic DNA.
DR PIR; T43588; T43588.
DR PDB; 1XKP; X-ray; Bsl-123.
DR GenomeReviews; AE017043.GR; pCD46.
DR BioCyc; YPES229193:PCD46-MONOMER; -.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III_SynN; 1.
KW 3D-structure; Chaperone; Complete proteome; Plasmid.
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FT TURN 3 4
FT HELIX 5 14
FT TURN 15 16
FT STRAND 21 22
FT STRAND 25 31
FT TURN 32 34
FT STRAND 35 42
FT TURN 43 44
FT STRAND 45 53
FT HELIX 56 69
FT TURN 70 70
FT STRAND 71 71
FT HELIX 72 74
FT STRAND 77 78
FT STRAND 81 85
FT TURN 86 88
FT STRAND 89 97
FT HELIX 98 100
FT TURN 103 121
FT CHAIN 123 121
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Best Local Similarity 61.5%; Pred. No. 1.8e-32;
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Db 1 MSWIEPIISHFCQDLGVPTSPSPLEQLQLEMAQSGTLQERHQGLTLWLARSLAWHRCE 60
Qy 61 EAIRAMTLTAAAGPALPVRSGLGEGQLILFVSLDERAVTLFQLHQAATTLTFLQREV 120
Db 61 DAMVKALTTLTAQKSGALPLRAGLWGESQLVLFVSLDERSLTLPLHQAEPQLRLQREV 120
Qy 121 LA 122
Db 121 LA 122

RESULT 9
SYCN YERPS
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AC P61381; P16162; Q663K3;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DT 07-MAR-2006, entry version 14.
DE Chaperone protein synN.
GN Name=synN; OrderedLocusNames=PYV0063;
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1, and Plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RX MEDLINE=91312137; PubMed=1857212;
RA Forsberg A., Viitanen A.-M., Skurnik M., Wolf-Watz H.;
RA "The surface-located YopN protein is involved in calcium signal
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transduction in Yersinia pseudotuberculosis. ";
RL Mol. Microbiol. 5:977-986(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I; PLASMID=pYV.
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis. ";
RC Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Functions as a specific chaperone for yopN. It could
CC facilitate the secretion and the subsequent translocation of yopN
CC (By similarity).
CC -!- SUBUNIT: Interacts with yscB to form a complex which specifically
CC binds to YOPN (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic or peripheral membrane protein
CC that is not exported across the inner membrane (By similarity).
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CC -----
DR EMBL; X51833; CAA36131.1; -; Genomic DNA.
DR EMBL; BX936399; CAF25406.1; -; Genomic DNA.
DR PIR; S15322; S15322.
DR SMR; P61381; 2-122.
DR GenomeReviews; BX936399.GR; pYV0063.
DR InterPro; IPR012673; TTSS_SynN.
DR TIGRFAMs; TIGR02503; type_III_SynN; 1.
KW Chaperone; Complete proteome; Plasmid.
FT CHAIN 1 123
FT Chaperone protein synN.
FT FTId=PRO_0000072361.
SQ SEQUENCE 123 AA; 13609 MW; 3771F865B6E3D9AD CRC64;

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Qy 61 EAIRAMTLTAAAGPALPVRSGLGEGQLILFVSLDERAVTLFQLHQAATTLTFLQREV 120
Db 61 DAMVKALTTLTAQKSGALPLRAGLWGESQLVLFVSLDERSLTLPLHQAEPQLRLQREV 120
Qy 121 LA 122
Db 121 LA 122

RESULT 10
Q91329.PSEAE
ID Q91329.PSEAE PRELIMINARY; PRT; 123 AA.
AC Q91329;
DT 01-MAR-2001, integrated into UniProtKB/TREMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
GN OrderedLocusNames=PA1700;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mitzoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
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RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.A., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RL opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -----
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CC -----
DR EMBL; AE004597; AAG05089.1; -; Genomic_DNA.
DR PIR; A83432;
DR BICCYC; PAER287; PA1700-MONOMER; -.
DR InterPro; IPR012673; TTSS SYN.
DR TIGRFAMs; TIGR02503; type_III; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 123 AA; 13674 MW; 500B35C61D4B757E CRC64;

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Best Local Similarity 44.7%; Pred. No. 9.4e-21;
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QY 121 LAS 123
Db 121 LAA 123

RESULT 11
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AC O30533;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Pcr2.
GN Name=Pcr2;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=388;
RA MEDLINE=38037517; PubMed=9371466;
RX Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7165-7168(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Broms J.E., Edqvist P.J., Carlsson K.E., Forsberg A., Francis M.S.;
RT "Mapping of a YscY Binding Domain within the LcrH Chaperone That Is
RT Required for Regulation of Yersinia Type III Secretion.";
RL J. Bacteriol. 187:7738-7752(2005).
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CC -----
CC EMBL; AF010150; AAC45941.1; -; Genomic_DNA.
DR ENBL; DQ000666; AAY17108.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS SYN.
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Query Match 44.3%; Score 279; DB 2; Length 123;
Best Local Similarity 44.7%; Pred. No. 9.4e-21;
Matches 55; Conservative 24; Mismatches 44; Indels 0; Gaps 0;

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QY 61 EAIRRAMTLTAAAGPALPVRSGWLGEEQILFVSLDERAVTLPOLHQAVTTLTRLOREV 120
Db 61 RGTLRALRLCHARAAGSLPLRCAWSGESRLLCITLEARQVGIPTLHQALQALRSARSEV 120
QY 121 LAS 123
Db 121 LAA 123

RESULT 12
O6QVR6 VIBHA PRELIMINARY; PRT; 124 AA.
AC O6QVR6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Vcr2.
GN Name=vcr2;
OS Vibrio Harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY524044; AAS13315.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS SYN.
DR TIGRFAMs; TIGR02503; type_III; 1.
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QY 60 GEAIRRAMTLTAAAGPALPVRSGWLGEEQILFVSLDERAVTLPOLHQAVTTLTRLORE 119
Db 61 NELIKKALSFCHAGQGWPELTKTGLLDEQTMVFSQIIEGDEVTLPTIEQAFALLVRLHKD 120
QY 120 VLAS 123
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RESULT 13
O87P53 VIBPA PRELIMINARY; PRT; 123 AA.
AC O87P53;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative type III secretion protein.
GN OrderedLocusNames=VP1665;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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SQ SEQUENCE 123 AA; 13682 MW; 000B24C6169073A5 CRC64;

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Db 1 MDWVELPVAQFCODLQSRVSPAPLARVVQLDFEDSGTLQLERHGEQLSLWLACDLAWHQAY 60
QY 61 EAIRRAMTLTAAAGPALPVRSGWLGEEQILFVSLDERAVTLPOLHQAVTTLTRLOREV 120
Db 61 RGTLRALRLCHARAAGSLPLRCAWSGESRLLCITLEARQVGIPTLHQALQALRSARSEV 120
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Db 121 LAA 123

RESULT 12
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AC O6QVR6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Vcr2.
GN Name=vcr2;
OS Vibrio Harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY524044; AAS13315.1; -; Genomic_DNA.
DR InterPro; IPR012673; TTSS SYN.
DR TIGRFAMs; TIGR02503; type_III; 1.
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Query Match 38.3%; Score 241.5; DB 2; Length 124;
Best Local Similarity 38.7%; Pred. No. 7.4e-17;
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QY 1 MNWIEPLLQFCODLGTITGD-NPHSLIQLEQSGTLQLERHQGLTLWLARAVPWHQS 59
Db 1 MNWIDASVDVDFCRGMGLEAVDFSSAGRVQLSFQSGTLHIERHQDCLFLMLAKPLPHQS 60
QY 60 GEAIRRAMTLTAAAGPALPVRSGWLGEEQILFVSLDERAVTLPOLHQAVTTLTRLORE 119
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QY 120 VLAS 123
Db 121 VVGS 124

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O87P53 VIBPA PRELIMINARY; PRT; 123 AA.
AC O87P53;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative type III secretion protein.
GN OrderedLocusNames=VP1665;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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1	180	28.6	262	2	US-09-252-991A-30169	Sequence 30169, A		
2	118	18.7	106	2	US-09-252-991A-29961	Sequence 29961, A		
3	84	13.3	167	2	US-09-252-991A-27865	Sequence 27865, A		
4	80	12.7	253	2	US-08-426-630-28	Sequence 28, Appl		
5	74	11.7	313	1	US-08-990-379-7	Sequence 7, Appl		
6	74	11.7	314	2	US-09-164-193-22	Sequence 22, Appl		
7	74	11.7	314	2	US-09-221-448A-22	Sequence 22, Appl		
8	73	11.6	421	2	US-08-840-713-6	Sequence 6, Appl		
9	73	11.6	565	2	US-10-104-047-2296	Sequence 2296, Ap		
10	71	11.3	332	2	US-09-252-991A-21159	Sequence 21159, A		
11	71	11.3	361	2	US-09-583-110-5129	Sequence 5129, Ap		
12	71	11.3	365	2	US-09-107-433-4556	Sequence 4556, Ap		
13	70.5	11.2	434	2	US-09-252-991A-37401	Sequence 37401, A		
14	70	11.1	618	2	US-09-252-991A-25459	Sequence 25459, A		
15	70	11.1	1028	2	US-09-543-681A-1781	Sequence 1781, Ap		
16	68.5	10.9	342	2	US-09-902-540-15825	Sequence 15825, A		
17	68.5	10.9	362	1	US-08-415-751-5	Sequence 5, Appl		
18	68.5	10.9	430	2	US-09-540-236-3267	Sequence 3267, Ap		
19	68	10.8	530	2	US-08-840-713-2	Sequence 2, Appl		
20	68	10.8	550	2	US-09-252-991A-25062	Sequence 25062, A		
21	68	10.8	637	1	US-08-235-838-14	Sequence 14, Appl		
22	68	10.8	637	1	US-08-465-473B-14	Sequence 14, Appl		
23	68	10.8	674	2	US-09-252-991A-25462	Sequence 25462, A		
24	68	10.8	3340	2	US-09-252-991A-23568	Sequence 23568, A		
25	67.5	10.7	2293	2	US-09-368-590-2	Sequence 2, Appl		
26	67.5	10.7	2600	2	US-09-949-016-7309	Sequence 7309, Ap		

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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29961
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29961

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Best Local Similarity 18.7%; Score 118; DB 2; Length 106;
Matches 31; Conservative 16; Mismatches 27; Indels 22; Gaps 4;

Qy 49 WLAR-AVP--WHQSGEARRAMTLT-----AAAQGPALPVRSGWLGE 87
Db 12 WISRTAACSNNAMANSRSGWPTVPTGTRPIAFCGRCALCHARAAG-SLPLRCANSGE 70

Qy 88 EQLILFVSLDERAVTLPOLHQAVTTLRLQREVLAAS 123
Db 71 SRLLLCITLEARQVGITPLHQALQALRSARSEVLAA 106

RESULT 3
US-09-252-991A-27865
; Sequence 27865, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; LENGTH: 167
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27865

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Matches 24; Conservative 10; Mismatches 24; Indels 16; Gaps 3;

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Db 14 BIDTGGDLSTHTPLGLDALMLTAVRLREQAGPLEDSEAVRQAL-----AQGGSLPRRI 68

Qy 80 -VRSGWLGEQILIL 92
Db 69 LTRAHWLGRREGLL 82

RESULT 4
US-08-426-630-28
; Sequence 28, Application US/08426630
; Patent No. 6656709
; GENERAL INFORMATION:
; APPLICANT: BLANCHE, FRANCIS; CAMERON, BEATRICE; CROUZET,
; APPLICANT: JOEL; DEBUSSCHE, LAURENT; LEVY SCHIL, SOPHIE;
; APPLICANT: THIBAUT, DENIS
; TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE
; TITLE OF INVENTION: BIOSYNTHESIS OF COBALAMINS AND/OR COBAMIDES, DNA SEQUENCES
; TITLE OF INVENTION: CODING FOR THESE POLYPEPTIDES, PREPARATION METHOD AND THEIR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 555 13TH STREET, N.W.
; CITY: WASHINGTON
```

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; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426.630
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/916,151
; FILING DATE: 14-SEP-1992
; APPLICATION NUMBER: PCT/FR91/00054
; FILING DATE: 30-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: F. F. CALVETTI
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: 1290-7213
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 857-7887
; TELEFAX: (202) 857-7929
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas denitrificans
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; FEATURE:
; NAME/KEY: COBM
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Translation product of SEQ ID NO:27
US-08-426-630-28

Query Match
Best Local Similarity 12.7%; Score 80; DB 2; Length 253;
Matches 35; Conservative 24; Mismatches 49; Indels 42; Gaps 7;

Qy 4 IEPLLVQFCQDLGITICGNPHSLIQLELE---QSGTLQLER-HQGLTLWLARAVPMHQ 58
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Qy 59 SGEAIRR-----AMTLTAAQGPALPVRSGWLGE-----QLILFVSLDERAVTLPQ 105
Db 92 --EQIRLEKHGIAYTWTGTV--PSFAAASALGRELTIPIPAVQSLVLTVRVGRASPMNP 147

Qy 106 -----LHQAVTTLRLQREV 120
Db 148 SETLSAFGATGSTLAIHAIHALQOQVVEEL 177

RESULT 5
US-08-990-379-7
; Sequence 7, Application US/08990379
; Patent No. 5998188
; GENERAL INFORMATION:
; APPLICANT: Stork, Philip J
; APPLICANT: Misra-Press, Anita
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; SEQ ID NO 22
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-221-448A-22

Query Match      11.7%; Score 74; DB 2; Length 314;
Best Local Similarity 32.2%; Pred. No. 0.81;
Matches 37; Conservative 10; Mismatches 42; Indels 26; Gaps 5;

QY      28 QLEQSGTQLERHOGQLTWL-----ARAVPHQSGEAL--PRAMTLT 70
DB      8 ELECAALGALLREFAERTLLDCRFLACRSHVRAARPVMN-----ALLRRRAPGTP 63

QY      71 AAAAGPALPVR--GWLGEQLILFYSLDERAVT---LPQLHQAVTTLTRELQEV 120
DB      64 AALACLLPDRLARLGRCELARAVVLDSSASVTLPDPGPAHLLAALQHEM 118

RESULT 8
US-08-840-713-6
; Sequence 6, Application US/08840713
; Patent No. 6498233
; GENERAL INFORMATION:
; APPLICANT: WELLS, Winfried, Dr.
; APPLICANT: FOYMINAYA, Jesus
; TITLE OF INVENTION: NUCLEIC ACID TRANSFER SYSTEM
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., N.W., Suite 330 - G St. Lobby
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,713
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1614-7014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638 - 5000
; TELEFAX: (202) 638 - 4810
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-840-713-6

Query Match      11.6%; Score 73; DB 2; Length 421;
Best Local Similarity 28.3%; Pred. No. 1.7;
Matches 32; Conservative 12; Mismatches 35; Indels 34; Gaps 4;

QY      9 VQFCQDLGITGNPHSLTQLELEQSGTQLE---RH-----QGQTLW 49
DB     139 ITFCQSIITLTLEGGSLAALTAHQACHLPLETFTTRHQPRGWLEQFCQGPVQRLVALY 198

QY     50 LARAVPHQSGEAIRAMTLTAAAGPALPVRSGWLGE-----EQILLFVSL 96
DB     199 LAARLSWNQDVIRNAL-----ASPGSGDLGEAIRPEQEARLALT 242

RESULT 9

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US-10-104-047-2296
; Sequence 2296, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2296
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2296

Query Match 11.6%; Score 73; DB 2; Length 565;
Best Local Similarity 27.4%; Pred. No. 2.6;
Matches 32; Conservative 7; Mismatches 42; Indels 36; Gaps 5;
QY 12 CQDLGITGDNPHSIIQLEBSGTLQLER-----HQQQLTLMAR-----AVPWHQSG 60
Db 189 CSDTGVV-----SSSLGPARRREASQPSLHRQLSDPNHGSPPOLYRANLKLGLGAYPWSQSS 244
QY 61 EAIRAMT--LTAAGQPALVRSCWLGEEQILFVSLDERAVTLPOLHQAVTTLTR 115
Db 245 PALNHNSTPLTAVESPLP-----RSRPLLOPHRGAPALSR 282

RESULT 10
US-09-252-991A-21159
; Sequence 21159, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21159
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21159

Query Match 11.3%; Score 71; DB 2; Length 332;
Best Local Similarity 28.5%; Pred. No. 2.1;
Matches 37; Conservative 20; Mismatches 53; Indels 20; Gaps 7;
QY 5 EPLLVOFCQDLGITGDNPHSIIQLEBSGTLQLERHQQQLTLMAR---RAVPWHQSGEA 62
Db 146 DAFLVFCEEA-----PHRTTQLDVDPGGGL-VEDQQARLVQDCAGDHOAPLHAAGEH 197
QY 63 IRRAMTITAAQA--GPALPVRSGWLGEBQILFVSLD--ERAVTLPQL-----HOAVTTLT 114
Db 198 PRGFVALVPQALGQVALGALLGLDRDVAVAGLGHDDVDLLELVEVELLRHAKATLE 257
QY 115 --RLQREVLA 122
Db 258 AGRVLVEVYA 267

RESULT 11
US-09-583-110-5129

; Sequence 5129, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5129
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5129

Query Match 11.3%; Score 71; DB 2; Length 361;
Best Local Similarity 33.9%; Pred. No. 2.4;
Matches 20; Conservative 7; Mismatches 28; Indels 4; Gaps 2;

QY 38 QLERHQQQLTLMARAVPWHQSGEAIIRAMT--LTAAGQGA--LPVRSWLGEEQLIL 92
Db 15 EYEPHHGTLMWPTPGSWPFGKAKRAFTQIETIAEGERVYLLVEQAYLSEAQSYL 73

RESULT 12
US-09-107-433-4556
; Sequence 4556, Application US/09107433
; Patent No. 8800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4556:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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RESULT 14
US-09-252-991A-25459
; Sequence 25459, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25459
; LENGTH: 618
; TYPE: PRT

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Query Match	11.1%	Score 70;	DB 2;	Length 1028;
Best Local Similarity	25.6%;	Pred. No. 15;		
Matches	32;	Conservative 17;	Mismatches 40;	Indels 36; Gaps 6

Qy	1	MNWI-----EPLLVOFCODLGITICDNPHSLLIQLESGTQLERHQGQLTLWLARA	53
Db	114	MMWIYNEKPOSTPLTLQFKQNNVALS-----FKTELNFTG-----WRGIA	154
Qy	54	VPMH-OSGEAIRRAMWTLTAAAOQPALPVRSGWLGEEOILFVSLDER----	AVTLPOLHQ 108
Db	155	VPRDMKSGATGLDKLVITA-----PDQAGTLFFDQIIMSVPLDNRWPIFDYQIPYNN	209
Qy	109	AVTTL	113
Db	210	AVNTM	214

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Job time : 23.7 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 68.8 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-2
Perfect score: 630
Sequence: 1 MNWIEPLLVPFCQDLGITIG.....POLHQA VTTLT LRLQREVLA S 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630	100.0	123	US-10-813-908-2	Sequence 2, Appli
2	89	14.1	252	US-10-732-923-2161	Sequence 2161, Ap
3	82	13.0	176	US-10-506-454-1585	Sequence 1585, Ap
4	80	12.7	253	US-10-732-923-2165	Sequence 2165, Ap
5	80	12.7	253	US-10-724-598-28	Sequence 28, Appl
6	79	12.5	289	US-10-156-761-9384	Sequence 9384, Ap
7	78	12.4	558	US-10-437-963-153335	Sequence 153335
8	77	12.2	652	US-10-369-493-8117	Sequence 8117, Ap
9	74.5	11.8	420	US-10-282-122A-78453	Sequence 78453, A
10	74	11.7	1224	US-10-282-122A-67550	Sequence 67550, A
11	73	11.6	450	US-10-282-122A-67552	Sequence 67552, A
12	73	11.6	565	US-10-104-047-2296	Sequence 2296, Ap
13	73	11.6	565	US-11-072-512-2296	Sequence 2296, Ap
14	72.5	11.5	3084	US-09-938-275-4	Sequence 4, Appli
15	72.5	11.5	3084	US-10-262-670-2	Sequence 2, Appli
16	71.5	11.3	243	US-09-866-099-2	Sequence 2, Appli
17	71.5	11.3	243	US-10-149-256-6	Sequence 6, Appli
18	71.5	11.3	243	US-10-243-552-594	Sequence 594, App
19	71.5	11.3	289	US-10-450-763-41657	Sequence 41657, A
20	71.5	11.3	760	US-10-732-923-12022	Sequence 12022, A
21	71.5	11.3	939	US-10-087-099-9073	Sequence 9073, Ap
22	71.5	11.3	939	US-10-292-798-1524	Sequence 1524, Ap
23	71.5	11.3	1068	US-10-017-161-1868	Sequence 1868, Ap
24	71	11.3	361	US-10-472-928-1798	Sequence 1798, Ap
25	71	11.3	365	US-10-617-320-4556	Sequence 4556, Ap
26	71	11.3	482	US-10-369-493-8828	Sequence 8828, Ap
27	71	11.3	560	US-11-097-143-19725	Sequence 19725, A

28	71	11.3	1162	4	US-10-282-122A-69725	Sequence 69725, A
29	71	11.3	1814	4	US-10-367-094-162	Sequence 162, App
30	70	11.1	402	4	US-10-369-493-22935	Sequence 22935, A
31	70	11.1	641	6	US-11-097-143-12591	Sequence 12591, A
32	69.5	11.0	305	4	US-10-437-963-186976	Sequence 186976, A
33	69	11.0	551	4	US-10-238-075-847	Sequence 847, App
34	69	11.0	747	4	US-10-408-765A-1495	Sequence 1495, Ap
35	69	11.0	2241	4	US-10-369-493-5240	Sequence 5240, Ap
36	69	11.0	2261	4	US-10-369-493-5241	Sequence 5241, Ap
37	69	11.0	6145	4	US-10-156-761-7962	Sequence 7962, Ap
38	68.5	10.9	412	4	US-10-282-122A-63228	Sequence 63228, A
39	68.5	10.9	502	4	US-10-282-122A-65008	Sequence 65008, A
40	68.5	10.9	788	5	US-10-485-395A-6	Sequence 6, Appli
41	68.5	10.9	788	6	US-11-097-143-19737	Sequence 19737, A
42	68.5	10.9	827	4	US-10-347-470A-26	Sequence 26, Appl
43	68	10.8	364	6	US-11-096-568A-15334	Sequence 15334, A
44	68	10.8	390	6	US-11-096-568A-15333	Sequence 15333, A
45	68	10.8	1403	5	US-10-732-923-8710	Sequence 8710, Ap

ALIGNMENTS

RESULT 1

US-10-813-908-2
; Sequence 2, Application US/10813908
; Publication No. US20050058662A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and U
; FILE REFERENCE: MICOI/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813,908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
US-10-813-908-2

Query Match	100.0%;	Score 630;	DB 5;	Length 123;
Best Local Similarity	100.0%;	Pred. No. 5.4e-63;		
Matches 123;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNWIEPLLVPFCQDLGITIGDNPHSLIQLELEQSGTQLQERHQGLTLWLARAVPMHQSG	60	
Db	1	MNWIEPLLVPFCQDLGITIGDNPHSLIQLELEQSGTQLQERHQGLTLWLARAVPMHQSG	60	
QY	61	EAIRAMTLTAAAOQPALPVRSGWLGEGEQLILFVSLDERAVTLPOLHQA VTTLT LRLQREV	120	
Db	61	EAIRAMTLTAAAOQPALPVRSGWLGEGEQLILFVSLDERAVTLPOLHQA VTTLT LRLQREV	120	
QY	121	LAS 123		
Db	121	LAS 123		
RESULT 2				
US-10-732-923-2161				
; Sequence 2161,		Application US/10732923		
; Publication No. US20050108791A1				
; GENERAL INFORMATION:				
; APPLICANT: Edgerton, Michael D				
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES				
; FILE REFERENCE: 38-15(52796)C				
; CURRENT APPLICATION NUMBER: US/10/732,923				
; CURRENT FILING DATE: 2003-12-10				
; PRIOR APPLICATION NUMBER: 10/310,154				

SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: Amino Acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: No
ORIGINAL SOURCE:
ORGANISM: Pseudomonas denitrificans
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
FEATURE:
NAME/KEY: COBM
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: Translation product of SEQ ID NO:27
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-724-598-28
Query Match 12.7%; Score 80; DB 5; Length 253;
Best Local Similarity 23.3%; Pred. No. 2.2;
Matches 35; Conservative 24; Mismatches 49; Indels 42; Gaps 7;
QY 4 IEPLLVQFCODLGITIGDNPHSLIQLELE-----QSGTQLQLER-HQGQLTLWLAARVPWHQ 58
DB 37 VSEPLLRYCPGARIVDTTPAPMSLDEIEAEYVKAEGLDVARLHSGDLSVMSAVA----- 91
QY 59 SGEAIR-----AMTLTAAAGPALPVRSGWLGE-----QLILFVSLDERAVTLPO 105
DB 92 --EQIRRLKEHGIAYTMTFGV--PSFAAASALGRELTIPAVAQSLVLRVSGRASPMEN 147
QY 106 -----LHQAVTTLRLQREV 120
DB 148 SETLSAFGATGSTLAITHLAHAIHQVVEEL 177
RESULT 6
US-10-156-761-9384
; Sequence 9384, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9384
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9384
Query Match 12.5%; Score 79; DB 4; Length 289;
Best Local Similarity 31.9%; Pred. No. 3.4;
Matches 23; Conservative 10; Mismatches 25; Indels 14; Gaps 1;

QY 21 DNPHSLIQLELEQSGTQLQLERHOGQLTLWLAARVPWHOSGEAIRRAMTTLTAAAGPALPV 80
DB 115 DPEVDLELTVELSGTTLHEQLAAGKLDLVLAKRPRQDPGRGELVRHD----- 160
QY 81 RSGWLGEELIIL 92
DB 161 RUVWIGAERLRL 172
RESULT 7
US-10-437-963-153335
; Sequence 153335, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 153335
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_532C.1.pap
US-10-437-963-153335
Query Match 12.4%; Score 78; DB 4; Length 558;
Best Local Similarity 32.6%; Pred. No. 10;
Matches 30; Conservative 6; Mismatches 36; Indels 20; Gaps 5;
QY 39 LERHOGQLTLWLAARVP--WHOSGEAIRRAMTTLTAAAGPALPVRSGW-----LGEEQLI 91
DB 89 LQTHNGSLT---GRVPPDAWHGVGHAANSVF-----VLPFRKWRALRRIGAELLL 136
QY 92 LFFVSLDERAVTIPQLHQAVTTLRLQREVLAS 123
DB 137 SARQLDGRRL-LPLLRDAVLDRRVSEMSAA 167
RESULT 8
US-10-369-493-8117
; Sequence 8117, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8117
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Thermobifida fusca
; FEATURE:
; NAME/KEY: unsure


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QY 114 TRLQREVLA 122
Db 317 QHLQOQLQA 325

RESULT 11
US-10-282-122A-67552
; Sequence 67552, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67552
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-67552

Query Match 11.6%; Score 73; DB 4; Length 450;
Best Local Similarity 36.9%; Pred. No. 28;
Matches 24; Conservative 7; Mismatches 16; Indels 18; Gaps 4;

QY 7 LLVQFCQ-----DLGITIGDNPHSLIQLELEQSGTLQLER-----HQQLTLWLARA 53
Db 387 LLEQCCORAVAEQRHLRAVLIGDEP-----QVSAELSGE-ELDRLLDPAHYLGQARVWVARA 441

QY 54 VFWHQ 58
Db 442 VSEHQ 446

RESULT 12
US-10-104-047-2296
; Sequence 2296, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2296
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2296

Query Match 11.6%; Score 73; DB 4; Length 565;
Best Local Similarity 27.4%; Pred. No. 37;
Matches 32; Conservative 7; Mismatches 42; Indels 36; Gaps 5;

QY 12 CQDLGITIGDNPHSLIQLELEQSGTLQLER-----HQQLTLWLAR-----AVPMHQSG 60
Db 189 CSDTGVW-----SSSLGPARREASQPSLHRQLSDPNHGSPPGLYRANLGLGAYPWSQSS 244

QY 61 EAIRRAMT--LTAAGQGPALPVRSGWLGBEEQLILFVSLDERAVTLPOLHQAVTTLTR 115
Db 245 PALNHNSTSPLTAVESPLP-----RSRPLLOFHRGAPALSR 282

RESULT 13
US-11-072-512-2296
; Sequence 2296, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAOBU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2296
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2296

Query Match 11.6%; Score 73; DB 6; Length 565;
Best Local Similarity 27.4%; Pred. No. 37;
Matches 32; Conservative 7; Mismatches 42; Indels 36; Gaps 5;

QY 12 CQDLGITIGDNPHSLIQLELEQSGTLQLER-----HQQLTLWLAR-----AVPMHQSG 60
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Db

189

CSDTGW-----SSSIGPARREASGOPSILHRQLSDPNHGSPPCLYRANLKLGAYPWSOSS

244

Qy

61

EAIRRAMT--LTAAAGPALPVRSGWLGEQILFVSLDERAVTLPOLHQAVTTILTR

115

Db

245

PALNHSTSPITLAVESPLP-----RSRPLQPHRGAPALSR

282

RESULT 14

US-09-938-275-4

; Sequence 4, Application US/09938275

; Patent No. US20020111309A1

; GENERAL INFORMATION:

; APPLICANT: Gerardo Castillo

; APPLICANT: Alan Snow

; TITLE OF INVENTION: Therapeutic and Diagnostic Applications

; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments

; FILE REFERENCE: PROTEO.P03

; CURRENT APPLICATION NUMBER: US/09/938,275

; CURRENT FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 3084

; TYPE: PRT

; ORGANISM: Mus Musculus

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: Swissprot P19137

; DATABASE ENTRY DATE: 1990-11-01

US-09-938-275-4

Qy

33

QSGTLQLERHOGQLTLWLARAVPHQSGEAI-----RRAMTLTAAAGGPA--LPVRSGLWG

86

Db

1836

QDTLTQLEHHRDELLW-ARKIRSHVDDLVNMQSKRRARDLVHRAEQHASELQSRAGALD

1894

Qy

87

EE-OLILFVSLDERAVTLPOLHQAVTTILTRLQREVLAS

123

Db

1895

RDLENVRNVSUN--ATSAAHVHSNIQILTTE-EAEMLAA

1929

Query Match 11.5%; Score 72.5; DB 3; Length 3084;

Best Local Similarity 32.7%; Pred. No. 3.6e+02;

Matches 32; Conservative 16; Mismatches 39; Indels 11; Gaps 6;

RESULT 15

US-10-262-670-2

; Sequence 2, Application US/10262670

; Publication No. US20030108540A1

; GENERAL INFORMATION:

; APPLICANT: Kalluri, Raghuram

; TITLE OF INVENTION: Anti-Angiogenic and Anti-Tumor

; TITLE OF INVENTION: Properties of Matin and Other Laminin Domains

; FILE REFERENCE: 1440-2004-008

; CURRENT APPLICATION NUMBER: US/10/262,670

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: PCT/US01/09921

; PRIOR FILING DATE: 2001-03-28

; PRIOR APPLICATION NUMBER: US 60/192,875

; PRIOR FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 3084

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-262-670-2

Qy

33

QSGTLQLERHOGQLTLWLARAVPHQSGEAI-----RRAMTLTAAAGGPA--LPVRSGLWG

86

Db

1836

QDTLTQLEHHRDELLW-ARKIRSHVDDLVNMQSKRRARDLVHRAEQHASELQSRAGALD

1894

Search completed: June 16, 2006, 20:25:01

Job time : 69.8 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 20:13:41 ; Search time 5.3 Seconds
(without alignments)
523.484 Million cell updates/sec

Title: US-10-813-908A-2
Perfect score: 630
Sequence: 1 MNWIEPLLVPQDLGITIG.....POLHQAVTTLRLQREVLA 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	10.8	441	US-10-449-902-32870	Sequence 32870, A
2	67	10.6	557	US-10-449-902-47436	Sequence 47436, A
3	65.5	10.4	305	US-11-122-986-5	Sequence 5, Appli
4	65.5	10.4	305	US-11-122-986-7	Sequence 7, Appli
5	65.5	10.4	308	US-10-449-902-28824	Sequence 28824, A
6	65	10.3	557	US-10-449-902-50128	Sequence 50128, A
7	64.5	10.2	249	US-10-953-349-32013	Sequence 32013, A
8	64.5	10.2	307	US-10-953-349-32012	Sequence 32012, A
9	64.5	10.2	354	US-10-953-349-32011	Sequence 32011, A
10	64.5	10.2	1333	US-10-449-902-41289	Sequence 41289, A
11	63.5	10.1	673	US-11-121-154-11	Sequence 11, Appli
12	63	10.0	152	US-10-449-902-38951	Sequence 38951, A
13	62	9.8	231	US-10-449-902-30176	Sequence 30176, A
14	61.5	9.8	153	US-10-953-349-12335	Sequence 12335, A
15	61.5	9.8	153	US-10-953-349-25973	Sequence 25973, A
16	61.5	9.8	156	US-10-449-902-51435	Sequence 51435, A
17	61.5	9.8	508	US-10-449-902-38213	Sequence 38213, A
18	61	9.7	433	US-10-953-349-17176	Sequence 17176, A
19	61	9.7	436	US-10-953-349-17175	Sequence 17175, A
20	61	9.7	454	US-10-953-349-17174	Sequence 17174, A
21	61	9.7	619	US-10-449-902-44299	Sequence 44299, A
22	60.5	9.6	163	US-11-293-697-2811	Sequence 2811, Ap
23	60	9.5	183	US-10-449-902-38622	Sequence 38622, A
24	60	9.5	485	US-11-293-697-2858	Sequence 2858, Ap
25	60	9.5	497	US-10-953-349-35183	Sequence 35183, A

ALIGNMENTS

RESULT 1

US-10-449-902-32870
; Sequence 32870, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-363870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32870
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-32870

Query Match 10.8%; Score 68; DB 6; Length 441;
Best Local Similarity 29.3%; Pred. No. 3.4;
Matches 27; Conservative 11; Mismatches 34; Indels 20; Gaps 5;
QY 16 GITIGDNPHSLIQLEBOSGTLQLEHOGQLTLWLRARVPHQSGEATRRAMTLTAAAG 75
Db 179 GFVLWQKPELMSLVSGCKISAGSDGKVA-W--RQTPWQS-----HASRG 224

QY 76 PALPVRSGLGEEQLI---LF---VSLDERAV 101
Db 225 PPRPULRSLOGLDPMLTATSLFADAVCIGERSV 256

RESULT 2

US-10-449-902-47436
; Sequence 47436, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

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; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47436
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-47436

Query Match      10.6%; Score 67; DB 6; Length 557;
Best Local Similarity 25.4%; Pred. No. 5.9;
Matches 29; Conservative 17; Mismatches 46; Indels 22; Gaps 4;

QY      26 LTQLEQSGTQLQLER-----HQQQLTLMLAR-----AVPWHQSGEAIRRAM 67
DB      403 LLSYEEDSEGLQLATKVLGTHVYVHPNGSSMEIVRAGPSTFTFPWQTDEES--RAV 460

QY      68 TLTAQAQGPALPVRSG--WLGEQILFVSLDERAVTLPQLHQAVTTLTRLORE 119
DB      461 EINRSFAGEIATGYGFRYPGSKGSLFVLLDGLRLAFVRENKAVLTQLRLDLE 514

RESULT 3
US-11-122-986-5
; Sequence 5, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-5

Query Match      10.4%; Score 65.5; DB 7; Length 305;
Best Local Similarity 28.6%; Pred. No. 4.2;
Matches 24; Conservative 14; Mismatches 23; Indels 23; Gaps 4;

QY      57 HQSGE-AIRRAMTLTAAQAQGPALPV-----RSGWLGEQIL-----FVS----- 95
DB      73 HKSGEKALNRYMNRNTASAALKDQVDVIFVVDRTWTEEDQWLVLRVQVSCPVLIAVNKT 132

QY      96 --LDERAVTLPQLHQAVTTLTRLO 117
DB      133 DRIEKAADLLPHLEWLTQQLPKAE 156

RESULT 4
US-11-122-986-7
; Sequence 7, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-7

Query Match      10.4%; Score 65.5; DB 7; Length 305;
Best Local Similarity 28.6%; Pred. No. 4.2;
Matches 24; Conservative 14; Mismatches 23; Indels 23; Gaps 4;

QY      57 HQSGE-AIRRAMTLTAAQAQGPALPV-----RSGWLGEQIL-----FVS----- 95
DB      73 HKSGEKALNRYMNRNTASAALKDQVDVIFVVDRTWTEEDQWLVLRVQVSCPVLIAVNKT 132

QY      96 --LDERAVTLPQLHQAVTTLTRLO 117
DB      133 DRIEKAADLLPHLEWLTQQLPKAE 156

RESULT 5
US-10-449-902-28824
; Sequence 28824, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
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; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30176
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-30176

Query Match 9.8%; Score 62; DB 6; Length 231;
Best Local Similarity 23.8%; Pred. No. 7.5;
Matches 19; Conservative 15; Mismatches 36; Indels 10; Gaps 3;

QY 44 GQTLMLARVPWHQSGEARRAMTLTAAAGPAPLVRSGWLGEQILFVSLDERAVTL 103
Db 161 GYLDVSLGAMIGWRAGEALHGRRTDATRS----PILNAWMER-----FAALDAAKAAM 211

QY 104 PQHQAVTTLRLQREVLA 123
Db 212 PDNNKLIV-EFVRVRRRAAAN 230

RESULT 14
US-10-953-349-12335
; Sequence 12335, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12335
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-12335

Query Match 9.8%; Score 61.5; DB 6; Length 153;
Best Local Similarity 34.4%; Pred. No. 5.2;
Matches 21; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 30 ELEQSGTLQLERHQGLTLMLARAVPWHQSGEARRAMTLTAAAGPAPLVRSGWLGEQ 89
Db 32 EREMAKSLRSKREKRLTLRREITAEFPYDKKEAKQA-AQAAALEAPKLPVRVHPAYEES 90

QY 90 L 90
Db 91 L 91

RESULT 15
US-10-953-349-25973
; Sequence 25973, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25973
; LENGTH: 153
; TYPE: PRT

; ORGANISM: Triticum aestivum
US-10-953-349-25973

Query Match 9.8%; Score 61.5; DB 6; Length 153;
Best Local Similarity 34.4%; Pred. No. 5.2;
Matches 21; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

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Db 32 EREMAKSLRSKREKRLTLRREITAEFPYDKKEAKQA-AQAAALEAPKLPVRVHPAYEES 90

QY 90 L 90
Db 91 L 91

Search completed: June 16, 2006, 20:25:57
Job time : 6.3 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 80.1748 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-3

Perfect score: 609

Sequence: 1 MSRTAAHIGIEQLSAISLD.....EQMADEQLMQMTLLHLHKV 121

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Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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- 1: Geneseq1980s.*
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- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*
- 10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	266	43.7	262	7	ABO81423
3	88.5	14.5	259	9	AEC75797
4	83.5	13.7	353	2	AAR20178
5	83	13.6	10917	6	AAE36132
6	81.5	13.4	366	4	AAU53181
7	81.5	13.4	366	6	ABM49700
8	81.5	13.4	452	6	ABU25842
9	80	13.1	1132	8	ADY06856
10	78.5	12.9	165	3	ABU41479
11	78.5	12.9	165	5	ABP10391
12	78.5	12.9	4924	4	AAB70968
13	78.5	12.9	4928	2	AAV39300
14	78	12.8	294	8	ADJ67793
15	78	12.8	294	8	ADJ68005
16	78	12.8	294	8	ADK01083
17	78	12.8	294	8	ADJ79302
18	78	12.8	294	8	ADJ84742
19	78	12.8	294	8	ADM77530
20	78	12.8	294	8	ADM66197
21	78	12.8	294	8	ADO04250
22	78	12.8	294	8	ADP82327
23	78	12.8	294	8	ADS15534

ALIGNMENTS

RESULT 1

ABB80771 ID ABB80771 standard; protein; 121 AA.

XX AC ABB80771;

XX DT 23-SEP-2002 (first entry)

XX DE A. salmonicida type III secretion protein acr3 sequence.

XX KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;

XX KW acrV; acrH; antibiotic; vaccine; fish.

XX OS Aeromonas salmonicida.

XX PN WO200240514-A2.

XX PD 23-MAY-2002.

XX PF 15-NOV-2001; 2001WO-CA001589.

XX PR 15-NOV-2000; 2000US-0248864P.

XX PA (FREY/) FREY J.

XX PA (STUB/) STUBER K.

XX PA (THOR/) THORNTON J C.

XX PA (KUZU/) KUZYK M A.

XX PA (BURI/) BURIAN J.

XX PA Frey J, Stuber K, Thornton JC, Kuzyk MA, Burian J;

XX WPI: 2002-537338/57.

XX N-PSDB: ABN86172.

XX Novel protein from Aeromonas salmonicida and nucleic acid encoding the protein, useful for reducing susceptibility of fish to infection by a virulent strain of Aeromonas salmonicida.

XX Claim 13; Page 27; 39pp; English.

XX The invention relates to A. salmonicida type III secretion genes and encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH. A. salmonicida type III secretion apparatus is useful for producing selected products, especially Aext. AcrV in vaccine, epitope or epitopic region of AcrV or any other protein of A. salmonicida type III secretion apparatus is useful for reducing the susceptibility of fish to infection

Ady55025 B. subtil
Adz76601 Bacillus
Aea24609 B. subtil
Aea34032 B. subtil
Aeb51436 DNA polym
Abb63035 Drosophil
Adm28904 Bacterial
Aas00477 sgal prot
Abo63231 Klebsiell
Abo81712 Pseudomon
Abo71440 Drosophil
Abo81630 Pseudomon
Adt60176 Plant pol
Adg22680 Cyanophag
Adx71223 Plant ful
Adx89677 Plant ful
Adm93022 M. xanthu
Ady22840 Plant ful
Ady04623 Plant ful
Adn27057 Bacterial
Abo71150 Pseudomon

CC by a virulent strain of A. salmonicida. The proteins and encoding DNA are
CC useful for manufacturing a diagnostic agent. Detecting the presence of
CC the genes of AcrD, AcrV or any other components of the A.salmonicida type
CC III secretion apparatus is useful for the production or quality control
CC or efficacy of vaccines made from A.salmonicida or its genes. The present
CC sequence represents the A. salmonicida type III secretion protein acr3
XX
XX
SQ Sequence 121 AA;

Query Match 100.0%; Score 609; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.3e-60;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTAAHIGIEQLSALSLDDQERSLPGRYALLPDGOSIEPHISRILYPERLADRVLLDFA 60
DB 1 MSRTAAHIGIEQLSALSLDDQERSLPGRYALLPDGOSIEPHISRILYPERLADRVLLDFA 60
QY 61 TPDGRGHDLRLRPVDFNQMGRLSVLAEGOSPRLRAAAALLEQWHADEQLMQMTLHLHK 120
DB 61 TPDGRGHDLRLRPVDFNQMGRLSVLAEGOSPRLRAAAALLEQWHADEQLMQMTLHLHK 120
QY 121 V 121
DB 121 V 121

RESULT 2
ABO81423
ID ABO81423 standard; protein; 262 AA.
AC ABO81423;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #13598.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD14994.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 30169; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences

CC of Pseudomonas species using biocchip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 262 AA;

Query Match 43.7%; Score 266; DB 7; Length 262;
Best Local Similarity 46.3%; Pred. No. 3.4e-21;
Matches 56; Conservative 20; Mismatches 45; Indels 0; Gaps 0;
QY 1 MSRTAAHIGIEQLSALSLDDQERSLPGRYALLPDGOSIEPHISRILYPERLADRVLLDFA 60
DB 142 MSRVGAWHIGIERLDLAHAEPFAPPLPERHLLAPDGRPVETHVASLYPQAQOQLFDYA 201
QY 61 TPDGRGHDLRLRPVDFNQMGRLSVLAEGOSPRLRAAAALLEQWHADEQLMQMTLHLHK 120
DB 202 RPQLEPHGLLRPGDFRQALRLRLALTLPRQALQAACLLGERDEDRLLQMAPNLLHK 261
QY 121 V 121
DB 262 V 262

RESULT 3
AEC75797
ID AEC75797 standard; protein; 259 AA.
XX
AC AEC75797;
XX
DT 01-DEC-2005 (first entry)
XX
DE P. cellulosum ambruticin ORF5 protein.
XX
KW ambruticin; fungal infection; fungicide; polyketide.
XX
OS Polyangium cellulosum.
XX
PN WO2005086907-A2.
XX
PD 22-SEP-2005.
XX
PF 08-MAR-2005; 2005WO-US007924.
XX
PR 08-MAR-2004; 2004US-0551103P.
PR 04-MAY-2004; 2004US-0568290P.
PR 07-MAR-2005; 2005US-00075185.
XX
PA (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI Reeves CD, Julien B, Reid RC;
XX
DR WPI; 2005-639088/65.
DR N-PSDB; AEC75775.
XX
PT New nucleic acids encoding polyketide synthases and polyketide
PT modification enzymes involved in or required for the biosynthesis of
PT ambruticin, useful for producing polyketides, e.g. ambruticins, for
PT treating fungal infections.
XX
PS Disclosure; SEQ ID NO 24; 285pp; English.
XX
CC The invention relates to a purified or recombinant nucleic acid (I)
CC comprising a nucleotide sequence encoding a polypeptide involved in or
CC required for the biosynthesis of ambruticin. The complement of the
CC nucleotide sequence hybridizes to a nucleic acid encoding a domain
CC selected from beta-ketoacylsynthase, acyltransferase, beta-ketoreductase,
CC dehydratase, enoylreductase, or acyl carrier protein domains of the
CC Sorangium cellulosum (synonym: Polyangium cellulosum) ambruticin gene
CC cluster, or where the complement of the nucleotide sequence hybridizes to
CC a nucleic acid encoding an amino acid sequence selected from (SEQ ID NO.
CC 11-19 (AEC75784-AEC75792). The nucleic acid is useful for producing

Matches 36; Conservative 12; Mismatches 36; Indels 23; Gaps 5;

[illegible]

XX Sequence 366 AA;
SQ Query Match 13.4%; Score 81.5; DB 6; Length 366;
Best Local Similarity 27.0%; Pred. No. 2.9;
Matches 24; Conservative 18; Mismatches 32; Indels 15; Gaps 3;

QY 8 HIGIEQLSAISLDDQERSLPGRYALPDGQSIIEPHISRLYPERLADRVLLDFATPDGRFH 67
Db 237 HRWIEELGGMNF-----MAISKDQLVTPELAGTILRGVTRRSILEVA-PDLGLE 285
QY 68 DLLRPVDFNQAMQGLRSVLARGQSPELRA 96
Db 286 PVERKIDVDELDGVR-----GEFPEVFA 310

RESULT 8
ABU25842
ID ABU25842 standard; protein; 452 AA.
XX
AC ABU25842;
DT 19-JUN-2003 (first entry)
DE Protein encoded by Prokaryotic essential gene #11369.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Corynebacterium diphtheriae.
XX
PN W0200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA29712.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 53766; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 452 AA;

Query Match 13.4%; Score 81.5; DB 6; Length 452;
Best Local Similarity 23.5%; Pred. No. 3.8;
Matches 36; Conservative 20; Mismatches 56; Indels 41; Gaps 4;

QY 2 SRITAAHIGIEQLSAISLDDQERSLPGRYAL---LPDGQSIIEPHISRLYPERLADRVLLD 58
Db 202 NRITISDEALEQLVLLSGGDARSLTYLEAASESLADGEELTPPIIR-----HNVDKAIVR 257
QY 59 FATPDGRGFHDL-----LRPVDFNQAMQGLRSVLARGQSPELRA----- 96
Db 258 YDRDGGQHYDVSAFIKSMRGSVDVAALHYLARIMIDAGEDPRFTARRLVIHASEDVGWAD 317
QY 97 -----AAALLEQWHADEQLMQMTLHL 117
Db 318 PQALSVAVAASQAVALIGMPEARINLAQATIH 350

RESULT 9
ADY06856
ID ADY06856 standard; protein; 1132 AA.
XX
AC ADY06856;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 62671.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content.
XX Unidentified.
XX
XX US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX

DR WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 62671; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 1132 AA;

Query Match 13.1%; Score 80; DB 8; Length 1132;
Best Local Similarity 27.2%; Pred. No. 19;
Matches 25; Conservative 16; Mismatches 27; Indels 24; Gaps 4;
QY 38 SIEPHSRUYPERLADRVLLDPATPGPHDLRLPVDVFNQAMQLRS-----VLAEGQ 90
Db 831 STEPH-----DVIAQDR-LTDLPPNDPNHTVMVHIOAQSTAQSHALDGGK 874
QY 91 SPELRAAAALLEGMHAD-EQLMQMTLHLHKV 121
Db 875 DPAHATSSLVKTHSNMEPVQKSI:SQLHDI 906

RESULT 10
AAB41479
ID AAB41479 standard; protein; 165 AA.
XX
XX AAB41479;
XX
XX 08-FEB-2001 (first entry)
XX
XX Human ORFX ORF1243 polypeptide sequence SEQ ID NO:2486.

XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; nontropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive.

XX Homo sapiens.
OS
XX
XX WO200058473-A2.
PN
XX
XX 05-OCT-2000.

XX
XX 31-MAR-2000; 2000WO-US008621.
XX
XX 31-MAR-1999; 99US-0127607P.
PR
XX 02-APR-1999; 99US-0127636P.
PR
XX 05-APR-1999; 99US-0127728P.
PR
XX 30-MAR-2000; 2000US-00540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2000-602362/57.
DR
XX N-PSDB; AAC75688.
DR
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 11; Page 1789-1790; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antipsoriatic; antiparkinsonian; nontropic; neuroprotective; vulnary;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
XX Sequence 165 AA;

Query Match 12.9%; Score 78.5; DB 3; Length 165;
Best Local Similarity 25.8%; Pred. No. 2-2;
Matches 23; Conservative 19; Mismatches 32; Indels 15; Gaps 3;
QY 8 HIGIEQLSAISLDQERSLPGRYALLPDQSQSIPIHISRLYPERLADRVLLDPATPGPH 67
Db 36 HRWIBELGGMF-----MAISKDQGLVTPELAGTILRGVTRKSILEVA-PDLGLE 84
QY 68 DLLRPVDFNQAMQGLRSVLAEGQSPELRA 96
Db 85 PVERKIDVDELDDGVR-----GEFFPEVFA 109

RESULT 11
AAB10391
ID AAB10391 standard; protein; 165 AA.
XX
XX AAB10391;
XX
XX 24-JUN-2002 (first entry)
XX
XX Human ORFX protein sequence SEQ ID NO:20764.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;

KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

OS Homo sapiens.

PN WO200192523-A2.

XX 06-DEC-2001.

PD 29-MAY-2001; 2001WO-US010836.

XX 30-MAY-2000; 2000US-0206132P.

PR 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

PA Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

DR N-PSDB; ABN26143.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.

XX Disclosure; SEQ ID NO 20764; 1037pp; English.

XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification)). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 165 AA;

Query Match 12.9%; Score 78.5; DB 5; Length 165;
Best Local Similarity 25.8%; Pred. No. 2.2;
Matches 23; Conservative 19; Mismatches 32; Indels 15; Gaps 3;

QY 8 HIGIEQLSALSDQERSLPGRYALLPDGQSIPIHISRLYPERLADRVLDLDFATPDRGFH 67

DB 36 HRVIEELGGWNF-----MAISKDGGQLVTPELAGTILRGVTRKSIILEVA-PDLGLE 84

QY 68 DLLRPVDFNQMOGLRSVLAEQSPPELRA 96

DB 85 PVERKIDVDELLDGVRS----GEFPEVFA 109

RESULT 12

AAB70968

ID AAB70968 standard; protein; 4924 AA.

XX AAB70968;

XX

DT

XX

DE

XX

XX

KW

KW

KW

XX

OS

XX

PN

XX

XX

PD

XX

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XX

XX

XX

XX

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28-AUG-2001 (first entry)

S. spinosa protein fragment encoded by ORF21, SEQ ID 48.

Forosamine; trimethylrhannose; polyketide synthase; biosynthesis;
spinosyn; polyketide aglycone; transgenic plant; insect resistance;
macrolide; insecticidal; polyketide synthase.

Saccharopolyspora spinosa.

DE19957268-A1.

08-MAR-2001.

29-NOV-1999; 99DE-01057268.

27-AUG-1999; 99DE-01040596.

(FARB) BAYER AG.

Eberz G, Moehrl V, Froede R, Velten R, Salas JA;

WPI; 2001-267102/28.

N-PSDB; AAF88338.

New nucleic acid encoding enzymes for spinosyn biosynthesis, useful for
recombinant production of insecticidal spinosyns and their derivatives.

Claim 57; Page 264-284; 354pp; German.

This invention describes a novel method nucleic acid (I) and its encoded
polypeptide (II) containing at least one region that encodes an enzymatic
activity involved in biosynthesis of spinosyns. (I) are used (i) to
identify, inactivate or modulate genes involved in the biosynthesis of
(II); (ii) to generate a library of polyketide synthases; (iii) for
adding forosamine or trimethylrhannose to a spinosyn or polyketide
aglycone; and (iv) for recombinant production of the corresponding
enzymes, which are used for production of (II), their precursors or
derivatives, including production of transgenic plants that express (II)
and thus have increased resistance to insects. (I) are also useful as
markers for sequencing of the Saccharopolyspora spinosa genome. (II) are
macrolides with insecticidal, but not antibacterial, activity, and can
also be used to raise specific antibodies, useful for identifying
expression clones in a gene bank. Cells transformed with (I) may produce
(II) at significantly increased levels or produce new derivatives of
(II). This sequence represents an S. spinosa polyketide synthase

Sequence 4924 AA;

Query Match 12.9%; Score 78.5; DB 4; Length 4924;
Best Local Similarity 27.5%; Pred. No. 1.9e+02;
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;

QY 5 TAAHIGIEQLSALSDQERSLPGRYALLPDGQSIPIHISRLYPERLADRVLDLDFATPDR 64

DB 4795 TFAELGFDLSLTAVELNRNLNAVTVG--LRUPPTLVFDHPTLALSEQLVPAIV---AFPDN 4849

QY 65 GFHDLLRPVDFNQMOGLRSVLAEQSPPELRAAAALAEQMHIA 106

DB 4850 GIESLLAELD-----RLDTTLAQGFSPLEDOAKVAERLHA 4885

RESULT 13

AAY39300

ID AAY39300 standard; protein; 4928 AA.

XX AAY39300;

01-DEC-1999 (first entry)

Spnd a polyketide synthase.

Spinosyn biosynthetic enzyme; open reading frame; ORF;

KW insecticidal microlides; arachnid; nematode; insect; polyketide;
 KW polyketide synthase; PKS; extender module; initiator module;
 KW acyl transferase domain; AT; acyl carrier protein; ACP;
 KW beta-ketosynthase domain; KS; KR; dehydratase domain; DH;
 KW enoyl reductase domain; ER; beta-ketoreductase; insecticide.
 XX
 XX Saccharopolyspora spinosa.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..424
 FT /label= KS5
 FT /note= "Beta-ketosynthase domain: part of extender module
 5"
 FT Domain 539..866
 FT /label= AT5
 FT /note= "Acyl transferase domain: part of extender module
 5"
 FT Domain 893..1078
 FT /label= DH5
 FT /note= "Dehydratase domain: part of extender module 5"
 FT Domain 1384..1565
 FT /label= KR5
 FT /note= "Beta-ketoreductase domain: part of extender
 module 5"
 FT Domain 1645..1726
 FT /label= ACP5
 FT /note= "Acyl carrier protein domain: part of extender
 module 5"
 FT Domain 1748..2172
 FT /label= KS6
 FT /note= "Beta-ketosynthase domain: part of extender module
 6"
 FT Domain 2283..2613
 FT /label= AT6
 FT /note= "Acyl transferase domain: part of extender module
 6"
 FT Domain 2916..3095
 FT /label= KR6
 FT /note= "Beta-ketoreductase domain: part of extender
 module 6"
 FT Domain 3188..3269
 FT /label= ACP6
 FT /note= "Acyl carrier protein domain: part of extender
 module 6"
 FT Domain 3291..3713
 FT /label= KS7
 FT /note= "Beta-ketosynthase domain: part of extender module
 7"
 FT Domain 3825..4153
 FT /label= AT7
 FT /note= "Acyl transferase domain: part of extender module
 7"
 FT Domain 4344..4638
 FT /label= KR7
 FT /note= "Beta-ketoreductase domain: part of extender
 module 7"
 FT Domain 4725..4806
 FT /label= ACP7
 FT /note= "Acyl carrier protein domain: part of extender
 module 7"
 XX
 XX WO9946387-A1.
 XX
 XX 16-SEP-1999.
 XX
 XX 16-FEB-1999; 99WO-US0003212.
 XX
 XX 09-MAR-1998; 98US-00036987.
 XX
 XX (DOWC) DOW AGROSCIENCES LLC.
 XX
 XX Baltz RH, Broughton MC, Crawford KP, Madduri K, Merlo DJ;
 PI treadway PJ, Turner JR, Waldron C;

XX WPI: 1999-551414/46.
 DR N-PSDB; AA221501.
 XX
 XX New spinosyn biosynthetic genes from Saccharopolyspora spinosa, useful
 FT for production of insecticidal spinosyn compounds.
 FT
 XX
 XX Claim 1; Page 113-129; 190pp; English.
 XX
 XX This is the amino acid sequence of the product of the spnD gene. The
 CC protein is involved in spinosyn biosynthesis. The spnD gene is one of 23
 CC genes and open reading frames contained in an 80kb DNA sequence AA221501.
 CC Spinosyns are insecticidal microlides which are useful for the control of
 CC arachnids, nematodes and insects. Biosynthesis of spinosyns occurs via
 CC stepwise condensation and modification of carboxylic acid precursors
 CC generating a linear polyketide which is modified further. The DNA
 CC sequence contains a central region of approximately 55kb which has
 CC homology to the DNA encoding the polyketide synthases (PKS) of known
 CC macrolide producers. The spinosyn PKS DNA region consists of 5 ORFs with
 CC stop codons at the end of acyl carrier protein (ACP) domains. Together
 CC the PKS polypeptides (AAV39297-Y39301) of which this sequence is one,
 CC form a complex consisting of an initiator module, spnA, and several
 CC extender modules spnB-spnE. Each extender module adds a specific acetyl
 CC Co-A precursor to a growing polyketide chain, and modifies the beta-keto
 CC group in a specific manner. A module in a PKS polypeptide consists of
 CC several domains with specific functions. The initiator module has an acyl
 CC transferase (AT) domain, and an acyl carrier protein (ACP) domain. The
 CC extender modules have the same domains plus a beta-ketosynthase (KS)
 CC domain, and optionally a beta-ketoreductase domain, a dehydratase (DH)
 CC domain, and an enoyl reductase (ER) domain. The last extender module
 CC terminates with a thioester domain. The products of the genes present in
 CC the upstream region the PKS genes have been assigned names spnF-spnS
 CC AAV39302-Y39315 and are responsible for different modifications in
 CC spinosyn biosynthesis. There are also two ORFs ORF15 and ORF16 present
 CC immediately upstream of spnS, producing polypeptides AAY39316-Y39317, and
 CC two ORFs ORF1 and ORF2 present downstream of the PKS region producing
 CC polypeptides AAY39318-Y39319. The genes are useful to improve yields of
 CC spinosyns, and for creating new spinosyns e.g. by mutagenesis, or
 CC interruption of steps in spinosyn biosynthesis. The modified spinosyns
 CC may be a new insect control agent or serve as substrates for further
 CC chemical modification and the creation of new semi-synthetic spinosyns.
 CC The genes are also useful to isolate similar sequences from S. spinosa or
 CC other species by hybridization
 XX
 SQ Sequence 4928 AA;
 Query Match 12.9%; Score 78.5; DB 2; Length 4928;
 Best Local Similarity 27.5%; Pred. No. 1.9e+02;
 Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;
 QY 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDDQSTEPHISRLYPERLADRVLLDFATPDR 64
 Db 4799 TFAELGFDLSLTAVELNRLNNAVTVG--LRLPPTLVDFDHPFLALSEQLVPLV---NEPDN 4853
 QY 65 GFHDLRPVDFNQAMQGLRSVLAEQGSPELRAAAALLEQMHA 106
 Db 4854 GIESLLAELE-----RLDTTLAQGPSIPLEDOAKVAERLHA 4889
 RESULT 14
 ADJ67793
 ID ADJ67793 standard; protein; 294 AA.
 XX
 XX ADJ67793;
 AC
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX
 XX B. subtilis gamma/tau ATP binding domain.
 DE
 XX
 XX DNA polymerase; DNA sequencing; DNA amplification.
 KW
 XX
 XX Bacillus subtilis.
 OS
 XX

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: June 16, 2006, 19:07:20 ; Search time 12.2967 Seconds
(without alignments)
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Perfect score: 609
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
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Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR 80:*
1: Piri:*
2: Piri2:*
3: Piri3:*
4: Piri4:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304.5	50.0	122	2	T43589
2	302	49.6	122	2	D35392
3	276	45.3	121	2	B83432
4	83.5	13.7	353	2	S36249
5	76	12.5	761	2	S20458
6	74.5	12.2	275	2	E83412
7	74	12.2	355	2	T36273
8	73	12.0	369	2	B81039
9	73	12.0	403	2	B36151
10	72.5	11.9	429	2	JC4986
11	72.5	11.9	2218	2	B84883
12	72	11.8	491	2	E87270
13	71.5	11.7	186	2	B75590
14	71.5	11.7	986	2	AB2209
15	70	11.5	149	2	T03477
16	70	11.5	310	2	C95950
17	70	11.5	314	2	AC2878
18	70	11.5	325	2	E97654
19	70	11.5	489	2	F65125
20	70	11.5	9376	2	T14593
21	69	11.3	246	2	S39726
22	69	11.3	436	2	A75311
23	69	11.3	451	2	E90011
24	69	11.3	506	2	A99252
25	69	11.3	506	2	AC3034
26	69	11.3	563	2	S13786
27	69	11.3	820	2	T51186
28	68.5	11.2	302	2	B82036
29	68.5	11.2	420	2	AG0867

30	68.5	11.2	448	2	T01814
31	68.5	11.2	621	2	D72491
32	68.5	11.2	958	2	T51148
33	68.5	11.2	1449	2	A12017
34	68	11.2	196	2	D70637
35	68	11.2	267	2	H75396
36	68	11.2	338	2	C82590
37	68	11.2	487	1	S52261
38	68	11.2	556	2	T39383
39	68	11.2	851	2	AD0407
40	68	11.2	948	2	S75991
41	67.5	11.1	119	2	D87656
42	67.5	11.1	212	2	C83186
43	67.5	11.1	577	2	E75621
44	67.5	11.1	2471	2	T03820
45	67.5	11.1	5762	2	A41819

ALIGNMENTS

RESULT 1
T43589
hypothetical protein Y0045 - Yersinia pestis plasmid pCD1
C;Species: Yersinia pestis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43589; T42884
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubake
J. Bacteriol. 180, 5192-5202, 1998
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: 222578; MUID:98422474; PMID:9748454
A;Accession: T43589
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-122 <HUP>
A;Cross-references: UNIPROT:P61416; UNIPARC:UPI0000005173; EMBL:AF053946; NID:G2996222,
A;Experimental source: strain KIM
R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
Infect. Immun. 66, 4611-4623, 1998
A;Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia
A;Reference number: 222273; MUID:98427122; PMID:9746557
A;Accession: T42884
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-122 <PER>
A;Cross-references: UNIPARC:UPI0000005173; EMBL:AF074612; NID:G3822037; PIDN:AAC69795.1
A;Experimental source: strain KIMS
C;Genetics:
A;Genome: plasmid pCD1
A;Note: Y0045
C;Superfamily: Yersinia pestis hypothetical protein Y0045

Query Match	50.0%;	Score	304.5;	DB	2;	Length	122;
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Matches	66;	Conservative	19;	Mismatches	36;	Indels	1;
Gaps	1;						
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Db	1	MSRIITAPHIGIEKLSAISLEELSCGLPERYALPPDGHVPVEPHLERLYPTAQSKRSLWDF	60				
Qy	60	ATPDGRFHLLRPVDFNQAMQGRSVLAECQSPELRAAALLRQMHAEOLMONTLHLH	119				
Db	61	ASPGYTFHGLHRAQDYRRELDTLQSLTTSSSELQAAALLKCCQDDRLQLIILNLH	120				
Qy	120	KV	121				
Db	121	KV	122				

RESULT 2
D35392
hypothetical protein 3 - Yersinia enterocolitica
C;Species: Yersinia enterocolitica

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C/Accession: D35392
R/Vitonen, A.M.; Tolvanen, P.; Skurnik, M.
J. Bacteriol. 172, 3152-3162, 1990
A>Title: The lcrE gene is part of an operon in the lcr region of *Yersinia enterocolitica*
A/Reference number: A35392; MUID:90264308; PMID:2160939
A/Accession: D35392
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-122 <VII>
A/Cross-references: UNIPARC:UPI00001798AF; GB:M32097
C/Superfamily: *Yersinia pestis* hypothetical protein Y0045

Query Match 49.6%; Score 302; DB 2; Length 122;
Best Local Similarity 53.4%; Pred. No. 3.5e-23;
Matches 63; Conservative 19; Mismatches 36; Indels 0; Gaps 0;

QY 4 ITAAHIGIEOLSAISLDDQERSLPGRYALLPDGQSIETHISRLYPERLADRVLLDPATPD 63
DB 5 ITAPHIGIEKLSAISLEELSCGLPDRYALPDGHPVEPHLERLYPTAQSKRSLWDFASPG 64
QY 64 RGFHDLRLRPVDFNQAMQGLRSVLAEGSQSPELRAAALAEQMHAEQMLQMTLHLHKV 121
DB 65 YTFGLHRAQDYRRELTQLSLTTQSSELSQAAALAKCQDDDLQLLIHLHKV 122

RESULT 3
B83432
Conserved hypothetical protein in type III secretion PA1701 [imported] - *Pseudomonas aeruginosa*
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: B83432
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: B83432
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-121 <STO>
A/Cross-references: UNIPROT:O30534; UNIPARC:UPI00000D425B; GB:AE004597; NID:AE004091; NID:AE004091
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA1701
C/Superfamily: *Yersinia pestis* hypothetical protein Y0045

Query Match 45.3%; Score 276; DB 2; Length 121;
Best Local Similarity 47.9%; Pred. No. 1.4e-20;
Matches 58; Conservative 19; Mismatches 44; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEOLSAISLDDQERSLPGRYALLPDGQSIETHISRLYPERLADRVLLDFA 60
DB 1 MSRVGAWHIGIERLDLAHAEPFAPPVPERHLLAPDGRVPVETHVASLYPAQQAQQLFDYA 60
QY 61 TPDGRGHDLRLRPVDFNQAMQGLRSVLAEGSQSPELRAAALAEQMHAEQMLQMTLHLHK 120
DB 61 RPQLEPHGLLRPGDFQALRDRLALTLRPQALQAACLLGGERDEDERLLQALNLLHK 120
QY 121 V 121
DB 121 V 121

RESULT 4
S36249
lipB protein - *Pseudomonas glumae*
C/Species: *Pseudomonas glumae*
C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C/Accession: S36249
R/Frenken, L.G.O.; Bos, J.W.; Visser, C.; Mueller, W.; Tommassen, J.; Verrips, C.T.
Mol. Microbiol. 9, 579-589, 1993

A>Title: An accessory gene, lipB, required for the production of active *Pseudomonas glumae*
A/Reference number: S36248; MUID:94018652; PMID:8412704
A/Accession: S36249
A/Molecule type: DNA
A/Residues: 1-353 <PRE>
A/Cross-references: UNIPROT:Q05490; UNIPARC:UPI000002CA54; EMBL:X70354; NID:949205; PDB:1Y940
C/Genetics:
A/Gene: lipB
C/Keywords: transmembrane protein
F:19-40/Domain: transmembrane #status predicted <TMM>

Query Match 13.7%; Score 83.5; DB 2; Length 353;
Best Local Similarity 33.6%; Pred. No. 1;
Matches 36; Conservative 12; Mismatches 36; Indels 23; Gaps 5;

QY 21 DQERSLPGRYALLPDGQSIETHISRLYPERLADRVLLDPATPD-----DRGFHDLRL 71
DB 157 DALAQLPDGGAVL--GDKLDPAAQALQALDQRAALADRTLGWEAEPFGDEQRQRHDLR 214
QY 72 PVDFNQAMQGLRSVLAEGSQSPELRAA--AALAEQMHAEQMLQMTLH 116
DB 215 -----IRIANDTTLSPEQKARLAALDAQLTPDERAQAALH 251

RESULT 5
S20458
pqgF protein - *Klebsiella pneumoniae*
C/Species: *Klebsiella pneumoniae*
C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C/Accession: S20458
R/Meulenbergh, J.J.M.; Sellink, E.; Riegman, N.H.; Postma, P.W.
Mol. Gen. Genet. 232, 284-294, 1992
A>Title: Nucleotide sequence and structure of the *Klebsiella pneumoniae* pqg operon.
A/Reference number: S20452; MUID:92212293; PMID:1313537
A/Accession: S20458
A/Molecule type: DNA
A/Residues: 1-761 <MEU>
A/Cross-references: UNIPROT:P27508; UNIPARC:UPI0000132135; EMBL:X58778; NID:943903; PDB:1Y940
C/Genetics:
A/Gene: pqgF
C/Superfamily: pyrroloquinoline quinone synthesis F protein

Query Match 12.5%; Score 76; DB 2; Length 761;
Best Local Similarity 29.4%; Pred. No. 15;
Matches 32; Conservative 13; Mismatches 26; Indels 38; Gaps 6;

QY 33 LPDQSQI-----EP-HISRLYPE-----RLADR--VLLDFATPPRGFH 67
DB 612 LPDGASLAALRLAQHCEPLFQRLRVEQIQGVVYVSCRQYRVADRDGLLMALQSPDRRAG 671
QY 68 DLLR-----PVD---FNQAMQGLRSVLAEGSQSPELRAAALAEQ 103
DB 672 ELLRCGKDFLRQLAPMDEATFPLQORLAQAQIRASRPPEARALSALRQE 720

RESULT 6
E83412
streptomycin 3''-phosphotransferase PA1858 [imported] - *Pseudomonas aeruginosa* (strain: ATCC 27852)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: E83412
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: E83412
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-275 <STO>
A/Cross-references: UNIPROT:Q912N7; UNIPARC:UPI00000C54D6; GB:AE004612; NID:AE004091; NID:AE004091
A/Experimental source: strain PA01

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 95.0293 Seconds
(without alignments)
1177.815 Million cell updates/sec

Title: US-10-813-908A-3
Perfect score: 609
Sequence: 1 MSRTAAHIGIEQSAISLD.....EQMHADEQLMQMTLHLHKV 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	609	100.0	121	2	Q8GA93	aeromonas s
2	588	96.6	121	2	Q699R5	aeromonas h
3	585	96.1	121	2	Q5CCA2	aeromonas s
4	502	82.4	121	2	Q5XL09	aeromonas h
5	500	82.1	124	2	Q6TLM7	aeromonas h
6	381	62.6	121	2	Q7N0W6	photorhabd
7	370	60.8	121	2	Q84GZ0	photorhabd
8	305.5	50.2	122	1	YSCX_YEREN	P21208 yersinia en
9	304.5	50.0	122	1	YSCX_YERPE	P61416 yersinia pe
10	304.5	50.0	122	2	Q663K4	YERPS
11	276	45.3	121	2	Q30534	PSEAE
12	193	31.7	125	2	Q6QVR7	VIBHA
13	187	30.7	125	2	Q66P00	PASPI
14	180	29.6	126	2	Q67P34	VIBPA
15	112.5	18.5	125	2	Q2SC40	9GAMM
16	92.5	15.2	202	2	Q2J353	RHOA
17	90.5	14.9	722	2	Q4Q0R9	DESAC
18	84	13.8	464	2	Q6N0H8	RHOA
19	83.5	13.7	205	2	Q3IXR4	RHOS4
20	83.5	13.7	353	1	LIFO_BURGL	
21	83.5	13.7	3574	2	Q5Y9G5	9ACTO
22	83	13.6	1462	2	Q3XUH1	9PROT
23	83	13.6	10917	2	Q33NW6	9ACTO
24	82.5	13.5	338	2	Q2IYP4	RHOA
25	82	13.5	456	2	Q7WP97	BORBR
26	82	13.5	589	2	Q3UJY8	MOUSE
27	82	13.5	618	2	Q3UK73	MOUSE
28	82	13.5	673	2	Q80T90	MOUSE
29	82	13.5	1316	2	Q6PGE3	MOUSE
30	81.5	13.4	325	2	Q6N3W9	RHOA
31	81.5	13.4	363	2	Q6A7Z4	PROAC

32	81.5	13.4	369	2	Q37N29	RHOA
33	81.5	13.4	456	2	Q6NGZ6	CORDI
34	81	13.3	252	2	Q407D6	9RHO
35	80.5	13.2	133	2	Q2SH42	9GAMM
36	80	13.1	233	2	Q21IE2	9REOV
37	80	13.1	332	2	Q3AUD6	CHLCH
38	80	13.1	688	2	Q3RUE9	RALME
39	79.5	13.1	202	2	Q37BB5	RHOA
40	79	13.0	331	2	Q2JN45	9CYAN
41	78.5	12.9	246	2	Q7MK07	VIBVY
42	78.5	12.9	450	2	Q5FU22	GLUOX
43	78.5	12.9	501	2	Q47T70	THERFY
44	78.5	12.9	514	2	Q2NYY0	XANOR
45	78.5	12.9	533	2	Q7U464	SYNPX

ALIGNMENTS

RESULT 1
Q8GA93_AERSA
ID Q8GA93_AERSA PRELIMINARY; PRT; 121 AA.
AC Q8GA93;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE AscX protein.
GN Name=ascX;
OS Aeromonas salmonicida subsp. salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=JF2267;
RC MEDLINE=22262111; PubMed=12374830;
RX DOI=10.1128/JB.184.21.5966-5970.2002;
RA Burr S.E., Stuber K., Wahli T., Frey J.;
"Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida.";
J. Bacteriol. 184:5966-5970(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=JF2267;
RC Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;
"Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";
Microbiol. 151:2111-2118(2005).
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AJ458292; CAD30216.1; -; Genomic DNA.
DR EMBL; AJ616218; CAB83103.1; -; Genomic DNA.
DR InterPro; IPR012672; TRSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 121 AA; 13576 MW; 3016F377DA9080C CRC64;

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Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSRTAAHIGIEQSAISLDQDQSRSLPGRYALLPDGQSI	PHISRLRYPERLADRVLLDFA	60
Db	1	MSRTAAHIGIEQSAISLDQDQSRSLPGRYALLPDGQSI	PHISRLRYPERLADRVLLDFA	60
Qy	61	TPDRGFHDLRLRPVDFNQAMQGLSVLAEGQSP	ELRAAAALLENQWHADEQLMNTLHLHK	120
Db	61	TPDRGFHDLRLRPVDFNQAMQGLSVLAEGQSP	ELRAAAALLENQWHADEQLMNTLHLHK	120
Qy	121	V	121	
Db	121	V	121	

```

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CC -----
DR EMBL; AJ749609; CAG44553.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type III YscX; 1.
SQ SEQUENCE 121 AA; 13651 MW; 9EAF6B74CA9B7C91 CRC64;

Query Match 96.1%; Score 585; DB 2; Length 121;
Best Local Similarity 95.9%; Pred. No. 5.6e-48;
Matches 116; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPRLADRVLLDFA 60
DB 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPRLADRVLLDFA 60
QY 61 TPDGRFHDLRLRPVDFNQAMGRLSVLAEGQSPELRAAAALLEQMHAEQMLQMTLHLHK 120
DB 61 TPDGRFHDLRLRPVDFNQAMGRLSVLAEGQSPELRAAAALLEQMHAEQMLQMTLHLHK 120
QY 121 V 121
DB 121 V 121

RESULT 4
OSXL09_AERHY PRELIMINARY; PRT; 121 AA.
AC OSXL09;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DE 07-FEB-2006, entry version 7.
DE AscX.
GN Name=ascX;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]_NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RA PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RX Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
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CC -----
DR EMBL; AY763611; AAV30228.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type III YscX; 1.
SQ SEQUENCE 121 AA; 13874 MW; 5083CE413D09F7D8 CRC64;

Query Match 82.4%; Score 502; DB 2; Length 121;
Best Local Similarity 81.0%; Pred. No. 4.9e-40;
Matches 98; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPRLADRVLLDFA 60
DB 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPRLADRVLLDFA 60
QY 61 TPDGRFHDLRLRPVDFNQAMGRLSVLAEGQSPELRAAAALLEQMHAEQMLQMTLHLHK 120
DB 61 EPDRGFYDLRRPRDFSLAMQGLRVAVLMGQTAEKAAAGLLERMEHEQMLQMTLHLHK 120
QY 121 V 121
DB 121 V 121

RESULT 5
Q6TLM7_AERHY

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RESULT 2
Q699R5_AERHY PRELIMINARY; PRT; 121 AA.
AC Q699R5;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DE 07-FEB-2006, entry version 8.
DE AscX.
GN Name=ascX;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]_NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
DR EMBL; AY528667; AAS91814.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type III YscX; 1.
SQ SEQUENCE 121 AA; 13635 MW; A136E074CA84665B CRC64;

Query Match 96.6%; Score 588; DB 2; Length 121;
Best Local Similarity 96.7%; Pred. No. 2.9e-48;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPRLADRVLLDFA 60
DB 1 MSRTAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPRLADRVLLDFA 60
QY 61 TPDGRFHDLRLRPVDFNQAMGRLSVLAEGQSPELRAAAALLEQMHAEQMLQMTLHLHK 120
DB 61 TPDGRFHDLRLRPVDFNQAMGRLSVLAEGQSPELRAAAALLEQMHAEQMLQMTLHLHK 120
QY 121 V 121
DB 121 V 121

RESULT 3
Q5CCA2_AERSO PRELIMINARY; PRT; 121 AA.
AC Q5CCA2;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE AscX protein.
GN Name=ascX;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]_NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca
RT fluviatilis.";
RL J. Fish Dis. 28:141-150(2005).
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ID Q6TLM7_AERHY PRELIMINARY; PRT; 124 AA.
AC Q6TLM7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE AscX.
GN Name=ascX;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
RT pathogenesis.";
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
DR EMBL: AY394563; AAR26334.1; -; Genomic_DNA.
DR InterPro: IPR012672; TTSS_YscX.
DR TIGRFAMs: TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 124 AA; 13979 MW; ECC3860471D7FBCE CRC64;

Query Match 82.1%; Score 500; DB 2; Length 124;
Best Local Similarity 81.0%; Pred. No. 7.9e-40;
Matches 98; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIPIHISRLYPERLADRVLLDFA 60
Db 4 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIPIHISRLYPERLADRVLLDFA 63

Qy 61 TPDGRGHDLRLPVDNFQMGRLSVLAEGQSPERAAALAEQMHADQLMOMTLHLHK 120
Db 64 APAHGFDLLRPDFTLMAQGLRLLKEGGTDELMAASVLLQEMHEDQLMOMTLHLHK 123

Qy 121 V 121
Db 124 V 124

RESULT 6
Q7NOW6_PHOLL PRELIMINARY; PRT; 121 AA.
AC Q7NOW6;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Type III secretion protein SctX.
GN Name=SctX; OrderedLocusNames=plu3763;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbr886;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Bouraux-Eude C., Chaudler M., Charles J.-F.,
RA Dassa E., Detose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
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CC -----
DR EMBL: BX571871; CAE16135.1; -; Genomic_DNA.
DR Photolabist; plu3763; -;
DR BioCyc: PLUM243265:PLU3763-MONOMER; -;
DR InterPro: IPR012672; TTSS_YscX.
DR TIGRFAMs: TIGR02502; type_III_YscX; 1.
KW Complete proteome.
SQ SEQUENCE 121 AA; 13453 MW; E13DEE33DE590A48 CRC64;

Query Match 62.6%; Score 381; DB 2; Length 121;
Best Local Similarity 62.8%; Pred. No. 1.9e-28;
Matches 76; Conservative 16; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIPIHISRLYPERLADRVLLDFA 60
Db 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSVETHAARLYPANKADQALLAFA 60

Qy 61 TPDGRGHDLRLPVDNFQMGRLSVLAEGQSPERAAALAEQMHADQLMOMTLHLHK 120
Db 61 CPDQGFHALLRPDHFQAVSGLRTILQOGNDIRVQHAVSLLENMNDQEQLLQMALHLHK 120

Qy 121 V 121
Db 121 V 121

RESULT 7
Q84GZ0_PHOLU PRELIMINARY; PRT; 121 AA.
ID Q84GZ0;
AC Q84GZ0;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE LesB.
GN Name=LesB;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
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CC -----
DR EMBL: AY144116; AAO18048.1; -; Genomic_DNA.
DR InterPro: IPR012672; TTSS_YscX.
DR TIGRFAMs: TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 121 AA; 13472 MW; CEE63BE1ED0E3802 CRC64;

Query Match 60.8%; Score 370; DB 2; Length 121;
Best Local Similarity 61.2%; Pred. No. 2.1e-27;
Matches 74; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIPIHISRLYPERLADRVLLDFA 60
Db 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSVETHAARLYPANKADQALLAFA 60

Qy 61 TPDGRGHDLRLPVDNFQMGRLSVLAEGQSPERAAALAEQMHADQLMOMTLHLHK 120
Db 61 CPDQGFHALLRPDHFQAVSGLRTILQOGNDIRVQHAVSLLENMNDQEQLLQMALHLHK 120

Qy 121 V 121
Db 121 V 121

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RESULT 8
YSCX_YEREN STANDARD; PRT; 122 AA.
AC P21208; O68696;
DT 01-MAY-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1991, sequence version 1.
DT 07-FEB-2006, entry version 30.
DE Yop proteins translocation protein X.
GN Names: yscX;
OS Versinia enterocolitica.
OG Plasmid pYV, Plasmid pYve227, Plasmid pYve8081, and
OG Plasmid pYval27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND INDUCTION.
RC STRAIN=Serotype O:3; PLASMID=pYV;
RA MEDLINE=90264308; PubMed=2160939;
RX Viitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrE gene is part of an operon in the lcr region of Versinia
RT enterocolitica O:3";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pYve227;
RA Iriarte M., Lambert M., Kerbouch C., Cornells G.R.;
RT "Detailed genetic map of the pYve227 plasmid of Versinia
RT enterocolitica serotype O:9";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYve8081;
RX MEDLINE=21295118; PubMed=11402007;
RX DOI=10.1128/IAI.69.7.4627-4638.2001;
RX Shellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Versinia enterocolitica serotype O:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYval27/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foulciet B., Cornells G.R.;
RT "DNA sequence and analysis of the pYval27/90 virulence plasmid of
RT Versinia enterocolitica strain A127/90.";
RL Res. Microbiol. 154:553-557(2003).
RN [5]
RP FUNCTION.
RC PLASMID=pYV;
RX MEDLINE=99102336; PubMed=9882687;
RA Iriarte M., Cornells G.R.;
RT "Identification of SYN, yscX, and yscY, three new elements of the
RT Versinia Yop virulon.";
RL J. Bacteriol. 181:675-680(1999).
CC -!- FUNCTION: Required for Yop secretion.
CC -!- SUBUNIT: Interacts with yscY (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted via the type III secretion system
CC (By similarity).
CC -!- INDUCTION: Temperature seems to play the major role in regulation
CC of transcription of the lcrE-containing operon of pYV, whereas
CC Ca(2+) concentration has only a moderate effect at 37 degrees
CC Celsius, and no effect at room temperature.
CC -!- DOMAIN: The region between residues 50 and 110, which contains the
CC predicted coiled coil domain, is essential for interaction with
CC yscY (By similarity).
CC -!- MISCELLANEOUS: May possess both an mRNA signal and a ysc-dependent
CC signal capable of directing its export through the type III
CC secretion system (By similarity).
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CC -----
DR EMBL; M32097; -; NOT ANNOTATED CDS; Genomic_DNA.
DR EMBL; AF102990; AD15820.1; -; Genomic_DNA.
DR EMBL; AF336309; AAK69218.1; -; Genomic_DNA.
DR EMBL; AY150843; AAN37521.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
KW Coiled coil; Plasmid.
FT CHAIN 1 122 Yop proteins translocation protein X.
FT /FTID=PRO_0000086499.
FT COILED 71 87 Potential.
FT VARIANT 29 29 D -> E (in plasmid pYve8081 and plasmid
FT pYval27/90).
SQ SEQUENCE 122 AA; 13742 MW; 050F5E2D6909BB00 CRC64;
Query Match 50.2%; Score 305.5; DB 1; Length 122;
Best Local Similarity 54.1%; Pred. No. 3.2e-21;
Matches 66; Conservative 19; Mismatches 36; Indels 1; Gaps 1;
QY 1 MSR-ITAAHIGTEQLSALSDDOERSLPGRYALLPDQSIPIHSLYPERLADRVLLDF 59
Db 1 MSRIITAPHIGIEKLSAISLELSCLPDRYALPPDCHPVEPHERLYPTAQSKRSLWDF 60
QY 60 ATPDGRFHDLRPVDFNQAGLSRVLAEGSQSPELRAAAALQEHMADQLQMQLHLH 119
Db 61 ASPGYTFHGLHRAQDYRRELTQLSLTTTSQSSELQAAALCKQDDRLQLILNLLH 120
QY 120 KV 121
Db 121 KV 122
RESULT 9
YSCX_YERPE STANDARD; PRT; 122 AA.
AC P61416; O68696;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DT 07-MAR-2006, entry version 17.
DE Yop proteins translocation protein X.
GN Name=yscX; Ordered locus names=YPCD1.36c, y5042, y0045, pCD47;
OS Versinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RT Versinia pestis KIM5.";
RN Infect. Immun. 66:4611-4623(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCreedy P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Versinia
RT pestis.";
RL J. Bacteriol. 180:5192-5202(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,
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RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-O.T., Ewin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.B., Coulter D.H., Folger K.K., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer S.N., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Brome J.E., Edqvist P.J., Carlsson K.E., Forberg A., Francis M.S.;
RT "Mapping of a YecY Binding Domain within the LcrH Chapterone That Is
RT Required for Regulation of Yersinia Type III Secretion.";
RL J. Bacteriol. 187:7738-7752(2005).
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CC -----
CC EMBL; AF010150; AAC45942.1; -; Genomic_DNA.
DR EMBL; AE004597; AAG05090.1; -; Genomic_DNA.
DR EMBL; DQ000666; AAY17109.1; -; Genomic_DNA.
DR PIR; B83432; B83432.
DR BioCyc; PAER287; PA1701-MONOMER; -.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
KW Complete proteome.
SQ SEQUENCE 121 AA; 13722 MW; 91EFP2450DEC87B6 CRC64;

Query Match 45.3%; Score 276; DB 2; Length 121;
Best Local Similarity 47.9%; Pred. No. 2.1e-18;
Matches 58; Conservative 19; Mismatches 44; Indels 0; Gaps 0;

QY 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIPTSPHISRLYPERLADRVLLDFA 60
Db 1 MSRVGAHWIGIERLDLAHAFPAFAPPLPERHLLAPDGRPVETHVASLYPAQAQQLFDYA 60

QY 61 TPDGRGHDLRLPVDNFQAMQGLRSVLAEQSPPELRAAAALLEGQMHAEQMLMQLTLH 120
Db 61 RPQLEFGLRLPGDFRQALRDRLALTLPRQALQAACLLGRDEDERLLQALNLLHK 120

QY 121 V 121
Db 121 V 121

RESULT 12
Q6QVR7 VIBHA PRELIMINARY; PRT; 125 AA.
AC Q6QVR7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE VscX.
GN Names=vscX;
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Basler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AY524044; AAS13314.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.

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SQ SEQUENCE 125 AA; 14484 MW; F48F6AD8560AA8F2 CRC64;

Query Match 31.7%; Score 193; DB 2; Length 125;
Best Local Similarity 36.0%; Pred. No. 2e-10;
Matches 45; Conservative 23; Mismatches 53; Indels 4; Gaps 1;

QY 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIPTSPHISRLYPERLADRVLLDFA 60
Db 1 MSRTSLNVGIEGFTHVSLQEVNDFPQRFQQLPDGQAIAATHLEKLYELRPSQYLMSLA 60

QY 61 TPDGRGHDLRLPVDNFQAMQGLRSVLAEQSPPELRAAAALLEGQMHAEQMLMQLTLH 116
Db 61 KPKLTRSELLRPDKYRQQFDTTQORLREVAQKNGSHALNQALETLQSTQDQRYLTMALN 120

QY 117 LLHKV 121
Db 121 LLIQV 125

RESULT 13
Q66PU0 PASPI PRELIMINARY; PRT; 125 AA.
AC Q66PU0;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative TTSS protein X.
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
RT "Photobacterium damsela subsp. piscicida encodes a functional type
RT three secretion system (TTSS) that is involved in pathogenesis.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AY647223; AAU11476.1; -; Genomic_DNA.
DR InterPro; IPR012672; TTSS_YscX.
DR TIGRFAMs; TIGR02502; type_III_YscX; 1.
SQ SEQUENCE 125 AA; 14447 MW; 0671D3457BD3860E CRC64;

Query Match 30.7%; Score 187; DB 2; Length 125;
Best Local Similarity 35.2%; Pred. No. 7.3e-10;
Matches 44; Conservative 24; Mismatches 53; Indels 4; Gaps 1;

QY 1 MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGQSIPTSPHISRLYPERLADRVLLDFA 60
Db 1 MSRTSLNVGIEGFTHVSLQEVNDFPQRFQQLPDGQAIAATHLEKLYELRPSQYLMSLA 60

QY 61 TPDGRGHDLRLPVDNFQAMQGLRSVLAEQSPPELRAAAALLEGQMHAEQMLMQLTLH 116
Db 61 RKPLTHLELLRPDKYRQQFDTTQORLQELAQKNGSHALNQALETLQSTQDQRYLTMALN 120

QY 117 LLHKV 121
Db 121 LLIQV 125

RESULT 14
Q87P54 VIBPA PRELIMINARY; PRT; 126 AA.
AC Q87P54;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Putative type III secretion protein.
GN OrderedLocusNames=vPI664;
OS Vibrio parahaemolyticus.

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RIWD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -----
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CC -----
CC
CC EMBL: BA000031; BAC59927.1; -; Genomic_DNA.
DR InterPro: IPR012672; TTSS_YscX.
DR TIGRFAMs: TIGR02502; type_III_YscX; 1.
KW Complete proteome.
SQ SEQUENCE 126 AA; 14280 MW; 3B43397A945C2A48 CRC64;

Query Match          29.6%; Score 180; DB 2; Length 126;
Best Local Similarity 32.0%; Pred. No. 3.5e-09;
Matches 40; Conservative 28; Mismatches 53; Indels 4; Gaps 1;

Qy 1 MSRTAAHIGIEQLSALDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA 60
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 2 MTRVSTLNVGIEATFVSHGEVDTFPKRFQLLPDGGAVATHLEKLYDLRPSDQYLLALA 61
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 61 TPDRGFHDLRLP-----VDFNQMOGLRSVLAEQSPELRAAAALLEGQHADEQLM 116
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 62 KPLNHGCELLRPEKYRQQFDNTLARVQQLAEGSGSANLAKAAETLQSTOLDQRYLTW 121
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 117 LLHKV 121
   ||::|
Db 122 LLIQV 126

RESULT 15
Q2SC40_9GAMM
ID Q2SC40_9GAMM PRELIMINARY; PRT; 125 AA.
AC Q2SC40;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=HCH_05103;
OS Haella chejuensis KCTC 2396.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales;
OC Haellaceae; Haella.
OX NCBI_TaxID=349521;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KCTC 2396;
RX PubMed=16352867; DOI=10.1093/nar/gk11016;
RA Jeong H., Yim J.H., Lee C., Choi S.-H., Park Y.K., Yoon S.H.,
RA Hur C.-G., Kang H.-Y., Kim D., Lee H.H., Park K.H., Park S.-H.,
RA Park H.-S., Lee H.K., Oh T.K., Kim J.F.;
RT "Genomic blueprint of Haella chejuensis, a marine microbe producing
RT an algicidal agent.";
RL Nucleic Acids Res. 33:7066-7073(2005).
CC -----
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CC -----
CC
CC EMBL: CP000155; ABC31784.1; -; Genomic_DNA.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 125 AA; 14381 MW; B1669B9084FEDF9E CRC64;

Query Match          18.5%; Score 112.5; DB 2; Length 125;
Best Local Similarity 35.3%; Pred. No. 0.0099;
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Matches 36; Conservative 13; Mismatches 48; Indels 5; Gaps 3;
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   ||::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 10 IEGLSLYNAAD-ERQLPSRKKTTPAGQGVVSHLRQLYSKGEESLLESFIKPRVSSSLL 68
   ||::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 71 RPYDFNQ---AMOGLRSVLAEQSPELRAAAALLEGQHADEQ 109
   ||::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 69 SPVDFERQYGEVRGLFQKLAQ-QSPEDRELFSKAETLRDQ 109
   ||::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Search completed: June 16, 2006, 19:23:05
Job time : 97.0293 secs
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 22.3309 Seconds
(without alignments)
474.285 Million cell updates/sec

Title: US-10-813-908A-3
Perfect score: 609
Sequence: 1 MSRTAAHIGIEQLSAISLD.....EQMHADEQLMQMTLLHLHKV 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	266	43.7	262	2	US-09-252-991A-30169
2	83.5	13.7	353	1	US-08-034-650-11
3	83.5	13.7	353	1	US-08-449-015-11
4	78.5	12.9	4928	2	US-09-036-987A-5
5	78.5	12.9	4928	2	US-09-370-700-5
6	78.5	12.9	4928	2	US-09-603-207-5
7	78.5	12.9	4928	3	US-10-329-148A-5
8	78	12.8	294	2	US-09-716-964B-23
9	76	12.5	810	2	US-09-489-039A-9748
10	74.5	12.2	602	2	US-09-252-991A-30458
11	73.5	12.1	429	2	US-09-252-991A-30376
12	73.5	12.1	513	2	US-09-833-745-50
13	72	11.8	2216	2	US-09-902-540-12221
14	71	11.7	293	2	US-09-252-991A-19896
15	71	11.7	386	2	US-09-270-767-42532
16	71	11.7	457	2	US-09-605-703B-2586
17	70.5	11.6	1651	2	US-09-252-991A-31384
18	70.5	11.6	1651	2	US-09-543-681A-6604
19	69.5	11.4	235	2	US-09-489-039A-13178
20	69.5	11.4	502	2	US-09-489-039A-10638
21	69.5	11.4	574	2	US-09-605-703B-2288
22	69.5	11.4	927	2	US-09-252-991A-20340
23	69	11.3	233	2	US-09-489-039A-10313
24	69	11.3	273	2	US-10-104-047-2397
25	69	11.3	370	2	US-09-489-039A-8211
26	69	11.3	452	2	US-09-925-637-16

27	69	11.3	485	2	US-09-252-991A-24868	Sequence 24868, A
28	69	11.3	748	1	US-08-997-080-154	Sequence 154, App
29	69	11.3	748	1	US-08-997-362-154	Sequence 154, App
30	69	11.3	748	2	US-09-095-855-154	Sequence 154, App
31	69	11.3	748	2	US-09-324-542-154	Sequence 154, App
32	69	11.3	748	2	US-09-205-426-154	Sequence 154, App
33	68.5	11.2	700	2	US-09-252-991A-29072	Sequence 29072, A
34	68.5	11.2	2560	2	US-09-949-016-11554	Sequence 11554, A
35	68	11.2	1147	2	US-09-902-540-13965	Sequence 13965, A
36	67.5	11.1	255	2	US-09-252-991A-17010	Sequence 17010, A
37	67.5	11.1	275	2	US-09-036-987A-7	Sequence 7, Appli
38	67.5	11.1	275	2	US-09-370-700-7	Sequence 7, Appli
39	67.5	11.1	275	2	US-09-603-207-7	Sequence 7, Appli
40	67.5	11.1	275	3	US-10-329-148A-7	Sequence 7, Appli
41	67.5	11.1	291	2	US-09-489-039A-13316	Sequence 13316, A
42	67.5	11.1	544	2	US-09-252-991A-19064	Sequence 19064, A
43	67.5	11.1	612	2	US-09-902-540-13545	Sequence 13545, A
44	67.5	11.1	684	2	US-09-605-703B-654	Sequence 654, App
45	67.5	11.1	684	2	US-09-605-703B-656	Sequence 656, App

ALIGNMENTS

RESULT 1
US-09-252-991A-30169
; Sequence 30169, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30169
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30169

Query Match	43.7%	Score 266;	DB 2;	Length 262;
Best Local Similarity	46.3%	Pred. No. 1.3e-21;		
Matches	56;	Conservative	20;	Mismatches 45; Indels 0; Gaps 0;
Qy	1	MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA	60	
Db	142	MSRVGAHWIGIERLDLAHAEPFPAPPLPERHLLAPDGRPVETHVASLYPAQQAQQLFDYA	201	
Qy	61	TPDRGFHLLRPVDFNQMOGLRSVLAEQSPELRAAAALLEGQMHAEQMLHLLHK	120	
Db	202	RPQLEFGLLRPGDFRQALRDLRLATLPQPALQAACLLGERDEQRLIQMAPNLHKK	261	
Qy	121	V 121		
Db	262	V 262		
RESULT 2				
		US-08-034-650-11		
		; Sequence 11, Application US/08034650		
		; Patent No. 5641671		
		; GENERAL INFORMATION:		
		; APPLICANT: BOS, Jannetje W.		
		; APPLICANT: FRENKEN, Leon G.		
		; APPLICANT: VEREIPS, Cornelis T.		
		; APPLICANT: VISSER, Christiaan		
		; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE		

;; TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS

;; NUMBER OF SEQUENCES: 13

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

;; STREET: 1615 L. Street, N.W.

;; CITY: Washington

;; STATE: D.C.

;; COUNTRY: USA

;; ZIP: 20036-5601

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/034,650

;; FILING DATE:

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/727,235

;; FILING DATE: 03-JUL-1991

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Kokulis, Paul N.

;; REGISTRATION NUMBER: 16,773

;; REFERENCE/DOCKET NUMBER: PNK/5970/91731

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202) 861-3000

;; TELEFAX: (202) 822-0944

;; TELEX: 6714627 CUSH

;; INFORMATION FOR SEQ ID NO: 11:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 353 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-034-650-11

Query Match 13.7%; Score 83.5; DB 1; Length 353;

Best Local Similarity 33.6%; Pred. No. 0.46; Mismatches 36; Conservative 12; Indels 23; Gaps 5;

QY 21 DQERSLPGRYALLPDGQSIPEPHISRLYPER---LADRVLLDFATP-----DRGFHDLRL 71

Db 157 DALAQLPGDGAVL--GDKLDPAAQMLADQRAALADRTLGEWAEPFFGDEQRQRHDLR 214

QY 72 PVDNFQAMQGLRSVLAEGOSPELRAA--RALLEQMHADQLMQMTLH 116

Db 215 -----IRIANDTTLSPEQKAARLAALDAQLTPDERAQQAAALH 251

RESULT 3

US-08-449-015-11

;; Sequence 11, Application US/08449015

;; Patent No. 5804409

;; GENERAL INFORMATION:

;; APPLICANT: BOS, Jannette W.

;; APPLICANT: FRENKEN, Leon G.

;; APPLICANT: VERIPS, Cornelis T.

;; APPLICANT: VISSER, Christiaan

;; TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE

;; NUMBER OF SEQUENCES: 13

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

;; STREET: 1615 L. Street, N.W.

;; STATE: D.C.

;; COUNTRY: USA

;; ZIP: 20036-5601

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/449,015

;; FILING DATE: 24-MAY-1995

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 07/727,235

;; FILING DATE: 03-JUL-1991

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Kokulis, Paul N.

;; REGISTRATION NUMBER: 16,773

;; REFERENCE/DOCKET NUMBER: PNK/5970/91731

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202) 861-3000

;; TELEFAX: (202) 822-0944

;; TELEX: 6714627 CUSH

;; INFORMATION FOR SEQ ID NO: 11:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 353 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-449-015-11

Query Match 13.7%; Score 83.5; DB 1; Length 353;

Best Local Similarity 33.6%; Pred. No. 0.46; Mismatches 36; Conservative 12; Indels 23; Gaps 5;

QY 21 DQERSLPGRYALLPDGQSIPEPHISRLYPER---LADRVLLDFATP-----DRGFHDLRL 71

Db 157 DALAQLPGDGAVL--GDKLDPAAQMLADQRAALADRTLGEWAEPFFGDEQRQRHDLR 214

QY 72 PVDNFQAMQGLRSVLAEGOSPELRAA--RALLEQMHADQLMQMTLH 116

Db 215 -----IRIANDTTLSPEQKAARLAALDAQLTPDERAQQAAALH 251

RESULT 4

US-09-036-987A-5

;; Sequence 5, Application US/09036987A

;; Patent No. 6143526

;; GENERAL INFORMATION:

;; APPLICANT: Baltz, Richard H.

;; APPLICANT: Broughton, Mary C.

;; APPLICANT: Crawford, Kathryn P.

;; APPLICANT: Madduri, Krishnamurthy

;; APPLICANT: Merlo, Donald J.

;; APPLICANT: Treadway, Patti J.

;; APPLICANT: Turner, Jan R.

;; APPLICANT: Waldrton, Clive

;; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

;; NUMBER OF SEQUENCES: 39

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Dow Agrosciences LLC Patent Department

;; STREET: 9330 Zionsville Road

;; CITY: Indianapolis

;; STATE: Indiana

;; COUNTRY: USA

;; ZIP: 46268

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/036,987A

;; FILING DATE: 09-MAR-1998

;; CLASSIFICATION: 435

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Stuart, Donald R.

;; REGISTRATION NUMBER: 28,479

;; REFERENCE/DOCKET NUMBER: 50,608

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4928 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-036-987A-5

Query Match      12.9%; Score 78.5; DB 2; Length 4928;
Best Local Similarity 27.5%; Pred. No. 61;
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;

Qy 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64
Db 4799 TFAELGFDSLTAVELNRNLNAVGTG--LRLPPTLVFDHPTPLALSEQLVPAIV---AEPDN 4853

Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMA 106
Db 4854 GIESLLAELD-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

RESULT 5
US-09-370-700-5
; Sequence 5, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 Div1
; CURRENT APPLICATION NUMBER: US/09/370,700
; EARLIER FILING DATE: 1998-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4928
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-5

Query Match      12.9%; Score 78.5; DB 2; Length 4928;
Best Local Similarity 27.5%; Pred. No. 61;
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;

Qy 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64
Db 4799 TFAELGFDSLTAVELNRNLNAVGTG--LRLPPTLVFDHPTPLALSEQLVPAIV---AEPDN 4853

Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMA 106
Db 4854 GIESLLAELD-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

RESULT 6
US-09-603-207-5
; Sequence 5, Application US/09603207B
; Patent No. 6521406
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4928 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-036-987A-5

Query Match      12.9%; Score 78.5; DB 2; Length 4928;
Best Local Similarity 27.5%; Pred. No. 61;
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;

Qy 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64
Db 4799 TFAELGFDSLTAVELNRNLNAVGTG--LRLPPTLVFDHPTPLALSEQLVPAIV---AEPDN 4853

Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMA 106
Db 4854 GIESLLAELD-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

RESULT 7
US-10-329-148A-5
; Sequence 5, Application US/10329148A
; Patent No. 7015001
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 Div1
; CURRENT APPLICATION NUMBER: US/10/329,148A
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/603,207B
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/370,700
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4928
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-10-329-148A-5

Query Match      12.9%; Score 78.5; DB 3; Length 4928;
Best Local Similarity 27.5%; Pred. No. 61;
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;

Qy 5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64
Db 4799 TFAELGFDSLTAVELNRNLNAVGTG--LRLPPTLVFDHPTPLALSEQLVPAIV---AEPDN 4853

Qy 65 GFHDLLRPVDFNQAMQGLRSVLAEQSQPELRAAAALAEQMA 106
Db 4854 GIESLLAELD-----RLDTTLAQGPSIPLEDQAKVAERLHA 4889

RESULT 8
US-09-716-964B-23
; Sequence 23, Application US/09716964B
```

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; Patent No. 6897053
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yuriyeva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/09/716,964B
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-716-964B-23

Query Match      12.8%; Score 78; DB 2; Length 294;
Best Local Similarity 29.0%; Pred. No. 1.5;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

QY 5 TAAGHIEQSALSDOERSLGRYALLPDGQSIAPHISRLYPERLADRVLLDFATPDR 64
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 208 SAAGGMR--DAUSLDQATSFSGDILKVEDALLITGAVSOLYIGKLA-----K 254

QY 65 GFHDLRPPVDFNQAGLSRVLAEGQSPELRAAAALLEQM 104
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 SLHD-----KNVSDALETINELLOQGRDP-----AKLIEDM 285
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RESULT 9
US-09-489-039A-9748
; Sequence 9748, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9748
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9748

Query Match      12.5%; Score 76; DB 2; Length 810;
Best Local Similarity 29.4%; Pred. No. 9.8;
Matches 32; Conservative 13; Mismatches 26; Indels 38; Gaps 6;

QY 33 LPDQSQI-----EP-HISRLYPE-----RLADR--VLLDFATPDRGFH 67
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 LPDGASLAALRLAQHCEFFQRLRVEQQIGYVWSCRYQRVADRDLGMLALQSPDRAG 720

QY 68 DLLR-----PVD---FNOAGQLRSVLAEGQSPELRAAAALLEQ 103
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 721 ELLRCGKDFURQAPMDEATFRPLQRLAAQIRASRPPEARALSALRQE 769
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```
RESULT 10
US-09-252-991A-30458
; Sequence 30458, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30458
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30458

Query Match      12.2%; Score 74.5; DB 2; Length 602;
Best Local Similarity 33.0%; Pred. No. 9.6;
Matches 29; Conservative 9; Mismatches 37; Indels 13; Gaps 3;

QY 29 RYALLPDGQSIAPHISRLYPER---LADRVLLDFATPDRGFHDLRPPVDFNQAGLSRV 85
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 RWALPDGPEFPFATHSRLLPVRHGAAMLKISSAEERFGHVLLNWD---GQGAARV 360

QY 86 LAEGQSPELRAAAALLEQMHADQLMQM 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 LAYDHO-----ALLMERATGGRSLLEM 382
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RESULT 11
US-09-252-991A-30376
; Sequence 30376, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30376
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30376

Query Match      12.1%; Score 73.5; DB 2; Length 429;
Best Local Similarity 27.2%; Pred. No. 7.8;
Matches 37; Conservative 11; Mismatches 41; Indels 47; Gaps 7;

QY 13 QLSAISLDQOERSLPGRYALLPDGQSIAPHISRLYPERLADRVLLDFATPDR-----64
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 QFPALRDLDSRR--PQRHLPADPLGLQLRHAQPLHPER-----HQPDRHRRFPVPR 100

QY 65 -----GFHDLRPPVDFNQAMQ-----GLRSVLAEGQSPEL-----RAAALLEQ 103
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 101 SQRAERTIDCGHRPVRPVRRTSLQWPDRERGIRG-----KPQLGGIQPAAGSALPR 154

QY 104 MHADEQLMQMTLHLH 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 155 ROADHR-QRRGLFLSH 169
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RESULT 12

US-09-833-745-50
; Sequence 50, Application US/09833745
; Patent No. 6939541

; GENERAL INFORMATION:
; APPLICANT: ROBERTS, JOSEPH

; APPLICANT: SETHURAMAN, NATARAJAN
; APPLICANT: MACALLISTER, THOMAS

; TITLE OF INVENTION: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF

; TITLE OF INVENTION: BIOACTIVE HISTIDINE AMMONIA LYASE

; FILE REFERENCE: 078728/0106

; CURRENT APPLICATION NUMBER: US/09/833,745

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 60/197,770

; PRIOR FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 50

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Vibrio cholerae

US-09-833-745-50

Query Match 12.1%; Score 73.5; DB 2; Length 513;

Best Local Similarity 26.0%; Pred. No. 10;

Matches 33; Conservative 17; Mismatches 44; Indels 33; Gaps 5;

QY 11 IEQLSALSLDDQERSL--PCRYALLPDGQSIPIHISRLYPERLADRVLLDFATPDGRGPHD 68

DB 389 IAGVTAALASENKTLAHPASVDSLPTSANQEDHVSMM---ATPAARLRDMGENTRG--- 442

QY 69 LRPVDFNQMOGL-----RSVLAEGQ-----SPELRAAAALAEQM 104

DB 443 -ILAVEYLAQAQGLDFRAPLKSSPRIETEARQILREKVPFYDKRYFAPDIERKANALLAQ 501

QY 105 HADEQLM 111

DB 502 AVHNRLM 508

RESULT 13

US-09-902-540-12221

; Sequence 1221, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 12221

; LENGTH: 2216

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-12221

Query Match 11.8%; Score 72; DB 2; Length 2216;

Best Local Similarity 24.7%; Pred. No. 1.1e+02;

Matches 43; Conservative 21; Mismatches 48; Indels 62; Gaps 9;

QY 5 TTAHIGIE--QLSALSLDDQERSLPGRYALLPDG-----QSIPIHISRLYPERLAD- 53

DB 520 SAPSAGIEPKSVDAEVDSEGIWVSLGICILPGGAKDPETYQWIRKIGSIGVQGLLP 579

QY 54 RVLLDFA----TPDRGF-----HDLIRPVDF-----NQAMOG 81

DB 580 ELVTDFAAGPAGTPDRTYTLTGTGYVRDEDLVPPGDPTRFQQYVREQKLLAIALSQAMQG 639

QY 82 LRSV-----LAEGOSPELRAAAALAEOMHADEQLMOWMTLHLLHKV 121

DB 640 LKPVASKTPGRTQCILGSGTAEG-SABYDAALS-----VEAGEALLSARGERVHDI 688

RESULT 14

US-09-252-991A-19896

; Sequence 19896, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 19896

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19896

Query Match 11.7%; Score 71; DB 2; Length 293;

Best Local Similarity 28.7%; Pred. No. 8.8;

Matches 33; Conservative 13; Mismatches 31; Indels 38; Gaps 7;

QY 11 IEQLSALSLDDQERSLPGRYALLPDGQSIPIHISRLYP-----ERLAD-----RVL 56

DB 14 VVQSGPASTDRGRQMP-RFA-----ANLSMLYPRHDFLERFAAAADGFEVYL 63

QY 57 LDFATP-----DRGFHDL-----RPVDFNQAMQGLRSVLAEQOSPRLAAAA 99

DB 64 PFYAVPAELKARLDDHGLRQMLFNAAAPGDWKGKGLASL--PGREAEFRRAIA 116

RESULT 15

US-09-270-767-42532

; Sequence 42532, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 42532

; LENGTH: 386

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-42532

Query Match 11.7%; Score 71; DB 2; Length 386;

Best Local Similarity 31.0%; Pred. No. 13;

Matches 26; Conservative 9; Mismatches 29; Indels 20; Gaps 4;

QY 46 LYPERLADRVLLDFAT-PDRGFHDLRLRPVDFNQ-----AMQGLRSVLAEQOSPRLA 96

DB 110 LFPSPNF---VTADLSVDPER-----LDINQOHKSAAGQRELDLSVAALQOKTEAAA 158

QY 97 AAALAEQMHAEQMLMOWMTLHLLHK 120

DB 159 AAAAAQPVEIDSKIDRLHLLHLE 182

Search completed: June 16, 2006, 19:29:00
Job time : 23.3309 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 67.6813 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-3
Perfect score: 609
Sequence: 1 MSRTAAHIGIEQLSAISLD.....EQMHADEQLMONTLLHLHKV 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	121	5	US-10-813-908-3
2	88.5	14.5	259	6	US-11-075-185-24
3	83	13.6	10917	5	US-10-732-923-20606
4	81.5	13.4	452	4	US-10-282-122A-53766
5	80	13.1	1108	4	US-10-425-115-223719
6	80	13.1	1132	4	US-10-425-114-62671
7	78.5	12.9	4928	4	US-10-329-148A-5
8	78	12.8	294	4	US-10-671-403-23
9	78	12.8	294	4	US-10-671-419-23
10	78	12.8	294	4	US-10-670-844-23
11	78	12.8	294	4	US-10-671-134-23
12	78	12.8	294	4	US-10-673-098-23
13	78	12.8	294	4	US-10-672-638-23
14	78	12.8	294	4	US-10-673-127-23
15	78	12.8	294	4	US-10-670-817-23
16	78	12.8	294	4	US-10-671-119-23
17	78	12.8	294	4	US-10-671-207-23
18	78	12.8	294	5	US-10-673-120-23
19	78	12.8	294	5	US-10-671-412-23
20	78	12.8	294	5	US-10-671-859-23
21	78	12.8	294	5	US-10-671-106-23
22	77.5	12.7	1486	6	US-11-097-143-15897
23	77	12.6	673	4	US-10-369-493-17937
24	76	12.5	709	6	US-11-188-298-11622
25	75	12.3	318	4	US-10-156-761-12913
26	75	12.3	326	4	US-10-425-115-223741
27	73.5	12.1	340	6	US-11-097-143-41112

28	73.5	12.1	513	3	US-09-833-745-50	Sequence 50, Appl
29	73.5	12.1	513	6	US-11-135-667-50	Sequence 50, Appl
30	72.5	11.9	524	5	US-10-739-930-10253	Sequence 10253, A
31	72.5	11.9	3571	5	US-10-732-923-8324	Sequence 8324, Ap
32	72.5	11.9	3574	5	US-10-732-923-8326	Sequence 8326, Ap
33	72.5	11.9	3574	5	US-10-732-923-8329	Sequence 8329, Ap
34	72	11.8	294	4	US-10-425-114-40589	Sequence 40589, A
35	72	11.8	313	4	US-10-425-115-306063	Sequence 306063, A
36	72	11.8	348	4	US-10-156-761-12267	Sequence 12267, A
37	72	11.8	413	4	US-10-425-115-306066	Sequence 306066, A
38	72	11.8	610	4	US-10-425-114-52341	Sequence 52341, A
39	72	11.8	689	4	US-10-437-963-125613	Sequence 125613, A
40	71.5	11.7	393	4	US-10-425-114-70624	Sequence 70624, A
41	71.5	11.7	393	4	US-10-425-115-292398	Sequence 292398, A
42	71.5	11.7	482	4	US-10-425-114-60438	Sequence 60438, A
43	71	11.7	261	4	US-10-369-493-9710	Sequence 9710, Ap
44	71	11.7	432	3	US-09-738-626-4678	Sequence 4678, Ap
45	71	11.7	477	5	US-10-494-672-246	Sequence 246, App

ALIGNMENTS

RESULT 1
US-10-813-908-3
; Sequence 3, Application US/10813908
; Publication No. US20050058662A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and
; FILE REFERENCE: MIC01/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813,908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
US-10-813-908-3

Query Match	100.0%	Score 609;	DB 5;	Length 121;
Best Local Similarity	100.0%	Pred. No. 8.3e-60;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA	60	
Db	1	MSRTAAHIGIEQLSAISLDQERSLPGRYALLPDGOSIEPHISRLYPERLADRVLLDFA	60	
Qy	61	TPDGRFHLLRPVDFNQMGRLSVLAEGOSPELRAAALLLEQMHADQLMONTLLHLHK	120	
Db	61	TPDGRFHLLRPVDFNQMGRLSVLAEGOSPELRAAALLLEQMHADQLMONTLLHLHK	120	
Qy	121	V 121		
Db	121	V 121		

RESULT 2
US-11-075-185-24
; Sequence 24, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185


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US-10-425-115-223719
Query Match      13.1%; Score 80; DB 4; Length 1108;
Best Local Similarity 27.2%; Pred. No. 16;
Matches 25; Conservative 16; Mismatches 27; Indels 24; Gaps 4;

Qy 38 STEPHISRLYPERLADRVLLDFATPDGRGFDHLLRPVDFNQMOGLRS-----VLAEGQ 90
Db 807 STEPH-----DVIAPDR-LTDLPPNDPNHTMWHIQASTAQSHALDGGK 850

Qy 91 SPELRAAALAEQMHAD-EQLMQMTLHLHLKV 121
Db 851 DPDAHATSSLVKNTSHNMEPVVQKSISQLHDI 882

RESULT 6
US-10-425-114-62671
; Sequence 62671, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62671
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-238-A9_FLI.pep
US-10-425-114-62671

Query Match      13.1%; Score 80; DB 4; Length 1132;
Best Local Similarity 27.2%; Pred. No. 17;
Matches 25; Conservative 16; Mismatches 27; Indels 24; Gaps 4;

Qy 38 SIEPHISRLYPERLADRVLLDFATPDGRGFDHLLRPVDFNQMOGLRS-----VLAEGQ 90
Db 831 STEPH-----DVIAPDR-LTDLPPNDPNHTMWHIQASTAQSHALDGGK 874

Qy 91 SPELRAAALAEQMHAD-EQLMQMTLHLHLKV 121
Db 875 DPDAHATSSLVKNTSHNMEPVVQKSISQLHDI 906

RESULT 7
US-10-329-148A-5
; Sequence 5, Application US/10329148A
; Publication No. US20040023343A1
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/10/329,148A
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/603,207B
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/370,700
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-09
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; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4928
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-10-329-148A-5

Query Match      12.9%; Score 78.5; DB 4; Length 4928;
Best Local Similarity 27.5%; Pred. No. 1.6e+02;
Matches 28; Conservative 18; Mismatches 45; Indels 11; Gaps 3;

Qy 5 TAAHIGIEQLSAISLDDOERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64
Db 4799 TFAELGFDLSLTAVELRNRLNAVTG--LRLPPTLVFDHPTPLALSEQLVPA LV---AEPDN 4853

Qy 65 GFHDLLRPVDFNQMOGLRSVLAEGQSPELRAAALAEQMH 106
Db 4854 GIESLLAELD-----RLDTTLAOGPSIPLDQAKVAERLHA 4889

RESULT 8
US-10-671-403-23
; Sequence 23, Application US/10671403
; Publication No. US20040038289A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yuzieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/671,403
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-671-403-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy 5 TAAHIGIEQLSAISLDDOERSLPGRYALLPDGQSIIEPHISRLYPERLADRVLLDFATPDR 64
Db 208 SAAHGGMR--DALSLDDQAISFGSDILKVEDALLITGANSQLYIGKLA-----K 254

Qy 65 GFHDLLRPVDFNQMOGLRSVLAEGQSPELRAAALAEQMH 104
Db 255 SLHD----KNVSDALETNELLOQKDP-----AKLIEDM 285

RESULT 9
US-10-671-419-23
; Sequence 23, Application US/10671419
; Publication No. US20040038290A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
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; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/673,098
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-673-098-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSTEPHISRLYPERLADRVLDDFATPDR 64
Db      :||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
208 SAAGGMR--DALSLLDQAISFGDILKVEDALLITGAVSOLYIGKLA-----K 254

Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEQSPELRAAAALAEQM 104
Db      :||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285

RESULT 13
US-10-672-638-23
; Sequence 23, Application US/10672638
; Publication No. US20040077012A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/672,638
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-672-638-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSTEPHISRLYPERLADRVLDDFATPDR 64
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Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEQSPELRAAAALAEQM 104
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RESULT 13
US-10-672-638-23
; Sequence 23, Application US/10672638
; Publication No. US20040077012A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/672,638
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
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; ORGANISM: Bacillus subtilis
US-10-672-638-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSTEPHISRLYPERLADRVLDDFATPDR 64
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255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285
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Qy      65 GFHDLLRPVDFNQAMQGLRSVLAEQSPELRAAAALAEQM 104
Db      :||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285

RESULT 14
US-10-673-127-23
; Sequence 23, Application US/10673127
; Publication No. US20040081995A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/673,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-673-127-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

Qy      5 TAAHIGIEQLSAISLDDQERSLPGRYALLPDGQSTEPHISRLYPERLADRVLDDFATPDR 64
Db      :||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
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Db      :||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
255 SLHD----KNVSDALETLNELLQGGKDP-----AKLIEDM 285

RESULT 15
US-10-670-817-23
; Sequence 23, Application US/10670817
; Publication No. US20040106137A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurieva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/670,817
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US/09/716,964
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
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; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 23
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-670-817-23

Query Match      12.8%; Score 78; DB 4; Length 294;
Best Local Similarity 29.0%; Pred. No. 4.8;
Matches 29; Conservative 16; Mismatches 33; Indels 22; Gaps 4;

QY      5  TAAHIGIEQLSAISLDDQERSLFGRYALLPDGQSIEPHISRILYPERLADRVLLDPATPDR 64
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Search completed: June 16, 2006, 20:25:00
Job time : 69.6813 secs

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioacceleration Ltd.
 OM protein - protein search, using sw model
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 Title: US-10-813-908A-3
 Perfect score: 609
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 Searched: 96747 seqs, 22556637 residues
 Total number of hits satisfying chosen parameters: 96747
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
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 Listing first 45 summaries
 Database : Published Applications AA New:*
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 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pap:*
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Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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1	70	11.5	562	6	US-10-449-902-47856
2	70	11.5	562	6	US-10-449-902-47856
3	69	11.3	451	6	US-10-471-571A-2280
4	68	11.2	467	6	US-10-449-902-49788
5	68	11.2	504	6	US-10-449-902-35636
6	68	11.2	547	6	US-10-449-902-55462
7	67	11.0	504	6	US-10-449-902-43064
8	67	11.0	504	6	US-10-449-902-53630
9	67	11.0	567	6	US-10-449-902-46221
10	66.5	10.9	458	6	US-10-449-902-37980
11	66	10.8	381	7	US-11-321-421-8
12	65.5	10.8	447	6	US-10-449-902-46260
13	65.5	10.8	3429	6	US-10-953-349-9275
14	65.5	10.8	3438	6	US-10-953-349-9274
15	65.5	10.8	3478	6	US-10-953-349-9273
16	65	10.7	800	6	US-10-449-902-53325
17	64	10.5	520	6	US-10-449-902-54451
18	64	10.5	521	6	US-10-449-902-43877
19	63.5	10.4	272	7	US-11-293-697-3682
20	63.5	10.4	343	6	US-10-449-902-43568
21	63.5	10.4	349	6	US-10-449-902-48899
22	63.5	10.4	489	6	US-10-449-902-41981
23	63.5	10.4	546	6	US-10-449-902-29819
24	63.5	10.4	859	6	US-10-449-902-51763
25	63.5	10.4	1568	7	US-11-330-363-5

26 63 10.3 846 6 US-10-449-902-43448 Sequence 43448, A
 27 62.5 10.3 493 6 US-10-449-902-53861 Sequence 53861, A
 28 62.5 10.3 839 7 US-11-293-697-3261 Sequence 3261, Ap
 29 62 10.2 291 7 US-11-252-276-10 Sequence 10, Appl
 30 62 10.2 513 6 US-10-953-349-8011 Sequence 8011, Ap
 31 62 10.2 553 6 US-10-953-349-8010 Sequence 8010, Ap
 32 62 10.2 571 6 US-10-449-902-42832 Sequence 42832, A
 33 62 10.2 580 6 US-10-953-349-8009 Sequence 8009, Ap
 34 62 10.2 910 6 US-10-953-349-9741 Sequence 9741, Ap
 35 62 10.2 991 6 US-10-449-902-55212 Sequence 55212, A
 36 62 10.2 1127 6 US-10-953-349-9740 Sequence 9740, Ap
 37 62 10.2 1139 6 US-10-953-349-9739 Sequence 9739, Ap
 38 61.5 10.1 810 6 US-10-953-349-33953 Sequence 33953, A
 39 61 10.0 226 6 US-10-953-349-16545 Sequence 16545, A
 40 61 10.0 479 6 US-10-449-902-55434 Sequence 55434, A
 41 61 10.0 1190 6 US-10-449-902-41233 Sequence 41233, A
 42 60.5 9.9 178 6 US-10-953-349-34473 Sequence 34473, A
 43 60.5 9.9 261 6 US-10-953-349-34472 Sequence 34472, A
 44 60.5 9.9 855 6 US-10-449-902-41097 Sequence 41097, A
 45 60.5 9.9 961 6 US-10-449-902-41296 Sequence 41296, A

ALIGNMENTS

RESULT 1
 US-10-449-902-47856
 ; Sequence 47856, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 47856
 ; LENGTH: 562
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-449-902-47856
 Query Match 11.5%; Score 70; DB 6; Length 562;
 Best Local Similarity 29.8%; Pred. No. 9.1;
 Matches 25; Conservative 14; Mismatches 35; Indels 10; Gaps 3;
 Qy 23 ERSLPGRYALLP-DGQSIPIHISRLYPERLADRVLLDFATPDRCGHLLRPVDPNQAMQG 81
 Db 225 EWSLPTVTHFRPHHGLCIIEPKHSRLSLKLGCCII----PPLOGFHALTK-----MTLQD 275
 Qy 82 LRSVLAEQSQPELRRAAALAEQWH 105
 Db 276 LRNSVAKASYEDVFKSCPQLQVLH 299
 RESULT 2
 US-10-449-902-50502
 ; Sequence 50502, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

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; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50502
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50502

Query Match      11.5%; Score 70; DB 6; Length 562;
Best Local Similarity 29.8%; Pred. No. 9.1;
Matches 25; Conservative 14; Mismatches 35; Indels 10; Gaps 3;

QY 23 ERSILPGRYALLP-DGQSIIEPHISRLYPERLADRVLLDFATPDGRGFDHLLRPVDFNQAMOG 81
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Db 225 EWSLPPVIVHFPFHGGLCIEPHKSRSLKLGCCII-----PPLQGPHALTK-----MTLQD 275
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QY 82 LRSVLAEQSPSELRAAAALLEQMH 105
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Db 276 LRNSVAKASYEDVFKSCPQLQVLH 299
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RESULT 3
US-10-471-571A-2280
; Sequence 2280, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2280
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(451)
; OTHER INFORMATION: phosphoglucosamine-mutase
US-10-471-571A-2280

Query Match      11.3%; Score 69; DB 6; Length 451;
Best Local Similarity 28.4%; Pred. No. 8.8;
Matches 23; Conservative 14; Mismatches 28; Indels 16; Gaps 3;

QY 34 PDGQSTIEPHISRLYPERLADRVL---LDPATPDGRGFDHLLRPVDEN-QAMQGLRSVLAEG 89
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QY 90 QSPELRAAAALLEQMHAEQOL 110
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RESULT 4
US-10-449-902-49788
; Sequence 49788, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
```

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; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49788
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49788

Query Match      11.2%; Score 68; DB 6; Length 467;
Best Local Similarity 29.1%; Pred. No. 12;
Matches 30; Conservative 16; Mismatches 29; Indels 28; Gaps 6;

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QY 76 NQAMQGLRSVLAEGQSPELRAAAALLEQMHAEQOLMQMTLHL 118
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RESULT 5
US-10-449-902-35636
; Sequence 35636, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35636
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35636

Query Match      11.2%; Score 68; DB 6; Length 504;
Best Local Similarity 24.6%; Pred. No. 13;
Matches 28; Conservative 20; Mismatches 46; Indels 20; Gaps 4;

QY 1 MSRIITAAHTGIEQLGSAISLDDQERSLPGRYALLPDGQSTIEPHISRL--YPERLADRVLLD 58
      :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 218 LHKITDEIINIDPNSIS-----FPGISFSPGMSEIRFVEEHCFD 263
      :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 59 FATPDGRGFDHLLRPVDFNQAMQGLRSVLAEGQSPELRAAAALLEQMHAEQOLMQ 112
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 264 ---PFKNYPLLDRIQIQILIRLEGLSAEGR-PKLRAPCFLKIESFCGSELOK 313
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 6
US-10-449-902-55462
; Sequence 55462, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
```

```
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55462
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Oryza sativa
;
US-10-449-902-55462

Query Match      11.2%; Score 68; DB 6; Length 547;
Best Local Similarity 24.6%; Pred. No. 14;
Matches 28; Conservative 20; Mismatches 46; Indels 20; Gaps 4;

Qy 1 MSRTAAHIGIEQLSALSLDQERSLPCRYALLPDGOSIEPHISRL--YPERLADRVLLD 58
Db 261 LHKITDEIINDPNSSIS-----FPKGISFSPGMSEIIRFVEEHCDFCVID 306

Qy 59 FATPDGRGHDLRLRPVDFNOAMQGLRSVLAEGSPELRAAAALLQMHAEQLMQ 112
Db 307 ---PFKNYPLDLRIQIEILIRLEGLSABGR-PKLAPCPFKIESFCGSELQK 356

RESULT 7
US-10-449-902-43064
; Sequence 43064, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43064
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
;
US-10-449-902-43064

Query Match      11.0%; Score 67; DB 6; Length 504;
Best Local Similarity 27.4%; Pred. No. 16;
Matches 23; Conservative 15; Mismatches 30; Indels 16; Gaps 3;

Qy 31 ALLPDGOSIEPHISRLYPERLADRVLLDFATPDGRGFHDLRLPVDFOAMQGLRSVLAEGQ 90
Db 357 AIIPGSSVP-----LLPKHICDDVLDY-----DALKAV---QSGLGTAAVIMDK 400

Qy 91 SPELRAAAALLOQMHAEQLMQMT 114
Db 401 STDVVDIAIRLSYFYKHSCGQCT 424

RESULT 8
US-10-449-902-53630
; Sequence 53630, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53630
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
;
US-10-449-902-53630

Query Match      11.0%; Score 67; DB 6; Length 504;
Best Local Similarity 27.4%; Pred. No. 16;
Matches 23; Conservative 15; Mismatches 30; Indels 16; Gaps 3;

Qy 31 ALLPDGOSIEPHISRLYPERLADRVLLDFATPDGRGFHDLRLPVDFOAMQGLRSVLAEGQ 90
Db 357 AIIPGSSVP-----LLPKHICDDVLDY-----DALKAV---QSGLGTAAVIMDK 400

Qy 91 SPELRAAAALLOQMHAEQLMQMT 114
Db 401 STDVVDIAIRLSYFYKHSCGQCT 424

RESULT 9
US-10-449-902-46221
; Sequence 46221, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46221
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Oryza sativa
;
US-10-449-902-46221

Query Match      11.0%; Score 67; DB 6; Length 567;
Best Local Similarity 24.8%; Pred. No. 19;
Matches 33; Conservative 19; Mismatches 37; Indels 44; Gaps 8;

Qy 27 PGRYALLPDQOSTE---PHISRLYPER-----LADRVLLDFATPD-----RGFH 67
Db 336 PAR-AILPYSQALEKFAPHIQQLSMESNGKVSIDGVQLSFETGEIDFGPFGTNGQHSFY 394
Qy 68 DLLR-----PVDFOAMQGLRSVLAEGQ-----SPELRAAAALLOQMHAE 108
Db 395 QLHQGRVPCDFIGVVKSOQPYLKGIVSNHDELMNSFFAQPDAALAYGKTPQLHSE- 453
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```
; Sequence 53630, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53630
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Oryza sativa
;
US-10-449-902-53630

Query Match      11.0%; Score 67; DB 6; Length 504;
Best Local Similarity 27.4%; Pred. No. 16;
Matches 23; Conservative 15; Mismatches 30; Indels 16; Gaps 3;

Qy 31 ALLPDGOSIEPHISRLYPERLADRVLLDFATPDGRGFHDLRLPVDFOAMQGLRSVLAEGQ 90
Db 357 AIIPGSSVP-----LLPKHICDDVLDY-----DALKAV---QSGLGTAAVIMDK 400

Qy 91 SPELRAAAALLOQMHAEQLMQMT 114
Db 401 STDVVDIAIRLSYFYKHSCGQCT 424

RESULT 9
US-10-449-902-46221
; Sequence 46221, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46221
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Oryza sativa
;
US-10-449-902-46221

Query Match      11.0%; Score 67; DB 6; Length 567;
Best Local Similarity 24.8%; Pred. No. 19;
Matches 33; Conservative 19; Mismatches 37; Indels 44; Gaps 8;

Qy 27 PGRYALLPDQOSTE---PHISRLYPER-----LADRVLLDFATPD-----RGFH 67
Db 336 PAR-AILPYSQALEKFAPHIQQLSMESNGKVSIDGVQLSFETGEIDFGPFGTNGQHSFY 394
Qy 68 DLLR-----PVDFOAMQGLRSVLAEGQ-----SPELRAAAALLOQMHAE 108
Db 395 QLHQGRVPCDFIGVVKSOQPYLKGIVSNHDELMNSFFAQPDAALAYGKTPQLHSE- 453
```


RESULT 14

US-10-953-349-9274
; Sequence 9274, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9274
; LENGTH: 3438
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9274

Query Match 10.8%; Score 65.5; DB 6; Length 3438;
Best Local Similarity 28.4%; Pred. No. 2.5e+02;
Matches 23; Conservative 11; Mismatches 28; Indels 19; Gaps 3;

QY 33 LPDQSQSTIEPHISRILYPERLADRVLLDFATPDGRGFHDLLRPVDFNQAMQGLRSVLAEQSP 92
DB 3255 VPSCGSTEPQIQ-----LSSSAEPEEGMHIHL-----EAAANSETVVTGSG-- 3295
QY 93 ELRAAAALLEGOMHADEQLMOM 113
DB 3296 ELPSSLPMTEDENADGQLAEV 3316

RESULT 15

US-10-953-349-9273
; Sequence 9273, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9273
; LENGTH: 3478
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9273

Query Match 10.8%; Score 65.5; DB 6; Length 3478;
Best Local Similarity 28.4%; Pred. No. 2.6e+02;
Matches 23; Conservative 11; Mismatches 28; Indels 19; Gaps 3;

QY 33 LPDQSQSTIEPHISRILYPERLADRVLLDFATPDGRGFHDLLRPVDFNQAMQGLRSVLAEQSP 92
DB 3295 VPSCGSTEPQIQ-----LSSSAEPEEGMHIHL-----EAAANSETVVTGSG-- 3335
QY 93 ELRAAAALLEGOMHADEQLMOM 113
DB 3336 ELPSSLPMTEDENADGQLAEV 3356

Search completed: June 16, 2006, 20:25:56
Job time : 6.21382 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model
Run on: June 16, 2006, 18:52:40 ; Search time 76.8618 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-4
Perfect score: 602
Sequence: 1 MTWVLTQQQDALLTTCWLQ.....ARFAYQQYLEEQNESTHP 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A Geneseq_8:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*
 - 9: Geneseqp2005s:*
 - 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	100.0	116	5	ABB80772 A. salmon
2	272	45.2	231	7	ABO81216 Pseudomon
3	111.5	18.5	470	9	ABM93219 M. xanthu
4	99	16.4	619	6	ABU22979 Protein e
5	96.5	16.0	143	2	AAI35024 Chlamydia
6	88.5	14.7	870	7	ABO79661 Pseudomon
7	86.5	14.0	719	8	ADX89002 Plant ful
8	84.5	14.0	122	3	AAI14133 Bordetell
9	84.5	14.0	737	8	ADX94619 Plant ful
10	83	13.8	1219	7	ABO80094 Pseudomon
11	83	13.8	1586	6	ABU21467 Protein e
12	81	13.5	953	9	ABM95482 M. xanthu
13	80	13.3	143	10	AE60312 Cat chlam
14	80	13.3	368	7	ABO81971 Pseudomon
15	79.5	13.2	517	9	AEBA49907 P. aerugi
16	79.5	13.2	956	7	ABM91196 M. xanthu
17	79.5	13.1	2519	7	ABM88218 Rice abio
18	78.5	13.0	169	2	AAW15044 G-CSF rec
19	78.5	13.0	1234	4	ABM68510 Drosophil
20	78	13.0	390	9	ABM97422 M. xanthu
21	78	13.0	577	9	AEBA41002 L. pneumo
22	78	13.0	587	9	AEBA37691 L. pneumo
23	77.5	12.9	171	2	AAW15045 G-CSF rec

24	77.5	12.9	171	2	AAW15046	Aaw15046 G-CSF rec
25	77.5	12.9	171	2	AAW15048	Aaw15048 G-CSF rec
26	77.5	12.9	171	2	AAW15050	Aaw15050 G-CSF rec
27	77.5	12.9	171	2	AAW15043	Aaw15043 G-CSF rec
28	77.5	12.9	171	2	AAW15049	Aaw15049 G-CSF rec
29	77.5	12.9	171	2	AAW15051	Aaw15051 G-CSF rec
30	77.5	12.9	238	2	AAW52089	Aay52089 Human ret
31	77.5	12.9	299	2	AAW17131	Aaw17131 Amino aci
32	77.5	12.9	302	2	AAW17108	Aaw17108 Amino aci
33	77.5	12.9	302	2	AAW17112	Aaw17112 Amino aci
34	77.5	12.9	302	2	AAW17106	Aaw17106 Amino aci
35	77.5	12.9	302	2	AAW17110	Aaw17110 Amino aci
36	77.5	12.9	302	2	AAW77845	Aaw77845 Multi-fun
37	77.5	12.9	302	2	AAW77839	Aaw77839 Multi-fun
38	77.5	12.9	302	2	AAW77841	Aaw77841 Multi-fun
39	77.5	12.9	302	2	AAW77843	Aaw77843 Multi-fun
40	77.5	12.9	317	2	AAW17113	Aaw17113 Amino aci
41	77.5	12.9	317	2	AAW17109	Aaw17109 Amino aci
42	77.5	12.9	317	2	AAW17111	Aaw17111 Amino aci
43	77.5	12.9	317	2	AAW17107	Aaw17107 Amino aci
44	77.5	12.9	317	2	AAW77842	Aaw77842 Multi-fun
45	77.5	12.9	317	2	AAW77840	Aaw77840 Multi-fun

ALIGNMENTS

RESULT 1
ABB80772
ID ABB80772 standard; protein; 116 AA.
XX
AC ABB80772;
XX
DT 23-SEP-2002 (first entry)
XX
DE A. salmonicida type III secretion protein acr4 sequence.
XX
KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;
KW acrV; acrH; antibiotic; vaccine; fish.
XX
OS Aeromonas salmonicida.
XX
PN WO200240514-A2.
XX
PD 23-MAY-2002.
XX
PF 15-NOV-2001; 2001WO-CA001589.
XX
PR 15-NOV-2000; 2000US-0248864P.
XX
PA (FREY/) FREY J.
PA (STUB/) STUBER K.
PA (THOR/) THORNTON J C.
PA (KUZ/) KUZYSK M A.
PA (BURI/) BURIAN J.
XX
PI Frey J, Stuber K, Thornton JC, Kuzysk MA, Burian J;
XX
DR WPI; 2002-537338/57.
XX
DR N-PSDB; ABN86172.
XX
PT Novel protein from Aeromonas salmonicida and nucleic acid encoding the
PT protein, useful for reducing susceptibility of fish to infection by a
PT virulent strain of Aeromonas salmonicida.
XX
PS Claim 13; Page 27; 39pp; English.
XX
CC The invention relates to A. salmonicida type III secretion genes and
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.
CC A. salmonicida type III secretion apparatus is useful for producing
CC selected products, especially AexT. AcrV in vaccine, epitope or epitopic
CC region of AcrV or any other protein of A. salmonicida type III secretion
CC apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of *A. salmonicida*. The proteins and encoding DNA are
CC useful for manufacturing a diagnostic agent. Detecting the presence of
CC the genes of AcrD, AcrV or any other components of the *A. salmonicida* type
CC III secretion apparatus is useful for the production or quality control
CC or efficacy of vaccines made from *A. salmonicida* or its genes. The present
CC sequence represents the *A. salmonicida* type III secretion protein acr4
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 602; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e-65; Indels 0; Gaps 0;
Matches 116; Conservative 0; Mismatches 0;

QY 1 MTWVLTSSQDDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 60
|||||
DB 1 MTWVLTSSQDDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 60
|||||

QY 61 EAAAHVDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQQYLEEQNESTHP 116
|||||
DB 61 EAAAHVDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQQYLEEQNESTHP 116
|||||

RESULT 2

ABO81216
ID ABO81216 standard; protein; 231 AA.

XX
AC ABO81216;

XX 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #13391.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD14787.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 29962; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO67826-
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 231 AA;

Query Match 45.2%; Score 272; DB 7; Length 231;
Best Local Similarity 55.1%; Pred. No. 1.2e-24; Indels 0; Gaps 0;
Matches 59; Conservative 13; Mismatches 35;

QY 2 TWVLTSSQDDALLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQEG 61
|||||
DB 122 SMTLKQTQORLLTLMGLHLCQGPRAQVLLLEALLSVAPERRDGRALLLQQLGLGE 181
|||||

QY 62 AALAHVDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQQYLELE 108
|||||
DB 182 PAVRLCRQLQEDGEBEPGLWLCLSRAEQLAGRLDAARAHAHALELE 228
|||||

RESULT 3

ABM93219
ID ABM93219 standard; protein; 470 AA.

XX
AC ABM93219;

XX 02-JUN-2005 (first entry)

XX M. xanthus protein sequence, seq id 12418.

XX Transgenic plant; DNA replication; gene regulation; gene expression.

XX Myxococcus xanthus.

XX US6833447-B1.

XX 21-DEC-2004.

XX 10-JUL-2001; 2001US-00902540.

XX 10-JUL-2000; 2000US-0217883P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX WPI; 2005-028716/03.

XX New substantially purified Myxococcus xanthus nucleic acid molecule
XX encoding a nitrite reductase, useful for determining gene expression,
XX identifying mutations in a gene of interest, and for constructing
XX mutations in a gene of interest.

XX Example 2; SEQ ID NO 12418; 25pp; English.

XX The invention relates to a substantially purified nucleic acid molecule
XX encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
XX recombinant DNA construct for expression of a nitrite reductase gene in a
XX plant cell, and a plant cell comprising the recombinant DNA construct.
XX The nucleic acid is useful for determining gene expression, identifying
XX mutations in a gene of interest, and for constructing mutations in a gene
XX of interest. Sequences given in records for SEQ IDs 9692-16825 represent
XX a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from USPTO

XX Sequence 470 AA;

Query Match 18.5%; Score 111.5; DB 9; Length 470;
Best Local Similarity 36.6%; Pred. No. 0.00018; Indels 7; Gaps 2;
Matches 34; Conservative 8; Mismatches 44;

QY 13 LLLTGMVLQYQY---GHPDK-----ASVLLAALLQIHPDHQGGRTLLVALLKQEGEALA 65
|||||
DB 56 LLLAGFLLDGYEPDGRPGQGPYAQLLRLLRSHPDHAGVHHAWQVLMNSGRPEARD 115
|||||

QY 66 HVDQLMOQGEADGPLWLCRSRACQLAGRLDEAR 98
DB 116 SAHRLVALAPRAGPALLSAGRLQRLVGLVAEAR 148

RESULT 4

ABU22979
ID ABU22979 standard; protein; 619 AA.

AC ABU22979;
XX

DT 19-JUN-2003 (first entry)
XX

DE Protein encoded by prokaryotic essential gene #8506.
XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX

OS Bordetella pertussis.
XX

PN WO200277183-A2.
XX

PD 03-OCT-2002.
XX

PF 21-MAR-2002; 2002WO-US009107.
XX

PR 21-MAR-2001; 2001US-00815242.
XX

PR 06-SEP-2001; 2001US-00948993.
XX

PR 25-OCT-2001; 2001US-0342923P.
XX

PR 08-FEB-2002; 2002US-00072851.
XX

PR 06-MAR-2002; 2002US-0362699P.
XX

PA (ELIT-) ELITRA PHARM INC.
XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlssen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX

DR WPI; 2003-029926/02.
XX

DR N-PSDB; ACA26849.
XX

PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX

PS Claim 25; SEQ ID NO 50903; 1766pp; English.
XX

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 619 AA;

Query Match 16.4%; Score 99; DB 6; Length 619;
Best Local Similarity 29.0%; Pred. No. 0.0088;
Matches 29; Conservative 21; Mismatches 46; Indels 4; Gaps 2;

QY 21 LOYG--HPDKASVLLAALLQIHPDHOGGRRTLLVALLKOGEGEAAAHVDQLMOQGEAD 77
DB 259 LEYGAKVDATRAQHQARAFINRNDARKLRLMLAGQIADGDYDGLAELQAMRRSPED 318

QY 78 GPLWLCRSRACQLAGRLDEARFAYQOYLEEEQNE-STHP 116
DB 319 FDLFMFQAQLAYKAGRLDQARGYLQQLVDVQNRQMATAP 358

RESULT 5

AAAY35024
ID AAY35024 standard; protein; 143 AA.

AC AAY35024;
XX

DT 17-OCT-2003 (revised)
DT 13-SEP-1999 (first entry)
XX

DE Chlamydia pneumoniae transmembrane protein sequence.
XX

KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope.
OS Chlamydothila pneumoniae.
XX

PN WO9927105-A2.
XX

PD 03-JUN-1999.
XX

PF 20-NOV-1998; 98WO-IB001890.
XX

PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX

PA (GEST) GENSET.
XX

PI Griffais R;
XX

DR WPI; 1999-357842/30.
XX

PT Genome sequence of Chlamydia pneumoniae.
XX

PS Page 921; Disclosure; 1912pp; English.
XX

CC AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91930) of Chlamydia pneumoniae. C.
CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
CC and is thought to be a contributing factor in heart disease, sarcoidosis,
CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
CC polypeptides encoded by the open reading frames of the C. pneumoniae
CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
CC be used as immunogenic compositions, especially where the vector directs
CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
CC -OCT-2003 to standardise OS field)
XX

SQ Sequence 143 AA;

Query Match 16.0%; Score 96.5; DB 2; Length 143;
Best Local Similarity 33.3%; Pred. No. 0.0026;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 11.7886 Seconds
(without alignments)
946.773 Million cell updates/sec

Title: US-10-813-908A-4
Perfect score: 602
Sequence: 1 MTWVLTQQDALLTGWLQ.....ARFAYQQYLEEONESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.80:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	
1	285	47.3	114	2 E35392	hypothetical prote	
2	285	47.3	114	2 T43590	hypothetical prote	
3	264	43.9	109	2 C83432	conserved hypotet	
4	96.5	16.0	142	2 E86543	CT274 hypothetical	
5	96.5	16.0	142	2 A72081	ct274 hypothetical	
6	88.5	14.7	827	2 H83217	probable transcrip	
7	86.5	14.4	384	2 S74806	hypothetical prote	
8	86	14.3	590	2 D83063	hypothetical prote	
9	84	14.0	698	2 A82593	hypothetical prote	
10	83	13.8	1193	2 F83264	hypothetical prote	
11	80.5	13.4	1334	2 T50568	probable multi-dom	
12	80	13.3	548	2 AH2962	cellulose biosynth	
13	80	13.3	553	2 F98320	hypothetical prote	
14	79.5	13.2	576	2 S49376	hypothetical prote	
15	78.5	13.0	139	2 G71534	hypothetical prote	
16	78	13.0	188	2 PQ0180	CytB protein - Syn	
17	77	12.8	520	2 S27137	hydroxymethylgluta	
18	77	12.8	673	2 F87636	TPR domain protein	
19	76.5	12.7	1810	2 E88481	protein Cl6A3.2 [i	
20	76	12.6	320	2 H64332	hypothetical prote	
21	75.5	12.5	844	2 T05227	hypothetical prote	
22	75	12.5	400	2 B64733	protein transport	
23	75	12.5	593	2 A83433	tetrairicopeptide	
24	74.5	12.4	265	2 S31070	rpcE protein - Syn	
25	74.5	12.4	724	2 AG1971	hypothetical prote	
26	74	12.3	400	2 F90642	probable integral	
27	74	12.3	400	2 F85493	probable integral	
28	74	12.3	593	1 XYVZFG	fzrG protein - Myx	
29	73.5	12.2	172	2 B83696	hypothetical prote	

30	73.5	12.2	460	2 D75493	cell division cycl
31	73.5	12.2	990	2 H90703	bacteriophage N4 a
32	73.5	12.2	990	2 C85554	bacteriophage N4 a
33	73	12.1	187	2 G75273	conserved hypotet
34	73	12.1	457	2 JC5422	FKS06-binding prot
35	73	12.1	559	2 T12680	peroxisomal target
36	72.5	12.0	990	2 B49351	bacteriophage N4 a
37	72	12.0	407	2 G83477	probable sigma-70
38	71.5	11.9	165	2 AG0619	probable bacteriop
39	71.5	11.9	267	2 E83858	hypothetical prote
40	71.5	11.9	460	2 T02544	hypothetical prote
41	71.5	11.9	802	2 C84733	probable O-GlcNAc
42	71	11.8	320	2 AB3630	taurine-binding pe
43	70.5	11.7	249	2 AIO350	probable fibrinall
44	70.5	11.7	761	2 G70393	conserved hypotet
45	70	11.6	204	1 FQHUGL	granulocyte colony

ALIGNMENTS

RESULT 1

E35392
hypothetical protein 4 - Yersinia enterocolitica
C:Species: Yersinia enterocolitica
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Oct-2004
C:Accession: E35392
R:Viitainen, A.M.; Toivanen, P.; Skurnik, M.
J. Bacteriol. 172, 3152-3162, 1990

A:Title: The lcrE gene is part of an operon in the lcr region of Yersinia enterocolitica
A:Reference number: A35392; MUID:90264308; PMID:2160939
A:Accession: E35392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <VII>
A:Cross-references: UNIPROT:Q93KU0; UNIPARC:UPI00000000246; GB:M32097; NID:g155454; PTDN
C:Superfamily: chaperone protein yscY

Query Match 47.3%; Score 285; DB 2; Length 114;
Best Local Similarity 52.2%; Pred. No. 1.6e-22;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

Qy	1	MTWVLTQQDALLTGWLQYCHPDKASVLAAALQIHPDQGGRTLLVALLKQEG 60
Db	1	MNITLTKRQOEFLLLNGWLQCGHAEACILLDALLTLNPEHLAGRRCRLVALLNNQ 60
Qy	61	EALAHVDQLMQOGEADGPLWLCRSACOLAGRLDEARFAYQOYLEEONES 113
Db	61	ERAKEAQLTISHDPLQAGNWLCLSRQAQLNGDLDKARHAYQHYLELKHNES 113

RESULT 2

T43590

hypothetical protein Y0046 - Yersinia pestis plasmid pCD1

C:Species: Yersinia pestis
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-Oct-2004
C:Accession: T43590; T42885
R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubake
J. Bacteriol. 180, 5192-5202, 1998
A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A:Reference number: Z22578; MUID:98422474; PMID:9748454
A:Accession: T43590
A:Status: preliminary;
A:Molecule type: DNA

A:Residues: 1-114 <HUP>

A:Cross-references: UNIPROT:P61417; UNIPARC:UPI00000000246; EMBL:AF053946; NID:g2996322;

A:Experimental source: strain KIM

R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.

Infect. Immun. 66, 4611-4623, 1998

A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia

A:Reference number: Z22273; MUID:98427122; PMID:9746557

A:Accession: T42885

A:Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-114 <PER>
A;Cross-references: UNIPARC:UPI0000000246; EMBL:AF074612; NID:g3822037; PIDN:AAC69796.1;
A;Experimental source: strain KIMS
C;Genetics:
A;Genome: plasmid pCD1
A;Note: Y0046
C;Superfamily: chaperrone protein yscY

Query Match 47.3%; Score 285; DB 2; Length 114;
Best Local Similarity 52.2%; Pred. No. 1.6e-22;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

QY 1 MTWLTSSQODALLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQEG 60
DB 1 MNTLTWRQGFLLNGWLQCGHAEACILDLALTLPNPELAGRRCLVALLNNQG 60

QY 61 EAAIAHVQDLMQOGEADGPLWLCRSRACQIAGRLDEARFAYQOYLEEONES 113
DB 61 ERAEKEAQLISHDPLQAGNWLCLSRAQQLNGDLDRKHAYQHYLEKOHNES 113

RESULT 3
C83432 conserved hypothetical protein in type III secretion PA1702 [imported] - Pseudomonas aer
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83432
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83432
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <STO>
A;Cross-references: UNIPROT:Q91328; UNIPARC:UPI000000C5452; GB:AE0044597; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1702

Query Match 43.9%; Score 264; DB 2; Length 109;
Best Local Similarity 54.7%; Pred. No. 2.4e-20;
Matches 58; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

QY 3 MVLTSQQODALLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQEGEA 62
DB 1 MTLKPTQRRLLMLGWLHLCQGPRAQVLLLEALLSVAPERRDGRALLALLIQQGLGEP 60

QY 63 ALAHVDLMQOGEADGPLWLCRSRACQIAGRLDEARFAYQOYLELE 108
DB 61 AVRLCRLQDGBEEFGLWRLCLSRABQLAGRLDAARAARALELE 106

RESULT 4
E85543
CT274 hypothetical protein [imported] - Chlamydomophila pneumoniae (strain J138)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86543
R;Shitai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: E86543
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <STO>
A;Cross-references: UNIPROT:Q928C0; UNIPARC:UPI000000D41E0; GB:BA000008; NID:g8978795; PI
A;Experimental source: strain J138
C;Genetics:

A;Gene: CPJ0423

Query Match 16.0%; Score 96.5; DB 2; Length 142;
Best Local Similarity 33.3%; Pred. No. 0.0083;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYGHDPDKASVLLAALLQIHP----DHQGRRTLLVALLKQEGEAALAH 66
DB 18 EELRISGYSFRLQGHYSKAILFFELVILDPISYIDHQ---TLGGLYLQIGENSQALAV 73

QY 67 VDQLMQOGEADGPLWLCRSRACQIAGRLDEARFAYQOYL 105
DB 74 LQALRMQGDHLPDLLNKTALFCLGRIBEAT-AIATYL 111

RESULT 5
A72081
ct274 hypothetical protein - Chlamydomophila pneumoniae (strain CWL029)
C;Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: A72081
R;Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: A72081
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <ARN>
A;Cross-references: UNIPROT:Q928C0; UNIPARC:UPI000000D41E0; GB:AE001625; GB:AE001363; NID
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: CPN0423

Query Match 16.0%; Score 96.5; DB 2; Length 142;
Best Local Similarity 33.3%; Pred. No. 0.0083;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYGHDPDKASVLLAALLQIHP----DHQGRRTLLVALLKQEGEAALAH 66
DB 18 EELRISGYSFRLQGHYSKAILFFELVILDPISYIDHQ---TLGGLYLQIGENSQALAV 73

QY 67 VDQLMQOGEADGPLWLCRSRACQIAGRLDEARFAYQOYL 105
DB 74 LQALRMQGDHLPDLLNKTALFCLGRIBEAT-AIATYL 111

RESULT 6
H83217
probable transcription regulator PA3420 [imported] - Pseudomonas aeruginosa (strain PAO
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83217
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83217
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-827 <STO>
A;Cross-references: UNIPROT:Q9HV15; UNIPARC:UPI000000C5A01; GB:AE004763; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3420
C;Superfamily: regulatory protein malt

Query Match 14.7%; Score 88.5; DB 2; Length 827;
Best Local Similarity 26.5%; Pred. No. 0.38;
Matches 36; Conservative 20; Mismatches 55; Indels 25; Gaps 5;

Qy 1 MTWLTSSQDALL-----LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLV 52
Db 354 MVLAIRDELPAALASTPRVLINAWTLTYAGRLAEEDCTGQARFLPMPFSASRQRVLL 413
Qy 53 A-----LLKQGEAALAH-----VDLMQOGEADGFLWLCRSRACOLA---GRIDEA 97
Db 414 AQWQGLFGILLHCRGERGAADYLRALBQLPEDAWSQG--LICRSALMQLAMIEGRMDQA 471
Qy 98 RFAYQOYLEEQNES 113
Db 472 RLIGRDALRLAREHDS 487

RESULT 7
S74806
hypothetical protein sll1628 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
C;Accession: S74806
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384 <KAN>
A;Cross-references: UNIPROT:P73719; UNIPARC:UPI00000C10C7; EMBL:D90909; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
F;286-299/Domain: tetratricopeptide repeat homology <TT1>
F;300-333/Domain: tetratricopeptide repeat homology <TT2>
F;334-367/Domain: tetratricopeptide repeat homology <TT3>

Query Match 14.4%; Score 86.5; DB 2; Length 384;
Best Local Similarity 28.1%; Pred. No. 0.27;
Matches 27; Conservative 15; Mismatches 49; Indels 5; Gaps 1;

Qy 18 WL-----QLQVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAALAHVDQLMQ 72
Db 269 WNLGIIQQAQGELETAIASHGEAISINPQMTSQAQNGSALGVNGKLEALANFDEALA 328

Qy 73 QGEADGFLWLCRSRACOLAGRLDEARFAYQOYLE 108
Db 329 QNPDDAEVWLSRGLLEAMERKEAIPSYEKALTLE 364

RESULT 8
D83063
hypothetical protein PA4667 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83063
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <STO>
A;Cross-references: UNIPROT:P42810; UNIPARC:UPI000013A09A; GB:AE004880; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4667

Query Match 14.3%; Score 86; DB 2; Length 590;
Best Local Similarity 29.1%; Pred. No. 0.48;
Matches 30; Conservative 15; Mismatches 58; Indels 0; Gaps 0;

Qy 13 LLTGWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAALAHVDQLMQ 72
Db 238 LLRSRLQSMKRSDEALPLLKAGIKEHPDDKRVLYARVLLVEQNRLDDAKAEFAGLVQ 297
Qy 73 QGEADGFLWLCRSRACOLAGRLDEARFAYQOYLEEQNESTH 115
Db 298 QFPDDDDLRFLSLVLCLEAQAWDEARLYLEELVERDSHVDAAH 340

RESULT 9
A82593
hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82593
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <SIM>
A;Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI00000C2968; GB:AE004030; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier,
as-Neto, E.; Docena, C.; El-Dorfi, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2169

Query Match 14.0%; Score 84; DB 2; Length 698;
Best Local Similarity 28.6%; Pred. No. 0.92;
Matches 26; Conservative 13; Mismatches 50; Indels 2; Gaps 1;

Qy 15 LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAALAHVDQLMQQ 74
Db 250 LTGEFELLAGHPDRALTHLRQVLATWPDPTLEALLTANKQLDMDDDDARITLDAALDIK 309
Qy 75 EADGFLWLCRSRACOLAGRLDEARFAYQOYL 105
Db 310 PRNHDLWLARLAVPVGS--DEARIVIERWL 338

RESULT 10
F83264
hypothetical protein PA3063 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83264
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83264
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1193 <STO>

Qy 13 LLLTGWLQYQHPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEGEAALAHVDQLMQ 72
Db 223 LLLRSRLQSMKRSDEALPLLKAGIKEHPDDKRVRLAYARLLVEQNRLDDAKAFAGLVQ 282
Qy 73 Q-GEADGPLWLCRSRACQACGLDEARFAYQOYLEBEQNESTH 115
Db 283 QFPDDDDDLRFSLALVCLCEAQANDEARIYLELVERDSDHDAAH 326

RESULT 15
G71534
hypothetical protein CT274 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: G71534
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: G71534
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-139 <ARN>
A:Cross-references: UNIPROT:O84276; UNIPARC:UPI00000C0B25; GB:AE001300; GB:AE001273; NID
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT274

Query Match 13.0%; Score 78.5; DB 2; Length 139;
Best Local Similarity 28.6%; Pred. No. 0,6;
Matches 28; Conservative 20; Mismatches 49; Indels 1; Gaps 1;
Qy 8 QQQDALLTGWLQYQHPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEGEAALAHV 67
Db 15 EELELRISGYSFLRQGHYQKAILFFEALVILDPLSVVDFQTLGGLYQISENTKALYVL 74
Qy 68 DQLMQQGEADGPLWLCRSRACQACGLDEARFAYQOYL 105
Db 75 DQALRMQGDHLPTLLNKTALFCLGRIEAS-AIASYL 111

Search completed: June 16, 2006, 19:25:05
Job time : 11.7886 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 91.1024 Seconds
(without alignments)
1177.815 Million cell updates/sec

Title: US-10-813-908A-4
Perfect score: 602
Sequence: 1 MTWVLTQQDALLLTGWLQ.....ARFAYQQYLEEQNESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*
1: uniprot_prot.*
2: uniprot_creml.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602	100.0	116	2 Q8GA92_AERSA	Q8GA92 aeromonas s
2	547	90.9	116	2 Q5CCAL_AERSO	Q5CCAL aeromonas s
3	537	89.2	116	2 Q699R4_AERHY	Q699R4 aeromonas h
4	483	80.2	116	2 Q6TLM6_AERHY	Q6TLM6 aeromonas h
5	467	77.6	116	2 Q5XL08_AERHY	Q5XL08 aeromonas h
6	338	56.1	109	2 Q84GV9_PHOLU	Q84GV9 photorhabdu
7	324	53.8	109	2 Q7N0W7_PHOLL	Q7N0W7 photorhabdu
8	285	47.3	114	1 YSCY_YEREN	Y93ku0 yersinia en
9	285	47.3	114	1 YSCY_YERPE	P61417 yersinia pe
10	270	44.9	114	2 Q663K5_YERPS	Q663K5 yersinia ps
11	264	43.9	109	2 Q30535_PSEAE	Q30535 pseudomonas
12	156.5	26.0	112	2 Q6QVR8_VIBHA	Q6QVR8 vibrio harv
13	148.5	24.7	108	2 Q66PT9_PASPI	Q66PT9 pasteurella
14	140.5	23.3	112	2 Q48IR6_PSE14	Q48IR6 pseudomonas
15	138.5	23.0	114	2 Q87P55_VIBPA	Q87P55 vibrio para
16	126	20.9	700	2 Q2JH05_9CYAN	Q2JH05 cyanobacter
17	118	19.6	798	2 Q2W4P4_MAGSA	Q2W4P4 magnetospir
18	116	19.3	788	2 Q31S90_SYN7	Q31S90 synecococc
19	116	19.3	788	2 Q5N228_SYN6	Q5N228 synecococc
20	114.5	19.0	142	2 Q9AN16_BRAJA	Q9AN16 bradyrhizob
21	107.5	17.9	467	2 Q5LTY9_SILPO	Q5LTY9 silicibacte
22	107.5	17.8	955	2 Q34XX4_9GAMM	Q34XX4 alkalilimni
23	107.5	17.5	192	2 Q34XH6_9GAMM	Q34XH6 alkalilimni
24	105.5	17.4	1837	2 Q2RRU7_RHURU	Q2RRU7 rhodospiril
25	104	17.3	313	2 Q39ZX0_PELCD	Q39ZX0 pelobacter
26	99.5	16.5	530	2 Q4C0T9_CROWT	Q4C0T9 crocosphaer
27	99.5	16.4	626	2 Q7W184_BORPA	Q7W184 bordetella
28	99	16.4	628	2 Q7VUG8_BORPE	Q7VUG8 bordetella
29	99	16.4	628	2 Q7WNY7_BORBR	Q7WNY7 bordetella
30	99	16.4	628	2 Q7WNY7_BORBR	Q7WNY7 bordetella
31	98	16.3	422	2 Q67NN9_SYNTH	Q67NN9 symbiobacte

32	97	16.1	443	2	Q40MR2_DESAC	Q40mr2 desulfuromo
33	96.5	16.0	142	2	Q9Z8C0_CHLPN	Q9Z8C0 chlamydia p
34	95	15.8	774	2	Q2JSZ1_9CYAN	Q2JSZ1 cyanobacter
35	94	15.6	582	2	Q5LPE5_SILPO	Q5LPE5 silicibacte
36	93.5	15.5	560	2	Q2ND56_9SPHN	Q2nd56 erythrobact
37	93	15.4	1138	2	Q46GI8_METEA	Q46gi8 methanosarc
38	93	15.4	1349	2	Q9L096_STRCO	Q9L096 streptomyce
39	92.5	15.4	161	2	Q3QHM9_9GAMM	Q3qhm9 shewanella
40	92.5	15.4	652	2	Q399P6_BURS3	Q399p6 burkholderi
41	92	15.3	718	2	Q2IFU6_9DELT	Q2ifu6 anaeromyxob
42	91	15.1	700	2	Q3X9C2_METFL	Q3x9c2 methylobaci
43	91	15.1	1198	2	Q4KCF4_PSEFS	Q4kcf4 pseudomonas
44	90	15.0	547	2	Q9X3W6_ZYMMO	Q9x3w6 zymomonas m
45	90	15.0	1129	2	Q8PTJ5_METWA	Q8ptj5 methanosarc

ALIGNMENTS

RESULT 1
Q8GA92_AERSA
ID Q8GA92_AERSA PRELIMINARY; PRT; 116 AA.
AC Q8GA92;
DT 01-MAR-2003, integrated into UniProtKB/TREMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE ASCY protein.
GN Name=ascy;
OS Aeromonas salmonicida subsp. salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RX MEDLINE=22262111; PubMed=12374830;
RX DOI=10.1128/JB.184.21.5966-5970.2002;
RA Burr S.E., Stuber K., Wahli T., Frey J.;
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida.";
RL J. Bacteriol. 184:5966-5970(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type =III secretion mutant in a rainbow trout model.";
RL Microbiol. 151:2111-2118(2005).
CC -----
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CC -----
CC EMBL: AJ458292; CAD30217.1; -; Genomic DNA.
CC EMBL: AJ616218; CAB83104.1; -; Genomic DNA.
CC GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR011990; TPR-like helical.
DR InterPro: IPR013105; TPR 2.
DR InterPro: IPR013026; TPR region.
DR PROSITE: PS50293; TPR_REGION; 1.
SQ SEQUENCE 116 AA; 12945 MW; AC1273193B180CB1 CRC64;

Query Match 100.0%; Score 602; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTWVLTQQDALLLTGWLQYCHPDKASVLLAALLQHPDHQGGRTLLVALLKQEG	60
Db	1	MTWVLTQQDALLLTGWLQYCHPDKASVLLAALLQHPDHQGGRTLLVALLKQEG	60
Qy	61	EALAHVDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQQYLEEQNESTHP	116
Db	61	EALAHVDQLMQQGEADGPLWLCRSRACQAGRLDEARFAYQQYLEEQNESTHP	116

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RESULT 2
Q5CCAL_AERSO
ID Q5CCAL_AERSO PRELIMINARY; PRT; 116 AA.
AC Q5CCAL;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Ascy protein.
GN Name=ascy;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca fluviatilis.";
RL J. Fish Dis. 28:141-150(2005).
CC -----
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CC -----
CC EMBL: AJ749609; CAG44554.1; -; Genomic_DNA.
CC GO: GO:0005488; F:binding; IEA.
CC DR InterPro: IPR011990; TPR-like_helical.
CC DR InterPro: IPR013105; TPR 2.
CC SQ SEQUENCE 116 AA; 13033 MW; ECDSE1A5569E48A CRC64;

Query Match 90.9%; Score 547; DB 2; Length 116;
Best Local Similarity 92.8%; Pred. No. 1.1e-45;
Matches 107; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTWVLTQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60
Db 1 MTWVLTQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60

QY 61 EAAAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116
Db 61 EAAAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116

RESULT 3
Q699R4_AERHY
ID Q699R4_AERHY PRELIMINARY; PRT; 116 AA.
AC Q699R4;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Ascy.
GN Name=ascy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Marino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
CC -----
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CC -----
CC EMBL: AY528667; AAS91815.1; -; Genomic_DNA.
CC GO: GO:0005488; F:binding; IEA.
```

```
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR013105; TPR 2.
SQ SEQUENCE 116 AA; 13140 MW; FF798C42CSA104E9 CRC64;

Query Match 89.2%; Score 537; DB 2; Length 116;
Best Local Similarity 90.5%; Pred. No. 1.1e-44;
Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTWVLTQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60
Db 1 MTWVLTQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60

QY 61 EAAAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116
Db 61 EAAAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116

RESULT 4
Q6TLM6_AERHY
ID Q6TLM6_AERHY PRELIMINARY; PRT; 116 AA.
AC Q6TLM6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ascy.
GN Name=ascy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1 pathogenesis.";
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
CC EMBL: AY394563; AAR26135.1; -; Genomic_DNA.
CC GO: GO:0005488; F:binding; IEA.
CC DR InterPro: IPR005158; BTAD.
CC DR InterPro: IPR011990; TPR-like_helical.
CC DR InterPro: IPR013026; TPR_region.
CC Pfam: PF03704; BTAD; 1.
CC DR PROSITE: PS0293; TPR_REGION; 1.
CC SQ SEQUENCE 116 AA; 13174 MW; C8CBF54A5459863D CRC64;

Query Match 80.2%; Score 483; DB 2; Length 116;
Best Local Similarity 79.3%; Pred. No. 2.2e-39;
Matches 92; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 MTWVLTQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60
Db 1 MTWVLTQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRLLVALLKQEG 60

QY 61 EAAAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116
Db 61 EAAAHVDQLMOQGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNESTHP 116

RESULT 5
Q5XL08_AERHY
ID Q5XL08_AERHY PRELIMINARY; PRT; 116 AA.
AC Q5XL08;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Ascy.
```

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GN Name=ascy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU; DOI=10.1128/IAI.73.10.6446-6457.2005;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RL Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
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CC -----
CC EMBL; AY763611; AAV30229.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013105; TPR_2.
DR InterPro; IPR013026; TPR_region.
DR PROSITE; PS0293; TPR_REGION; 1.
SQ SEQUENCE 116 AA; 12997 MW; 48E0C804287AB265 CRC64;

Query Match 77.6%; Score 467; DB 2; Length 116;
Best Local Similarity 78.1%; Pred. No. 8.2e-38;
Matches 89; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTWLTSSQDDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 60
DB 1 MTWLTSSQDDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 60

QY 61 EAAAHVDQLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEEQNEST 114
DB 61 EAAAHVDQLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEEQNEPT 114

RESULT 6
ID Q84GY9 PHOLU PRELIMINARY; PRT; 109 AA.
AC Q84GY9;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE LscC.
GN Name=LscC;
OS Photorhabdus luminescens (Xenorhabdus luminescens);
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
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CC -----
CC EMBL; AY144116; AA018049.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
SQ SEQUENCE 109 AA; 12103 MW; 3D6DB56BD1B84FD2 CRC64;

Query Match 56.1%; Score 338; DB 2; Length 109;
Best Local Similarity 63.1%; Pred. No. 3.5e-25;
Matches 65; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 3 MWLTSSQDDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 62
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DB 1 MTLSSAKQOQSALLLTGWLQYGHDPDRARILLDALLALHPHQERRALVSLKLQEGSA 60
QY 63 ALAHVDQLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYL 105
DB 61 AKEHCSLLQEGQESAAALWLCVSRACQOEGNLEARSAYQYLL 103

RESULT 7
ID Q7NOW7 PHOLL PRELIMINARY; PRT; 109 AA.
AC Q7NOW7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Type III secretion protein SctY.
GN Name=SctY; OrderedLocNames=plu3762;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Kusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyassinat G., Gaudriault S.,
RA Medigue C., Lanois K., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RT Nat. Biotechnol. 21:1307-1313(2003).
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CC -----
CC EMBL; BX571871; CAE16134.1; -; Genomic_DNA.
DR Photolista; plu3762; -.
DR BioCyc; PLUM243265; PLU3762-MONOMER; -.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
KW Complete proteome.
SQ SEQUENCE 109 AA; 12176 MW; 516493CB4A65312D CRC64;

Query Match 53.8%; Score 324; DB 2; Length 109;
Best Local Similarity 60.2%; Pred. No. 8.4e-24;
Matches 62; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 3 MWLTSSQDDALLLTGWLQYGHDPDKASVLLAALLQIHPDHOGGRRTLLVALLKQGG 62
DB 1 MTLSSAKQOQSALLLTGWLQYGHDPDRARILLDALLALHPHQERRALVSLKLQKGS 60
QY 63 ALAHVDQLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYL 105
DB 61 AKEHCTLLQEGQESAAALWLCVSRACQOEGNLEARSAYQYLL 103

RESULT 8
ID YSCY_YEREN STANDARD; PRT; 114 AA.
AC Q93KU0; F21209;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 2.
DT 07-MAR-2006, entry version 17.
DE Chapterone protein yscY (Yop proteins translocation protein Y).
GN Name=yscY;
OS Yersinia enterocolitica.
OG Plasmid pYV, Plasmid pYve227, Plasmid pYve8081, and
OG Plasmid pYal27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
```

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND INDUCTION.
RC STRAIN=serotype O:3; PLASMID=pyV;
RX MEDLINE=90264308; PubMed=2160939;
RA Viitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrE gene is part of an operon in the lcr region of Yersinia
enterocolitica O:3.";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pyVe227;
RA Iriarte M., Lambermont I., Kerbouch C., Cornelis G.R.;
RT "Detailed genetic map of the pyVe227 plasmid of Yersinia
enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pyVe8081;
RX MEDLINE=21295118; PubMed=11402007;
RA DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Snellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-
calcium-response plasmid reveals a new virulence plasmid-associated
replicon";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pyVal27/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foulter B., Cornelis G.R.;
RT "DNA sequence and analysis of the pyVal27/90 virulence plasmid of
Yersinia enterocolitica strain A127/90.";
RL Res. Microbiol. 154:553-557(2003).
RN [5]
RP PLASMID=pyV;
RC MEDLINE=99102236; PubMed=9882687;
RA Iriarte M., Cornelis G.R.;
RT "Identification of SynE, YscX, and YscY, three new elements of the
Yersinia Yop virulon.";
RL J. Bacteriol. 181:675-680(1999).
RN [6]
CC -!- FUNCTION: Required for Yop secretion. Functions probably as a
chaperone which stabilizes yscX within the cell, before its
secretion (by similarity).
CC -!- SUBUNIT: Binds to yscX (by similarity).
CC -!- INDUCTION: Temperature seems to play the major role in regulation
of transcription of the lcrE-containing operon of pyV, whereas
Ca(2+) concentration has only a moderate effect at 37 degrees
Celsius, and no effect at room temperature.
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CC -----
DR EMBL: M22097; AAA98432.1; -; Genomic DNA.
DR EMBL: AF102990; AAD16819.1; -; Genomic DNA.
DR EMBL: AF336309; AAK69217.1; -; Genomic DNA.
DR EMBL: AY150843; AAN37530.1; -; Genomic DNA.
DR PIR: E35392; E35392.
DR InterPro: IPR011950; TPR-like_helical.
KW Chaperone; Plasmid.
FT CHAIN 1 114 Chaperone protein yscY.
FT FTID=PRO_000066501.
FT VARIANT 38 38 T -> M (in plasmid pyVe8081).
FT VARIANT 114 114 P -> L (in plasmid pyVe8081).
SQ SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;
Query Match 47.3%; Score 285; DB 1; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
QY 1 MTWLTQQQDALLTGWLQLOVGHDPKASVLLAALQHPHQGGRRTLLVALLKQGG 60
Db 1 MNITLTKRQEFELLNGWLQCGHAERACILLDALLTLNPEHLAQRRCRLVALLNNQ 60

QY 61 EAALAHVDLMQGGADGPWLRCRSRACLAGRLDEARFAYQOYLEBONES 113
Db 61 ERAEKAQWLISHDPLQAGNWLCLSRAQQLGDLKARHAYQHYLELKOHNES 113
RESULT 9
YSCY YERPE
ID YSCY_YERPE STANDARD; PRT; 114 AA.
AC Pe1417; P21209;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DE Chaperone protein yscY (Yop proteins translocation protein Y).
GN Name=yscY; Ordered locus names=YPCD1.35c, Y5043, Y0046, pCD48;
OS Yersinia pestis.
OG Plasmid pCD1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]_TaxID=632;
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
Yersinia pestis KIM5.";
RL Infect. Immun. 66:4611-4623(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
pestis.";
RL J. Bacteriol. 180:5192-5202(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Fellwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
avirulent to humans.";
RL DNA Res. 11:179-197(2004).
RN [5]
RP FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC STRAIN=KIM8;
RX PubMed=10714987; DOI=10.1128/JB.182.7.1834-1843.2000;
RA Day J.B., Plano G.V.;
RT "The Yersinia pestis yscY protein directly binds YscX, a secreted
component of the type III secretion machinery.";
RL J. Bacteriol. 182:1834-1843(2000).
CC -!- FUNCTION: Required for Yop secretion. Functions probably as a
chaperone which stabilizes yscX within the cell, before its
secretion.
CC

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CC -!- SUBUNIT: Binds to yscY.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
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DR EMBL; AF074612; AAC69796.1; -; Genomic_DNA.
DR EMBL; AF053946; AAC62570.1; -; Genomic_DNA.
DR EMBL; AL117189; CAB54912.1; -; Genomic_DNA.
DR EMBL; AE017043; AAS58567.1; -; Genomic_DNA.
DR PIR; T43590; T43590.
DR GenomeReviews; AE017043 GR; pCD48.
DR GenomeReviews; AL117189 GR; YPCD1.35C.
DR BioCyc; YPES229193:PCD48-MONOMER; -.
DR InterPro; IPR011990; TPR-like_helical.
KW Chaperone; Complete proteome; Plasmid.
FT CHAIN 1 114
FT   Chaperone protein yscY.
FT   /FTID=PRO.0000066502
FT SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;
Query Match 47.3%; Score 285; DB 1; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MTWVLTQQDALLTGWLOQYHPDKASVLLAALQIHPDHOGGRRTLLVALLKQGE 60
Db 1 MNITLTTRQQEFLLNGWLQCCGHAERACILLDALLTLNPEHLAGRRCRLVALLNNQ 60
Qy 61 EAALAHVDQLMQOGEADGPLWLCRSRACOLAGRLDEARFAYQOYLEEONES 113
Db 61 ERAEKEAQLSHDPLQAGNWLCLSLRAQQLGDLKARHAYQHYLELKHNES 113
RESULT 10
Q663K5 YERPS
ID O663K5 YERPS PRELIMINARY; PRT; 114 AA.
AC O663K5
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE yscY; putative type III secretion protein.
GN OrderedLocusNames=pYV0061;
OS Versinia pseudotuberculosis.
OG Plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chausser-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
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DR EMBL; BX936399; CAF25404.1; -; Genomic_DNA.
DR GO; GO:0005488; F-binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
KW Complete proteome; Plasmid.
FT CHAIN 1 114
FT SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;
Query Match 47.3%; Score 285; DB 2; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
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Qy 1 MTWVLTQQDALLTGWLOQYHPDKASVLLAALQIHPDHOGGRRTLLVALLKQGE 60
Db 1 MNITLTTRQQEFLLNGWLQCCGHAERACILLDALLTLNPEHLAGRRCRLVALLNNQ 60
Qy 61 EAALAHVDQLMQOGEADGPLWLCRSRACOLAGRLDEARFAYQOYLEEONES 113
Db 61 ERAEKEAQLSHDPLQAGNWLCLSLRAQQLGDLKARHAYQHYLELKHNES 113
RESULT 11
O30535_PSEAE
ID O30535_PSEAE PRELIMINARY; PRT; 109 AA.
AC O30535;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Pcr4.
GN Name=pCr4;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=388;
RX MEDLINE=98037517; PubMed=9371466;
RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7165-7168(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Broms J.E., Edqvist P.J., Carlsson K.E., Forsberg A., Francis M.S.;
RT "Mapping of a YscY Binding Domain within the LcrH Chaperone That Is
RT Required for Regulation of Yersinia Type III Secretion.";
RL J. Bacteriol. 187:7738-7752(2005).
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CC -----
DR EMBL; AF010150; AAC45943.1; -; Genomic_DNA.
DR EMBL; DQ000666; AAY17110.1; -; Genomic_DNA.
DR GO; GO:0005488; F-binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013026; TPR region.
DR PROSITE; PS50293; TPR_REGION; 1.
DR SEQUENCE 109 AA; 12222 MW; 3C3F19535EB038C9 CRC64;
Query Match 44.9%; Score 270; DB 2; Length 109;
Best Local Similarity 55.7%; Pred. No. 1.7e-18;
Matches 59; Conservative 12; Mismatches 35; Indels 0; Gaps 0;
Qy 3 MVLTSQQDALLTGWLOQYHPDKASVLLAALQIHPDHOGGRRTLLVALLKQGEA 62
Db 1 MTLKPTQQRLLMLGWLHLQCGQPRRAQVLLLEALLSVAPRRDGRALLALLQQQLGEP 60
Qy 63 ALAHVDQLMQOGEADGPLWLCRSRACOLAGRLDEARFAYQOYLEE 108
Db 61 AVRLCRQLQDGEPEGPLWLCRLSRAQLAGRLDAARAHAHALELE 106
RESULT 12
Q91328_PSEAE
ID Q91328_PSEAE PRELIMINARY; PRT; 109 AA.
AC Q91328;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
GN OrderedLocusNames=PA1702;
OS Pseudomonas aeruginosa.
```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 15692 / PAOI;
 RX MEDLINE=2043737; PubMed=10984043; DOI=10.1038/35023079;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.B., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAOI, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964 (2000).
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 DR EMBL: AE004597; AAC05091.1; -; Genomic_DNA.
 DR PRJ: C83432; C83432.
 DR BIOCyc; PAER287:PAI702-MONOMER; -.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like helical.
 DR InterPro; IPR013026; TPR region.
 DR PROSITE; PS50293; TPR_REGION; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 109 AA; 12265 MW; 3C3F19535EAFD937 CRC64;
 Query Match 43.9%; Score 264; DB 2; Length 109;
 Best Local Similarity 54.7%; Pred. No. 6.5e-18;
 Matches 58; Conservative 12; Mismatches 36; Indels 0; Gaps 0;
 OY 3 MVLTSQQDALLTGWLQYQHPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEA 62
 DB 1 MTLKPTQRRLLMLGWLHLCQGPRAQVLEALLSVAPERRDGRALLLALLQQLGEP 60
 OY 63 ALAHVDQLMOQGEADGFWLCSRACQLAGRLDEARFAVQOYLE 108
 DB 61 AVRLCRQLQEDGEEFGLMRLSRAEQLAGRLDAARAHAHALELE 106
 RESULT 13
 O6QVR8_VIBHA PRELIMINARY; PRT; 112 AA.
 ID Q6QVR8; VIBHA
 AC Q6QVR8; integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Vacy.
 GN Name=vacy;
 OS Vibrio Harveyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=669;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Henke J.M., Bassler B.L.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: AY524044; AA513313.1; -; Genomic_DNA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like helical.
 DR InterPro; IPR013026; TPR region.
 DR PROSITE; PS50293; TPR_REGION; 1.
 SQ SEQUENCE 112 AA; 12913 MW; BAB232661790D401 CRC64;
 Query Match 26.0%; Score 156.5; DB 2; Length 112;
 Best Local Similarity 36.3%; Pred. No. 2.4e-07;

Matches 41; Conservative 22; Mismatches 45; Indels 5; Gaps 3;
 OY 4 VLTSSQQDALLTGWLQYQHPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEA 63
 DB 1 MLQSKDVELLLHAALQVQYQKPEQAITLLDALLEPQHQEAVROTAVACLNSGRYTRS 60
 OY 64 LAHVVDQLMOQGEADGFWLCSRACQLAGRLDEARFAVQOYLE 112
 DB 61 IELCESLLKTEHSNKAGLWFLCSQARWKQDVEGARHARRHYLQSLNESNE 112
 RESULT 14
 O66PT9_PASPI PRELIMINARY; PRT; 108 AA.
 ID O66PT9_PASPI
 AC O66PT9; integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Putative TTSS protein Y.
 OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Photobacterium.
 OX NCBI_TaxID=38294;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
 RT "Photobacterium damsela subsp. piscicida encodes a functional type
 RT three secretion system (TTSS) that is involved in pathogenesis.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AY647223; AAU11477.1; -; Genomic_DNA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like helical.
 DR InterPro; IPR013026; TPR region.
 DR PROSITE; PS50293; TPR_REGION; 1.
 SQ SEQUENCE 108 AA; 12478 MW; 75C85FDF70C1470C CRC64;
 Query Match 24.7%; Score 148.5; DB 2; Length 108;
 Best Local Similarity 34.6%; Pred. No. 1.4e-06;
 Matches 36; Conservative 24; Mismatches 43; Indels 1; Gaps 1;
 OY 4 VLTSSQQDALLTGWLQYQHPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEA 63
 DB 1 MLQTKDVELLLHAALQVQYQKPEQAITLLDALLEPQHQEAVROTAVACLNSGRYTRS 60
 OY 64 LAHVVDQLMOQGEADGFWLCSRACQLAGRLDEARFAVQOYLE 106
 DB 61 IELCESLLKTEHSNKAGLWFLCSQARWKQDVEGARHARRHYLQ 104
 RESULT 15
 Q48IR6_PSE14 PRELIMINARY; PRT; 112 AA.
 ID Q48IR6_PSE14
 AC Q48IR6; integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 21-FEB-2006, entry version 7.
 DE Type III secretion component, putative (EC 2.4.1.-).
 GN OrderedLocusNames=PSPPH_2519;
 OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=264730;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
 RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
 RA Crabtree J., Creasy T., Davidsen T.M., Haft D.H., Zafar N., Zhou L.,

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RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,
RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,
RA Mansfield J., Collmer A., Buehl R.;
RT "Whole-genome sequence analysis of Pseudomonas syringae pv.
RT phaseolicola 1448A reveals divergence among pathovars in genes
RT involved in virulence and transposition.";
RL J. Bacteriol. 187:6488-6498(2005).
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CC -----
DR EMBL; CP000058; AA234406.1; -: Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07721; TPR_4; 1.
DR SMART; SM00028; TPR; 1.
DR PROSITE; PS50005; TPR; 2.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 112 AA; 12534 MW; 1DACD78D6FAE2C59 CRC64;

Query Match      23.3%; Score 140.5; DB 2; Length 112;
Best Local Similarity 34.0%; Pred. No. 9e-06;
Matches 35; Conservative 23; Mismatches 42; Indels 3; Gaps 1;

Qy 7 SQQDALLL---TGWLQYGHDPKASVLLAALLQIHDPHQGRRTLIVALLKQGEAA 63
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 4 SQDRECIELHGMGLYRRSGQPQRALVLLLIATLQAPTNSALLHSLVLAFTDSGDTDRA 63
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||

Qy 64 LAHVDOLMOQGEADGPLWLCRSRACQLAGRLDEARFAYQOYLE 106
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 64 IAAIDLIVEQOGESAALLLLRSRALWKAGRKDDARQCFFRYLE 106
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||
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Job time : 91.1024 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 21.4081 Seconds
(without alignments)
474.285 Million cell updates/sec

Title: US-10-813-908A-4
Perfect score: 602
Sequence: 1 MTWLTSSQDALLLTGWLQ.....ARFAYQYLEEQNESTHP 116

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	45.2	231	2	US-09-252-931A-29962
2	111.5	18.5	470	2	US-09-902-540-12418
3	96.5	16.0	143	2	US-09-198-452A-442
4	96.5	16.0	143	2	US-09-438-185A-425
5	88.5	14.7	870	2	US-09-252-991A-28407
6	83	13.8	1219	2	US-09-252-991A-28840
7	81	13.5	953	2	US-09-902-540-14681
8	80	13.3	368	2	US-09-252-991A-30717
9	79.5	13.2	956	2	US-09-902-540-10395
10	78.5	13.0	169	2	US-08-833-167-58
11	78.5	13.0	169	2	US-09-344-837A-58
12	78	13.0	325	2	US-09-510-238A-273
13	78	13.0	390	2	US-09-902-540-16621
14	77.5	12.9	171	2	US-08-833-167-44
15	77.5	12.9	171	2	US-08-833-167-45
16	77.5	12.9	171	2	US-08-833-167-47
17	77.5	12.9	171	2	US-08-833-167-57
18	77.5	12.9	171	2	US-08-833-167-59
19	77.5	12.9	171	2	US-08-833-167-60
20	77.5	12.9	171	2	US-09-344-837A-44
21	77.5	12.9	171	2	US-09-344-837A-45
22	77.5	12.9	171	2	US-09-344-837A-47
23	77.5	12.9	171	2	US-09-344-837A-57
24	77.5	12.9	171	2	US-09-344-837A-59
25	77.5	12.9	171	2	US-09-344-837A-60
26	77.5	12.9	299	2	US-09-510-238A-193

27	77.5	12.9	302	2	US-09-510-238A-168	Sequence 168, App
28	77.5	12.9	302	2	US-09-510-238A-170	Sequence 170, App
29	77.5	12.9	302	2	US-09-510-238A-172	Sequence 172, App
30	77.5	12.9	302	2	US-09-510-238A-174	Sequence 174, App
31	77.5	12.9	302	2	US-08-957-610A-474	Sequence 474, App
32	77.5	12.9	302	2	US-08-957-610A-476	Sequence 476, App
33	77.5	12.9	302	2	US-08-957-610A-478	Sequence 478, App
34	77.5	12.9	302	2	US-08-957-610A-480	Sequence 480, App
35	77.5	12.9	317	2	US-09-510-238A-169	Sequence 169, App
36	77.5	12.9	317	2	US-09-510-238A-171	Sequence 171, App
37	77.5	12.9	317	2	US-09-510-238A-173	Sequence 173, App
38	77.5	12.9	317	2	US-09-510-238A-175	Sequence 175, App
39	77.5	12.9	317	2	US-08-957-610A-475	Sequence 475, App
40	77.5	12.9	317	2	US-08-957-610A-477	Sequence 477, App
41	77.5	12.9	317	2	US-08-957-610A-479	Sequence 479, App
42	77.5	12.9	317	2	US-08-957-610A-481	Sequence 481, App
43	77.5	12.9	319	2	US-09-510-238A-199	Sequence 199, App
44	77.5	12.9	319	2	US-09-510-238A-201	Sequence 201, App
45	77.5	12.9	319	2	US-08-957-610A-505	Sequence 505, App

ALIGNMENTS

RESULT 1
US-09-252-991A-29962
; Sequence 29962, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29962
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29962

Query Match 45.2% Score 272; DB 2; Length 231;
Best Local Similarity 55.1%; Pred. No. 1.5e-26;
Matches 59; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

Qy 2 TMVLTSSQDALLLTGWLQYGHPRKASVLLAALQIHDPDHQGRRTLLVALLKQGE 61
Db 122 SMTLKQTQQRLLMLGWLHLQCGOPRAQVLLLEALLSVAPERRDGRALLLALLOQGLGE 181

Qy 62 AALAHVDQLMQQGEADGPLWLCRSQCQLAGRLDEARFAYQOYLELE 108
Db 182 PAVRLCQLOEGDEEPEGLWLCLSRAEQLAGRLDARAARAAHALELE 228

RESULT 2
US-09-902-540-12418
; Sequence 12418, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12418
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12418

Query Match 18.5%; Score 111.5; DB 2; Length 470;
Best Local Similarity 36.6%; Pred. No. 1.5e-05;
Matches 34; Conservative 8; Mismatches 44; Indels 7; Gaps 2;

QY 13 LLTGTWGLQY---GHPDK-----ASVLLAALLQIHDPDHQGRRTLLVALLKQGEAAALA 65
Db LLLAGFLDCYEPDGRPGQGPYAQALLRELLRSHDPDHAGVHHAWQVQMLNSGRPEAARD 115

QY 66 HVQLMQGGEADGPLWLCRACQAGRLDEAR 98
Db 116 SAHRLVALAPRAGPALLSAGRLLRQVGLVAEAR 148

RESULT 3
US-09-198-452A-442
; Sequence 442, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 442
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-442

Query Match 16.0%; Score 96.5; DB 2; Length 143;
Best Local Similarity 33.3%; Pred. No. 0.00025;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLTGTWGLQYGHDPKASVLLAALLQIHP----DHQGRRTLLVALLKQGEAAALAH 66
Db 19 EELRISGYSFLRQGHYSKAILFPEALVILDPLSIYDHQ-----TLGGYLQIGENSQALAV 74

QY 67 VDQLMQGGEADGPLWLCRACQAGRLDEARFAYQOYL 105
Db 75 LDQALRMQGDHLPTLLNKTKALFCLGRIBEAT-AIATYL 112

RESULT 4
US-09-438-185A-425
; Sequence 425, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 425
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0423
US-09-438-185A-425

Query Match 16.0%; Score 96.5; DB 2; Length 143;
Best Local Similarity 33.3%; Pred. No. 0.00025;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLTGTWGLQYGHDPKASVLLAALLQIHP----DHQGRRTLLVALLKQGEAAALAH 66
Db 19 EELRISGYSFLRQGHYSKAILFPEALVILDPLSIYDHQ-----TLGGYLQIGENSQALAV 74

QY 67 VDQLMQGGEADGPLWLCRACQAGRLDEARFAYQOYL 105
Db 75 LDQALRMQGDHLPTLLNKTKALFCLGRIBEAT-AIATYL 112

RESULT 5
US-09-252-991A-28407
; Sequence 28407, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28407
; LENGTH: 870
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28407

Query Match 14.7%; Score 88.5; DB 2; Length 870;
Best Local Similarity 26.5%; Pred. No. 0.032;
Matches 36; Conservative 20; Mismatches 55; Indels 25; Gaps 5;

QY 1 MTWVLTSQQDDALL-----LTGWLQYGHDPKASVLLAALLQIHPDHQGRRTLLV 52
Db 367 MVLLALRDELPAALLASTPRVLINAWTLLYAGRLAEAEDCIGQLARFLPMPASRQRVLL 426

QY 53 A-----LLKQGEAAALAH-----VDQLMQGGEADGPLWLCRACQAGRLDEAR 97
Db 427 AQWQGLFGILLHCRGERGAADYLRLEALQEPEDAWSQG--LICRSALMQLAIEGRMDQA 484

QY 98 RFAYQOYLEERQNES 113
Db 485 RLIGRDALRLAREHDS 500

RESULT 6
US-09-252-991A-28840
; Sequence 28840, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18


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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15774
; FILING DATE: 06-OCT-1996
; APPLICATION NUMBER: US 60/004,834
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: 2910/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-09-510-238A-273

Query Match          13.0%; Score 78; DB 2; Length 325;
Best Local Similarity 28.2%; Pred. No. 0.18; Indels 24; Gaps 4;
Matches 31; Conservative 15; Mismatches 40; Indels 24; Gaps 4;

Qy 24 GHPDKASVLLAALQIHPDHOGGRTLLVALLK-----QGGEA-----ALAH 66
Db 120 GSPGPGPISTINPPSPKSHKSPNMAFLKLSLEQVRKIQDGAALQEKLCATYKLC 179

Qy 67 VDQLMQQGEADG-----PLWLCRSRACQIAG---RLDEARFAYQVYLEEE 109
Db 180 PEELVLLGSLGIPWAPLSSCPSCFQALQALAGLSQLHSLGLFYQGLQALE 229

RESULT 13
US-09-902-540-16621
; Sequence 16621, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16621
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16621

Query Match          13.0%; Score 78; DB 2; Length 390;
Best Local Similarity 27.3%; Pred. No. 0.23; Indels 45; Gaps 8;
Matches 39; Conservative 17; Mismatches 17; Indels 45; Gaps 8;

Qy 10 QDALLLTGWLQYGHDPK--ASVLLAALQIHPDH-----QGGR--TLLV 52
Db 35 KDSALLGLARLRLAQHDETAARAVLQRLVALHPHPEALSHLARLDAEKGDARQLDLA 94

Qy 53 ALLKQ-----GGEAALAH-----VDQL-----MQQGEADGPLWLCRSRACQIAG 92
Db 95 ALAAQPKAGPFVFNHGRALLGHDRYAAAIPELERALALQPNQAQTLLTL--GNALQGDK 152

Qy 93 RLDEARFAYQVYLEEONESTH 115
Db 153 QLDR---ALRRYLEAAEANKTEH 172
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RESULT 14
US-08-833-167-44
; Sequence 44, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,167
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-167-44

Query Match          12.9%; Score 77.5; DB 2; Length 171;
Best Local Similarity 32.6%; Pred. No. 0.088;
Matches 28; Conservative 12; Mismatches 25; Indels 21; Gaps 4;

Qy 45 GGRRTLLVALLK-----QGGEA-----ALAHVDQLMQQGEADG-----PLWLCRSR 86
Db 83 GGSQFLKLSLEQVRKIQDGAALQEKLCATYKLCHEELVLLGSLGIPWAPLSSCPSCFQ 142

Qy 87 ACQIAG---RLDEARFAYQVYLEEE 109
Db 143 ALQIAGLSQLHSLGLFYQGLQALE 168

RESULT 15
US-08-833-167-45
; Sequence 45, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
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; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRADFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,167
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-167-45

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Query Match      12.9%; Score 77.5; DB 2; Length 171;
Best Local Similarity 32.6%; Pred. No. 0.088;
Matches 28; Conservative 12; Mismatches 25; Indels 21; Gaps 4;

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QY 45 GGRRTLLVLLK-----QGEGEA-----ALAHVDQLMQOGEADG---PLWLCSR 86
Db 47 GGSQSFLLKSLQVRKIQDGAAALQKLCATYKLCHPPELVLLGHSIGIPWAPLSSCP 106
QY 87 ACQLAG---RLDEARFAYQQYLEEE 109
Db 107 ALQLAGCLSQLHSGFLYQGLLQALE 132

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Search completed: June 16, 2006, 19:28:56
Job time : 22.4081 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 64.8846 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-4
Perfect score: 602
Sequence: 1 MTWVLTSSQDDALLLTGWLQ.....ARFAYQQYLEEQNESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main.*

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	100.0	116	5	US-10-813-908-4
2	141.5	23.5	113	6	US-11-098-686-10792
3	99	16.4	619	4	US-10-282-122A-50903
4	96.5	16.0	143	4	US-10-289-762-442
5	86.5	14.4	713	4	US-10-425-115-201172
6	86.5	14.4	719	4	US-10-425-114-51666
7	84.5	14.0	643	4	US-10-425-115-201174
8	84.5	14.0	737	4	US-10-425-114-57283
9	83	13.8	1586	4	US-10-282-122A-49391
10	83	13.8	1864	5	US-10-732-923-2391
11	79.5	13.2	1743	5	US-10-732-923-18400
12	79	13.1	107	6	US-11-096-568A-26393
13	79	13.1	108	6	US-11-096-568A-26392
14	79	13.1	124	6	US-11-096-568A-26391
15	78.5	13.0	1234	6	US-11-097-143-32322
16	78	13.0	325	4	US-10-695-584A-273
17	77.5	12.9	238	3	US-09-920-552-3
18	77.5	12.9	299	4	US-10-695-584A-193
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20	77.5	12.9	302	4	US-10-695-584A-170
21	77.5	12.9	302	4	US-10-695-584A-172
22	77.5	12.9	302	4	US-10-695-584A-174
23	77.5	12.9	317	4	US-10-695-584A-169
24	77.5	12.9	317	4	US-10-695-584A-171
25	77.5	12.9	317	4	US-10-695-584A-173
26	77.5	12.9	317	4	US-10-695-584A-175
27	77.5	12.9	319	4	US-10-695-584A-199

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28 77.5 12.9 319 4 US-10-695-584A-201 Sequence 201, App
29 77.5 12.9 321 4 US-10-695-584A-186 Sequence 186, App
30 77.5 12.9 321 4 US-10-695-584A-187 Sequence 187, App
31 77.5 12.9 321 4 US-10-695-584A-188 Sequence 188, App
32 77.5 12.9 321 4 US-10-695-584A-189 Sequence 189, App
33 77.5 12.9 329 3 US-09-920-552-9 Sequence 9, Appli
34 77.5 12.9 329 4 US-10-695-584A-190 Sequence 190, App
35 77.5 12.9 329 4 US-10-695-584A-191 Sequence 191, App
36 77.5 12.9 329 4 US-10-695-584A-192 Sequence 192, App
37 77.5 12.9 332 3 US-09-920-552-17 Sequence 17, Appl
38 77.5 12.9 352 5 US-10-481-935A-219 Sequence 219, App
39 77.5 12.9 367 5 US-10-481-935A-220 Sequence 220, App
40 77.5 12.9 1814 3 US-09-920-552-103 Sequence 103, App
41 77 12.8 233 4 US-10-369-493-11128 Sequence 11128, A
42 77 12.8 518 4 US-10-193-295-5 Sequence 5, Appli
43 77 12.8 518 4 US-10-622-516-5 Sequence 5, Appli
44 77 12.8 518 5 US-10-971-001A-5 Sequence 5, Appli
45 77 12.8 520 5 US-10-732-923-19653 Sequence 19653, A

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ALIGNMENTS

RESULT 1

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US-10-813-908-4
; Sequence 4, Application US/10813908
; Publication No. US20050058662A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and
; FILE REFERENCE: MIC01/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813,908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
US-10-813-908-4

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Query Match 100.0%; Score 602; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.6e-61;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTWVLTSSQDDALLLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG 60
Db 1 MTWVLTSSQDDALLLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG 60

Qy 61 EALAHVDQLMQQGEADGPLWLCRSACLAGRLDEARFAYQQYLEEQNESTHP 116
Db 61 EALAHVDQLMQQGEADGPLWLCRSACLAGRLDEARFAYQQYLEEQNESTHP 116

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RESULT 2

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US-11-098-686-10792
; Sequence 10792, Application US/11098686
; Publication No. US2006002496A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04

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QY 71 MQQGEADGPLWLCRSRACQLA-----GRLDARFAYQOYLEL-----EEQNEST 114
DB 405 SMSMVANGQETEVASVDCSIGDIYLSLGRYDEAVFAVQKALTVPKTSKGENHAT 458

RESULT 6
US-10-425-114-51666
; Sequence 51666, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51666
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700207818_FLI.pep
US-10-425-114-51666

Query Match 14.4%; Score 86.5; DB 4; Length 719;
Best Local Similarity 29.8%; Pred. No. 0.73;
Matches 34; Conservative 15; Mismatches 42; Indels 23; Gaps 4;

QY 19 LQLOYGHPDKASVLLAALQIHPDHQ-----GGRITLVALKKGEGEAAALAHVDQL 70
DB 356 LQL-----DEAQRICQIALDIHREHGCTASLEETADRRMLGLIYDTKGDHEAALEHLVMA 410

QY 71 MQQGEADGPLWLCRSRACQLA-----GRLDARFAYQOYLEL-----EEQNEST 114
DB 411 SMSMVANGQETEVASVDCSIGDIYLSLGRYDEAVFAVQKALTVPKTSKGENHAT 464

RESULT 7
US-10-425-115-201174
; Sequence 201174, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201174
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115056C.1.pep
US-10-425-115-201174

Query Match 14.0%; Score 84.5; DB 4; Length 643;
Best Local Similarity 30.7%; Pred. No. 1.1;
Matches 35; Conservative 14; Mismatches 42; Indels 23; Gaps 4;

QY 19 LQLOYGHPDKASVLLAALQIHPDHQ-----GGRITLVALKKGEGEAAALAHVDQL 70

DB 350 LQL-----DEAQRICQIALDIHREHGCTASLEETADRRMLGLIYDTKGDHEAALEHLVMA 404
QY 71 MQQGEADGPLWLCRSRACQLA-----GRLDARFAYQOYLEL-----EEQNEST 114
DB 405 GTAMIANGQETEVASVDCSIGDIYLSLGRYDEAVFAVQKALTVPKTSKGENHAT 458

RESULT 8
US-10-425-114-57283
; Sequence 57283, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57283
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17278G10_FLI.pep
US-10-425-114-57283

Query Match 14.0%; Score 84.5; DB 4; Length 737;
Best Local Similarity 30.7%; Pred. No. 1.3;
Matches 35; Conservative 14; Mismatches 42; Indels 23; Gaps 4;

QY 19 LQLOYGHPDKASVLLAALQIHPDHQ-----GGRITLVALKKGEGEAAALAHVDQL 70
DB 444 LQL-----DEAQRICQIALDIHREHGCTASLEETADRRMLGLIYDTKGDHEAALEHLVMA 498

QY 71 MQQGEADGPLWLCRSRACQLA-----GRLDARFAYQOYLEL-----EEQNEST 114
DB 499 GTAMIANGQETEVASVDCSIGDIYLSLGRYDEAVFAVQKALTVPKTSKGENHAT 552

RESULT 9
US-10-282-122A-49391
; Sequence 49391, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49391
; LENGTH: 1586
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49391
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Query Match 13.8%; Score 83; DB 4; Length 1586;
Best Local Similarity 28.8%; Pred. No. 4.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;
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QY 3 MVLTSQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEA 62
Db 391 IALNPSDVTVAQVLLGEMLLANGDPVGAEQAYRWALRRQADNPDAVRLVGALAAQGRGDE 450
QY 63 ALAHVDQL--MQQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 451 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAAREAGDLGARSILFEDAL 501
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RESULT 10
US-10-732-923-2391
; Sequence 2391, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 2391
; LENGTH: 1864
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-732-923-2391
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Query Match 13.8%; Score 83; DB 5; Length 1864;
Best Local Similarity 28.8%; Pred. No. 5.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;
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QY 3 MVLTSQQDALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGRRTLLVALLKQGEA 62
Db 669 IALNPSDVTVAQVLLGEMLLANGDPVGAEQAYRWALRRQADNPDAVRLVGALAAQGRGDE 728
QY 63 ALAHVDQL--MQQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 729 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAAREAGDLGARSILFEDAL 779
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RESULT 11
US-10-732-923-18400
; Sequence 18400, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
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; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18400
; LENGTH: 1743
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-732-923-18400
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Query Match 13.2%; Score 79.5; DB 5; Length 1743;
Best Local Similarity 23.8%; Pred. No. 14;
Matches 25; Conservative 21; Mismatches 40; Indels 19; Gaps 3;
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QY 9 QQDALLTCWLQYGHDPD--KASVLLAALLQIHPDHQGRRTLLVALLKQGEAALAH 66
Db 1627 QQHVQLISKFAQLFEPKHGDAERGRTLLEGLVTAHPKKTDLWLVAEAVLK----HLGIEH 1682
QY 67 VQQLMQQGEADGGLWLCRSRACQLAGRLDEARFAYQQYLELEEQN 111
Db 1683 ARKVLSE-----RACNLGFSIHKMRPLYKKWLEMSK 1714
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RESULT 12
US-11-096-568A-26393
; Sequence 26393, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26393
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(107)
; OTHER INFORMATION: Ceres Seq. ID no. 13564029
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (93)..(93)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (97)..(97)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-26393
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Query Match 13.1%; Score 79; DB 6; Length 107;
Best Local Similarity 35.7%; Pred. No. 0.55;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;
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QY 49 TLLVALLKQGEAALAHVDQLMQ--QGEADGGLWLCRSRACQLAGRLDEARFAYQQYLE 106
Db 11 TWISGLMHGHPQEAL---DLFQMQDRPDGATLLAVLRACSLAGRIDDARW----YFE 62
QY 107 LEEQNESTHP 116
Db 63 SMERVYGINP 72
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RESULT 13
US-11-096-568A-26392
; Sequence 26392, Application US/11096568A
; Publication No. US20060048240A1
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Perfect score: 602
Sequence: 1 MTWVLTQQDALLTTCWLQ.....ARFAYQVLELEQNESTHP 116
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 96747 seqs, 22556637 residues
Total number of hits satisfying chosen parameters: 96747
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications AA New:*
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2: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US06_NEW_PUB.pbp:*
3: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US07_NEW_PUB.pbp:*
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5: /EMC Celerra_SIDS3/ptodata/2/pubppaa/PCT_NEW_PUB.pbp:*
6: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US10_NEW_PUB.pbp:*
7: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US11_NEW_PUB.pbp:*
8: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US60_NEW_PUB.pbp:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	13.0	737	6	US-10-449-902-53938
2	74	12.3	599	6	US-10-449-902-47030
3	73.5	12.2	711	6	US-10-449-902-46399
4	73	12.1	457	7	US-11-221-332-32
5	71.5	11.9	570	6	US-10-953-349-4630
6	71.5	11.9	772	6	US-10-953-349-4629
7	71.5	11.9	802	6	US-10-953-349-4628
8	71	11.8	495	6	US-10-953-349-31757
9	71	11.8	530	6	US-10-953-349-31756
10	71	11.8	610	6	US-10-953-349-31755
11	70.5	11.7	228	7	US-11-289-102-381
12	70.5	11.7	804	6	US-10-449-902-38463
13	70	11.6	174	7	US-11-183-218-2
14	70	11.6	177	7	US-11-330-353-14
15	70	11.6	204	6	US-10-511-337-2461
16	70	11.6	787	7	US-11-330-353-16
17	69.5	11.5	599	6	US-10-449-902-53783
18	67	11.1	840	6	US-10-449-902-41113
19	66.5	11.0	469	6	US-10-953-349-24112
20	66.5	11.0	473	6	US-10-449-902-47334
21	66.5	11.0	876	6	US-10-449-902-44948
22	66	11.0	525	6	US-10-953-349-34744
23	66	11.0	699	6	US-10-449-902-45095
24	65	10.8	622	6	US-10-505-928-735
25	64.5	10.7	330	6	US-10-449-902-30918

26	64.5	10.7	626	6	US-10-449-902-46528	Sequence 46528, A
27	64.5	10.7	690	6	US-10-449-902-41502	Sequence 41502, A
28	64	10.6	272	6	US-10-449-902-37122	Sequence 37122, A
29	64	10.6	272	6	US-10-449-902-48530	Sequence 48530, A
30	64	10.6	711	6	US-10-449-902-48230	Sequence 48230, A
31	63.5	10.5	519	7	US-11-293-697-4747	Sequence 4747, Ap
32	63.5	10.5	842	7	US-11-266-446-68	Sequence 68, Appl
33	63.5	10.5	2364	7	US-11-289-102-242	Sequence 242, App
34	63	10.5	325	6	US-10-953-349-35099	Sequence 35099, A
35	63	10.5	515	6	US-10-449-902-37134	Sequence 37134, A
36	63	10.5	1011	6	US-10-449-902-36207	Sequence 36207, A
37	62.5	10.4	440	7	US-11-122-986-266	Sequence 266, App
38	62.5	10.4	440	7	US-11-122-986-268	Sequence 268, App
39	62.5	10.4	507	6	US-10-449-902-39176	Sequence 39176, A
40	62.5	10.4	794	6	US-10-449-902-42587	Sequence 42587, A
41	62.5	10.4	972	6	US-10-449-902-41157	Sequence 41157, A
42	62	10.3	236	6	US-10-449-902-34843	Sequence 34843, A
43	62	10.3	408	6	US-10-449-902-46992	Sequence 46992, A
44	62	10.3	587	6	US-10-449-902-40565	Sequence 40565, A
45	62	10.3	623	6	US-10-449-902-47699	Sequence 47699, A

ALIGNMENTS

RESULT 1
US-10-449-902-53938
; Sequence 53938, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53938
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53938
Query Match 13.0%; Score 78; DB 6; Length 737;
Best Local Similarity 34.7%; Pred. No. 0.81;
Matches 26; Conservative 17; Mismatches 20; Indels 12; Gaps 5;
Qy 28 KASVLLAALQIHPDHQGRRTLLVALLKQGEAAALAHVDQLMQQGEADGP-----LWLC 83
Db 289 KARLLKSVTQTPKHPGP--WIAAARLEEVAGKLQVA--QLLTQRCCECPTNEDVWL- 343
Qy 84 RSRACOLAGRLDEAR 98
Db 344 --KACRLASP-DEAK 355
RESULT 2
US-10-449-902-47030
; Sequence 47030, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF


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; SEQ ID NO 4629
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4629

Query Match      11.9%; Score 71.5; DB 6; Length 772;
Best Local Similarity 22.9%; Pred. No. 4.3;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 378 DALYNLGLGYMDLGRFORASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETEAKRAK 437
Qy 63 -----ALAHVDQLMQ-----GEADGPLWLCRSRAQCLAG 92
Db 438 LKMTNRVELHDAVSHLKQLQKKKKVKKGNSANESEGGPFIVVSSKPKTVG 486

RESULT 7
US-10-953-349-4628
; Sequence 4628, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4628
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4628

Query Match      11.9%; Score 71.5; DB 6; Length 802;
Best Local Similarity 22.9%; Pred. No. 4.5;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 408 DALYNLGLGYMDLGRFORASEMYTRVLAVPNHWRQAQLNKAVSLLGAGETEAKRAK 467
Qy 63 -----ALAHVDQLMQ-----GEADGPLWLCRSRAQCLAG 92
Db 468 LKMTNRVELHDAVSHLKQLQKKKKVKKGNSANESEGGPFIVVSSKPKTVG 516

RESULT 8
US-10-953-349-31757
; Sequence 31757, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31757
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31757

Query Match      11.8%; Score 71; DB 6; Length 495;
Best Local Similarity 25.4%; Pred. No. 2.9;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;
```

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Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 121 LQF---DEAEKLCRKALEIHREHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 177
Qy 73 QGEADGPLWLCRSRAQCLA-----GRLDEARFAYQOYLE-LEEONESTHP 116
Db 178 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 228

RESULT 9
US-10-953-349-31756
; Sequence 31756, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31756
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31756

Query Match      11.8%; Score 71; DB 6; Length 530;
Best Local Similarity 25.4%; Pred. No. 3.2;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 156 LQF---DEAEKLCRKALEIHREHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 212
Qy 73 QGEADGPLWLCRSRAQCLA-----GRLDEARFAYQOYLE-LEEONESTHP 116
Db 213 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 263

RESULT 10
US-10-953-349-31755
; Sequence 31755, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31755
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31755

Query Match      11.8%; Score 71; DB 6; Length 610;
Best Local Similarity 25.4%; Pred. No. 3.7;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYCHPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 236 LQF---DEAEKLCRKALEIHREHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 292
Qy 73 QGEADGPLWLCRSRAQCLA-----GRLDEARFAYQOYLE-LEEONESTHP 116
Db 293 TMVANG-----RDVEVATIDVAIGNTYLALARFDESVSFYQKALTVLKSARGDDHP 343
```


STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/330,353
FILING DATE: 12-Jan-2006
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
FILING DATE: 10-Sep-2002
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-Jan-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-Jan-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-Jan-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-330-353-14

Query Match 11.6%; Score 70; DB 7; Length 177;
Best Local Similarity 34.8%; Pred. No. 1.2;
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;
QY 57 QGGEA-----ALAHVDQLMQQGEADG----PLWLCSRACQLAG---RLDEARFA 100
Db 28 QGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAPLSSCPSQLAGCLSQLHSGFL 87
QY 101 YQYVLEEE 109
Db 88 YQGLLQALE 96

RESULT 15
US-10-511-937-2461
Sequence 2461, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2461
LENGTH: 204
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2461
Query Match 11.6%; Score 70; DB 6; Length 204;
Best Local Similarity 34.8%; Pred. No. 1.4;
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;
QY 57 QGGEA-----ALAHVDQLMQQGEADG----PLWLCSRACQLAG---RLDEARFA 100
Db 55 QGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAPLSSCPSQLAGCLSQLHSGFL 114
QY 101 YQYVLEEE 109
Db 115 YQGLLQALE 123
Search completed: June 16, 2006, 20:25:53
Job time : 5.99837 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 76.8618 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-5
Perfect score: 602
Sequence: 1 MTWLTSSQQDALLLTGWLQ.....ARFAYQQYLEEQNESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_8.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*
 - 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	100.0	116	5	ABB80772 A. salmon
2	272	45.2	231	7	ABO81216 Pseudomon
3	111.5	18.5	470	9	ABM93219 M. xanthu
4	99	16.4	619	6	ABU22979 Protein e
5	96.5	16.0	143	2	AA35024 Chlamydia
6	88.5	14.7	870	7	ABO79661 Pseudomon
7	86.5	14.4	122	8	ADx89002 Plant ful
8	84.5	14.0	123	3	AA14133 Bordetell
9	84.5	14.0	737	8	ADx94619 Plant ful
10	83	13.8	1219	7	ABO80094 Pseudomon
11	83	13.8	1586	6	ABU21467 Protein e
12	81	13.5	953	3	ABM95482 M. xanthu
13	80	13.3	143	10	Aee60312 Cat chlam
14	80	13.3	368	7	ABO81971 Pseudomon
15	79.5	13.2	517	9	Aeb49907 P. aerugi
16	79.5	13.2	956	9	ABM91196 M. xanthu
17	79	13.1	2519	7	ABM88218 Rice abio
18	78.5	13.0	169	2	AAW15044 G-CSF rec
19	78.5	13.0	1234	4	AB68510 Drosophil
20	78	13.0	390	9	ABM97422 M. xanthu
21	78	13.0	577	9	AEB41002 L. pneumo
22	78	13.0	587	9	AEB37691 L. pneumo
23	77.5	12.9	171	2	AAW15045 G-CSF rec

24	77.5	12.9	171	2	AAW15046	Aaw15046 G-CSF rec
25	77.5	12.9	171	2	AAW15048	Aaw15048 G-CSF rec
26	77.5	12.9	171	2	AAW15050	Aaw15050 G-CSF rec
27	77.5	12.9	171	2	AAW15043	Aaw15043 G-CSF rec
28	77.5	12.9	171	2	AAW15049	Aaw15049 G-CSF rec
29	77.5	12.9	171	2	AAW15051	Aaw15051 G-CSF rec
30	77.5	12.9	238	2	AA52089	Aay52089 Human ret
31	77.5	12.9	299	2	AAW17131	Aaw17131 Amino aci
32	77.5	12.9	302	2	AAW17108	Aaw17108 Amino aci
33	77.5	12.9	302	2	AAW17112	Aaw17112 Amino aci
34	77.5	12.9	302	2	AAW17106	Aaw17106 Amino aci
35	77.5	12.9	302	2	AAW17110	Aaw17110 Amino aci
36	77.5	12.9	302	2	AAW77845	Aaw77845 Multi-fun
37	77.5	12.9	302	2	AAW77839	Aaw77839 Multi-fun
38	77.5	12.9	302	2	AAW77841	Aaw77841 Multi-fun
39	77.5	12.9	302	2	AAW77843	Aaw77843 Multi-fun
40	77.5	12.9	317	2	AAW17113	Aaw17113 Amino aci
41	77.5	12.9	317	2	AAW17109	Aaw17109 Amino aci
42	77.5	12.9	317	2	AAW17111	Aaw17111 Amino aci
43	77.5	12.9	317	2	AAW17107	Aaw17107 Amino aci
44	77.5	12.9	317	2	AAW77842	Aaw77842 Multi-fun
45	77.5	12.9	317	2	AAW77840	Aaw77840 Multi-fun

ALIGNMENTS

RESULT 1
ABB80772
ID ABB80772 standard; protein; 116 AA.
XX AC ABB80772;
XX AC
DT 23-SEP-2002 (first entry)
XX DE
DE A. salmonicida type III secretion protein acr4 sequence.

XX KW Type III secretion protein; acrl; acr2; acr3; acr4; acrD; acrR; acrG;
XX KW acrv; acrH; antibiotic; vaccine; fish.
XX OS Aeromonas salmonicida.

XX PN WO200240514-A2.
XX PD 23-MAY-2002.
XX PF 15-NOV-2001; 2001WO-CA001589.
XX PR 15-NOV-2000; 2000US-0248864P.

XX (FREY/) FREY J.
XX (STUB/) STUBER K.
XX (THOR/) THORNTON J C.
XX (KUZU/) KUZYSK M A.
XX (BURI/) BURIAN J.

XX Frey J, Stuber K, Thornton JC, Kuzysk MA, Burian J;
XX WPI; 2002-537338/57.
XX N-ESDB; ABN86172.

XX Novel protein from Aeromonas salmonicida and nucleic acid encoding the
XX protein, useful for reducing susceptibility of fish to infection by a
XX virulent strain of Aeromonas salmonicida.

XX Claim 13; Page 27; 39pp; English.

XX The invention relates to A. salmonicida type III secretion genes and
XX encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.
XX A. salmonicida type III secretion apparatus is useful for producing
XX selected products, especially AexT. AcrV in vaccine, epitope or epitopic
XX region of AcrV or any other protein of A. salmonicida type III secretion
XX apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of A. salmonicida. The proteins and encoding DNA are
CC useful for manufacturing a diagnostic agent. Detecting the presence of
CC the genes of AcrD, AcrV or any other components of the A. salmonicida type
CC III secretion apparatus is useful for the production or quality control
CC or efficacy of vaccines made from A. salmonicida or its genes. The present
CC sequence represents the A. salmonicida type III secretion protein acr4
XX
SQ Sequence 116 AA;

Query Match 100.0%; Score 602; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e-65;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTWLTSSQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG 60
Db 1 MTWLTSSQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEG 60

Qy 61 EALAHVDQLMQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLEEQNESTHP 116
Db 61 EALAHVDQLMQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLEEQNESTHP 116

RESULT 2
ABO81216
ID ABO81216 standard; protein; 231 AA.

AC ABO81216;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #13391.

DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

KW Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

PA (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

DR N-PSDB; ABD14787.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 29962; 455pp; English.

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html

XX Sequence 231 AA;

Query Match 45.2%; Score 272; DB 7; Length 231;
Best Local Similarity 55.1%; Pred. No. 1.2e-24;
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

Qy 2 TMVLTSSQQDALLTGWLQYGHDPKASVLLAALQIHPDHQGGRTLLVALLKQEGE 61
Db 122 SMTLKQTQORLLMLWHLQCGPRAQVLLLEALLSVAPERRDGRALLALLQQGLGE 181

Qy 62 AALAHVDQLMQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLELE 108
Db 182 PAVRLCRQLQEDGEEBPGMLWLCLSRAEQLAGRLDAARAHAHALELE 228

RESULT 3
ABM93219
ID ABM93219 standard; protein; 470 AA.

AC ABM93219;

DT 02-JUN-2005 (first entry)

XX M. xanthus protein sequence, seq id 12418.

DE Transgenic plant; DNA replication; gene regulation; gene expression.

XX Myxococcus xanthus.

XX US6833447-B1.

XX 21-DEC-2004.

XX 10-JUL-2001; 2001US-00902540.

PR 10-JUL-2000; 2000US-0217883P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX WPI; 2005-028716/03.

XX New substantially purified Myxococcus xanthus nucleic acid molecule
XX encoding a nitrite reductase, useful for determining gene expression,
XX identifying mutations in a gene of interest, and for constructing
XX mutations in a gene of interest.

PS Example 2; SEQ ID NO 12418; 25pp; English.

CC The invention relates to a substantially purified nucleic acid molecule
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
CC a group of 7134 Myxococcus xanthus proteins and peptides. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO

XX Sequence 470 AA;

Query Match 18.5%; Score 111.5; DB 9; Length 470;
Best Local Similarity 36.6%; Pred. No. 0.00018;
Matches 34; Conservative 8; Mismatches 44; Indels 7; Gaps 2;

Qy 13 LLLTGWLQLOQY---GHPDK----ASVLLAALQIHPDHQGGRTLLVALLKQEGEAAALA 65
Db 56 LLLAGFLLDGVEPDGRPGQGPQAQALLRELLRSHPDHAGVHVWQVAMLNSGRPEAARD 115

QY 66 HVDQLMOQGEADGDLWLCSRACQLAGRLDEAR 98
Db 116 SAHRLVALPRAGPALLSAGRLQRLVGLVAEAR 148

RESULT 4

ABU22979
ID ABU22979 standard; protein; 619 AA.

XX AC ABU22979;
XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #8506.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Bordetella pertussis.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA26849.

XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 50903; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids
XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
XX CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 619 AA;

Query Match 16.4%; Score 99; DB 6; Length 619;
Best Local Similarity 29.0%; Pred. No. 0.0088;

Matches 29; Conservative 21; Mismatches 46; Indels 4; Gaps 2;

QY 21 LOYG--HPDKASVLLAALLQIHDPHQGGRTLLVALLKOGEGEAALAHVDQLMQQGEAD 77
Db 259 LEYGAKVDATRAQHQARAFINRNPDKRLRLMLAGQADGGDYGALAELOAMGRSPED 318

QY 78 GPLWLCRSRACQLAGRLDEARFAYQOYLEEEQNE-STHP 116
Db 319 FDLMFMAQLAYKAGRLDQARGYLQOYLDVQNOQMATAP 358

XX ID AAY35024 standard; protein; 143 AA.

XX AC AAY35024;

XX DT 17-OCT-2003 (revised)

XX DT 13-SEP-1999 (first entry)

XX DE Chlamydia pneumoniae transmembrane protein sequence.

XX KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
XX KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
XX KW neutralising epitope.

XX OS Chlamydothiia pneumoniae.

XX PN WO9927105-A2.

XX PD 03-JUN-1999.

XX PF 20-NOV-1998; 98WO-IB001890.

XX PR 21-NOV-1997; 97FR-00014673.

XX PR 04-NOV-1998; 98US-0107078P.

XX PA (GEST) GENSET.

XX PI Griffais R;

XX DR WPI; 1999-357842/30.

XX PT Genome sequence of Chlamydia pneumoniae.

XX PS Page 921; Disclosure; 1912pp; English.

XX CC AAY34584-Y35879 represent the proteins encoded by all the open reading
XX CC frames in the complete genome (see AAX9190) of Chlamydia pneumoniae. C.
XX CC pneumoniae causes respiratory disease such as pneumonia and bronchitis
XX CC and is thought to be a contributing factor in heart disease, sarcoidosis,
XX CC sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The
XX CC polypeptides encoded by the open reading frames of the C. pneumoniae
XX CC genome (see AAY34584-Y35879) can be used in immunogenic compositions as
XX CC vaccines. Vectors containing C. pneumoniae nucleotide sequences can also
XX CC be used as immunogenic compositions, especially where the vector directs
XX CC the expression of a neutralising epitope of C. pneumoniae. (Updated on 17
XX CC -OCT-2003 to standardise OS field)

XX SQ Sequence 143 AA;

Query Match 16.0%; Score 96.5; DB 2; Length 143;
Best Local Similarity 33.3%; Pred. No. 0.0026;

Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;


```
CC invention.
```

XX
SQ Sequence 719 AA; Query Match 14.4%; Score 86.5; DB 8; Length 719;
Best Local Similarity 29.8%; Pred. No. 0.37; Mismatches 15; Indels 23; Gaps 4

QY 19 LQLVGHGPKASVLAAALQLIHPDHQ-----GGRTLLVALLKQGEGEALAHLAVDQL 70
 ||| : | : | : | : | : | : | : | : | : | :
Db 356 LQL-----DEAQRLCQIALDIHREHRITASLEETADRLMGLICTKGDEHAALHLYWA 410
 ||| : | : | : | : | : | : | : | : | : | :

QY 71 MQQEAGDCPLWCLRSRACOLA-----GRLDARFAYQQYLEL---BEQNEST 114
 ||| : | : | : | : | : | : | : | : | : | :
Db 411 SMSVMANGQETEVAUSDGSIGDYILSLGRYDAVFAYOKALTVPFKTSKENHAT 464
 ||| : | : | : | : | : | : | : | : | : | :

RESULT 8
AAB14133 ID AAB14133 standard; protein; 122 AA.
XX AC AAC14133;
DT 02-FEB-2001 (first entry)
XX Bordetella pertussis class II gene protein Orf2.
DE Orf2; bacterial infection; anti-bacterial; vaccine; whooping cough;
KW type III secretion system; virulence factor; pathogenicity island;
XX
OS Bordetella pertussis.
XX WO200037493-A2.
PN
PD 29-JUN-2000.
PP 21-DEC-1999; 99WO-EPO10297.
PR 21-DEC-1998; 98GB-00028217.
PS (ULBR) UNIV LIBRE BRUXELLES.
PA Bollen A, Fauconnier A, Godfried E;
PI WPI; 2000-452178/39.
DR N-PSDB; AAA64871, AAA64890.
XX Novel polypeptides derived from Bordetella pertussis, useful for treating
PT and diagnosing Bordetella infection.
XX Claim 1; Page 127; 165pp; English.
XX
CC Bordetella pertussis possesses a type III secretion system. Type III
secretion systems allow bacteria to target virulence factors directly at
host cells. The present sequence is the Orf2 protein of B. pertussis. The
present protein is encoded by a class II type gene and is an effector
protein involved in the type III secretion system of B. pertussis i.e. a
Bordetella pathogenicity protein. The gene of the present protein is
located within a pathogenicity island (see AAA64890). A pathogenicity
island is a compact, distinct genetic unit carrying virulence genes. The
present protein may be used to treat or diagnose B. pertussis infection,
e.g. as a vaccine. Whooping cough is a disease caused by infection by B.
pertussis
XX SQ Sequence 122 AA;

Query Match 14.0%; Score 84.5; DB 3; Length 122;
Best Local Similarity 32.6%; Pred. No. 0.062; Mismatches 11; Indels 3; Gaps 1

QY 19 LQLVGHGPKASVLAAALQLIHPDHQGGRTLLVALLKQGEGEALAHLAVDQMCGGEADG 78
 ||| : | : | : | : | : | : | : | : | : | :
Db 26 LBORQW----SKTVALLDALDLADAIDSQSLLALGYLHQGFPMVALVTLDKRALRPDA 82
 ||| : | : | : | : | : | : | : | : | : | :

QV	79	PLWLCRSRACQAGRLDEARFAYQOYLEL 107
		: : : : : :
DB	83	AGHLVRAQAMQALNRPDDARQMRDYMAL 111
RESULT 9		
ADX94619		
ID	ADX94619	standard; protein; 737 AA.
XX		
AC	ADX94619;	
XX		
DT	21-APR-2005	(first entry)
XX		
DE	Plant full length insert polypeptide seqid 57283.	
XX		
KW	plant protectant; plant growth regulant; gene therapy; plant;	
KW	recombinant DNA construct; physical array; plant breeding marker;	
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;	
KW	growth rate; cell cycle pathway; disease resistance;	
KW	galactomannan production; lignin production; plant growth regulator;	
KW	yield; plant growth; plant development; seed oil; protein yield;	
KW	protein content.	
XX		
OS	Unidentified.	
XX		
PN	US2004034888-A1.	
XX		
PD	19-FEB-2004.	
XX		
PF	28-APR-2003; 2003US-00425114.	
XX		
PR	06-MAY-1999; 99US-00304517.	
PR	05-NOV-2001; 2001US-00985678.	
XX		
PA	(LTUJ/) LIU J.	
PA	(ZHOU/) ZHOU Y.	
PA	(KOVA/) KOVALIC D K.	
PA	(SCRE/) SCREEN S E.	
PA	(TABA/) TABASKA J E.	
PA	(CAOY/) CAO Y.	
XX		
PI	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;	
XX		
DR	WPI; 2004-180133/17.	
XX		
PT	New recombinant DNA construct, useful for improving plant tolerance to	
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or	
PT	pests, for conferring increased resistance to plant disease, or for	
PT	improving yield.	
XX		
PS	Claim 1; SEQ ID NO 57283; 15pp; English.	
XX		
CC	The invention describes a recombinant DNA construct comprising a	
CC	polynucleotide consisting of a sequence encoding an amino acid sequence	
CC	available in electronic form from the US patent office at	
CC	ftp.segdata.uspco.gov/sequence.html?docID:2004034888. The polynucleotide	
CC	of the invention are also useful in physical arrays of molecules and as	
CC	plant breeding markers. The recombinant DNA construct is useful for	
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme	
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in	
CC	plant cells by modification of the cell cycle pathway, for conferring	
CC	increased resistance to plant disease, for producing galactomannan,	
CC	lignin or plant growth regulators, for increasing the rate of homologous	
CC	recombination in plants, for improving yield by modification of	
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake	
CC	or by providing improved plant growth and development under at least one	
CC	stress condition or for modifying seed oil or protein yield and/or	
CC	content. This is the amino acid sequence of a plant full length insert	
CC	polypeptide that can be used in the recombinant DNA construct of the	
CC	invention.	
XX		

SQ	Sequence 737 AA;		
QY	Query Match Best Local Similarity 14.0%; Score 84.5; DB 8; Length 737; Matches 35; Conservative 14; Mismatches 42; Indels 23; Gaps 4;		
QY	19 LQYQYGHDPKASVLLAALQIHPDHQ-----GRTLLVALLKQGEAALAHVDQL 70	1 MTWVLTSQQDALLLTGWLQYQYGHDPKASVLLA-ALLOIHPDHQGRRTLLVALLKQGE 59	
Db	444 LQL-----DEAQRCLQIALDIHREHGGTASLEETADRLMGLIYDTKGDHEAALEHLVMA 498	56 LVILWLTFSSEVFMSG-----DGEFPAVSVMYAEELLQAHPENDALRLTLDLLVLKGD 110	
QY	71 MQQGEADGPLWLCRSACQLA-----GRLEARFAYQVLEL-----EQNEST 114	60 GEAAALAHVDQLMQQGEADGPLW 81	
Db	499 GTAMIANGOETEVASVDCSIGDIYLSLGRYDEAVFAYQKALTVPKTSKGENHAT 552	111 FEQARHHLARLRGKDRLATPFY 132	
RESULT 10		RESULT 11	
ABO80094		ABU21467	
ID	ABO80094 standard; protein; 1219 AA.	ID	ABU21467 standard; protein; 1586 AA.
AC	ABO80094;	AC	ABU21467;
XX		XX	
DT	29-JUL-2004 (first entry)	DT	19-JUN-2003 (first entry)
XX		XX	
DE	Pseudomonas aeruginosa polypeptide #12269.	DE	Protein encoded by Prokaryotic essential gene #6994.
KW	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.	KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.
OS	Pseudomonas aeruginosa.	OS	Burkholderia fungorum.
XX		XX	
PN	US6551795-B1.	PN	WO200277183-A2.
XX		XX	
PD	22-APR-2003.	PD	03-OCT-2002.
XX		XX	
PF	16-FEB-1999; 99US-00252991.	PF	21-MAR-2002; 2002WO-US009107.
XX		XX	
PR	18-FEB-1998; 98US-0074788P.	PR	21-MAR-2001; 2001US-00815242.
XX		PR	06-SEP-2001; 2001US-00948993.
PR	27-JUL-1998; 98US-0094190P.	PR	25-OCT-2001; 2001US-0342923P.
XX		PR	08-FEB-2002; 2002US-00072851.
XX	(GENO-) GENOME THERAPEUTICS CORP.	PR	06-MAR-2002; 2002US-0362699P.
PA		XX	
PI	Rubenfield MJ, Nolling J, Deloughery C, Bush D;	PA	(ELIT-) ELITRA PHARM INC.
XX		XX	
DR	WPI; 2003-615309/58.	PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
DR	N-PSDB; ABD13665.	PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX		XX	
PT	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.	DR	WPI; 2003-029926/02.
XX		XX	N-PSDB; ACA25337.
PS	Disclosure; SEQ ID NO 28840; 455pp; English.	PT	New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
XX		XX	
CC	The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biotech technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html	PS	Claim 25; SEQ ID NO 49391; 1766pp; English.
XX		XX	
CC	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required	CC	The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 11.7886 Seconds
(without alignments)
946.773 Million cell updates/sec

Title: US-10-813-908A-5
Perfect score: 602
Sequence: 1 MTWVTSQQQDALLLTGWLQ.....ARFAYQVYLEEQNESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs. 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

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1: _pirl:*
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```
2: pir2:*
```

```
3: pir3:*
```

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	285	47.3	114	2	E35392	hypothetical prote
2	285	47.3	114	2	T43590	hypothetical prote
3	264	43.9	109	2	C83432	conserved hypothet
4	96.5	16.0	142	2	E86543	CT274 hypothetical
5	96.5	16.0	142	2	A72081	CT274 hypothetical
6	88.5	14.7	87	2	H83217	probable transcrip
7	86.5	14.4	384	2	S74806	hypothetical prote
8	86	14.3	590	2	D83063	hypothetical prote
9	84	14.0	698	2	A82593	hypothetical prote
10	83	13.8	1193	2	F83264	hypothetical prote
11	80.5	13.4	1334	2	T50568	probable multi-dom
12	80	13.3	548	2	AH2962	cellulose biosynth
13	80	13.3	553	2	F98320	hypothetical prote
14	79.5	13.2	576	2	G49376	hypothetical prote
15	78.5	13.0	139	2	G71534	hypothetical prote
16	78	13.0	188	2	PQ0180	CytB protein - Syn
17	77	12.8	520	2	S27197	hydroxymethylgluta
18	77	12.8	673	2	F87636	TPR domain protein
19	76.5	12.7	1810	2	E88481	protein C16A3.2 li
20	76	12.6	320	2	H64332	hypothetical prote
21	75.5	12.5	844	2	T05227	hypothetical prote
22	75	12.5	400	2	B64733	protein transport
23	75	12.5	593	2	AE3443	tetratricopeptide
24	74.5	12.4	265	2	S31070	rpcE protein - Syn
25	74.5	12.4	724	2	AG1571	hypothetical prote
26	74	12.3	400	2	F90642	probable integral
27	74	12.3	400	2	F85493	probable integral
28	74	12.3	593	1	XY22FG	frzG protein - Myx
29	73.5	12.2	172	2	B83696	hypothetical prote

ALIGNMENTS

RESULT 1

hypothetical protein 4 - Yersinia enterocolitica
E35392
C:Species: Yersinia enterocolitica
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Oct-2004
C:Accession: E35392
R:Viitainen, A.M.; Toivanen, P.; Skurnik, M.

J. Bacteriol. 172, 3152-3162, 1990

A:Title: the lcrE gene is part of an operon in the lcr region of *Yersinia enterocolitica*

A:Reference number: A35392; MUID:90284308; PMID:2160939

A:Accession: E35392

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-114 <VII>

A:Cross-references: UNIPROT:Q93KU0; UNIPARC:UPI0000000246; GB:M32097; NID:G155454; PID:G155454

C:Superfamily: chaperone protein vscy

Query Match	47.3%	Score	285;	DB 2;	Length	114;	
Best Local Similarity	52.2%;	Pred. No.	1.6e-22;				
Matches	59;	Conservative	14;	Mismatches	40;	Indels	0;

Qy	1	MTWLVTSQOQDALLTGWLOLOQHPDKASVLLAALLQIHPDHQCGRRLLVALLKQGBG	60
Db	1	MTWLVTSQOQDALLTGWLOLOQHPDKASVLLAALLQIHPDHQCGRRLLVALLKQGBG	60
Qy	61	EALAAHVDDLMQOQGEADGPLWLCRSRACQAGRLDEARFAYQYILELEEQNES	113
Db	61	EAAKEAAMLVISHDPLQAGNWLCLSRQOQNGDQKARHAYOHYLELKDHNES	113

RESULT 2

T43590
hypothetical protein Y0046 - Yersinia pestis plasmid pCD1
C:Species: Yersinia pestis
C:/date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-Oct-2004
C:/Accession: T43590; T42885
R/Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi,
T. Bacterial 180 5192-5202 1998

J. Bacteriol. 180, 3192-3202, 1998
 A;Title: Structural organization of virulence-associated plasmids of *Yersinia pestis*.
 A;Reference number: Z23578; MUID:98422474; PMID:9748454
 A;Accession: T43590
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Molecule type: DNA
 A;Residues: 1-114 <HUP>
 A;Cross-references: UNIPROT:P61417; UNIPARC:UPI0000000246; EMBL:AF053946; NID:g2996222,
 A;Experimental source: strain KIM
 R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
 Infect. Immun. 66, 4611-4623, 1998
 A;Title: DNA sequencing and analysis of the low-Ca²⁺-response plasmid pCD1 of *Yersinia*
 A;Reference number: Z22273; MUID:98427122; PMID:9746557
 A;Accession: T42885
 A;Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA
A:Residues: 1-114 <PER>
A:Cross-references: UNIPARC:UPI0000000246; EMBL:AF074612; NID:G3822037; PIDN:AAC69796.1;
A:Experimental source: strain KIMS
C:Genetics:
A:Genome: plasmid pCD1
A>Note: Y0046
C:Superfamily: chaperone protein yscY

Query Match 47.3%; Score 285; DB 2; Length 114;
Best Local Similarity 52.2%; Pred. No. 1.6e-22;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;

QY 1 MTWVLSQQDALLTGWLQYGHDPKASVLLAALLQIHPDHOGGRRRTLLVALLKQGG 60
DB 1 MNTILTKRQQEFLLNGWLQCGHAEACILLDALTNPHELAGRRCKRLVALLNNQG 60

QY 61 EAAIAHVQDLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYLEEQNES 113
DB 61 ERAEKAQWLISHDPLQAGNWLCLSRQAQLNGLDKARHAYQHYLELKDNES 113

RESULT 3
C83432
Conserved hypothetical protein in type III secretion PA1702 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: C83432
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83432
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-109 <STO>
A:Cross-references: UNIPROT:Q91328; UNIPARC:UPI000000C5452; GB:AE0044597; GB:AE004091; NID:G89878795; PIDN:G89878795; PMD:10871362
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1702

Query Match 43.9%; Score 264; DB 2; Length 109;
Best Local Similarity 54.7%; Pred. No. 2.4e-20;
Matches 58; Conservative 12; Mismatches 36; Indels 0; Gaps 0;

QY 3 MVLTSQQDALLTGWLQYGHDPKASVLLAALLQIHPDHOGGRRRTLLVALLKQGEA 62
DB 1 MTLKPTQORLLMLGWLHLQCGQPRRAQVLLLEALLSVAPERDGRALLALLQQLGEP 60

QY 63 ALAHVQDLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYLELE 108
DB 61 AVRLCKLOQEDGEEPLWLRCSRAEQLAGRLDAARAHARALELE 106

RESULT 4
E86543
Ct274 hypothetical protein [imported] - Chlamydomophila pneumoniae (strain J138)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86543
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Inoue, K.
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86543
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <STO>
A:Cross-references: UNIPROT:Q928C0; UNIPARC:UPI000000D41E0; GB:BA000008; NID:G89878795; PIDN:G89878795; PMD:10871362
A:Experimental source: strain J138
C:Genetics:
A:Gene: PA3420

A:Gene: CPj0423

Query Match 16.0%; Score 96.5; DB 2; Length 142;
Best Local Similarity 33.3%; Pred. No. 0.0083;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYGHDPKASVLLAALLQIHP----DHQGRRTLLVALLKQGEAALAH 66
DB 18 EELRISGYSFLRQGHYSKAILFREALVILDPISYDHQ----TLGGLYLIQIGNSQALAV 73

QY 67 VDQLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYL 105
DB 74 LDQALRMQGDHLPTLLNKTALFCLGRIEAT-AIATYL 111

RESULT 5
A72081
Ct274 hypothetical protein - Chlamydomophila pneumoniae (strain CWL029)
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: A72081
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: A72081
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <ARN>
A:Cross-references: UNIPROT:Q928C0; UNIPARC:UPI000000D41E0; GB:AE001625; GB:AE001363; NID:G89878795; PIDN:G89878795; PMD:10871362
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: CPn0423

Query Match 16.0%; Score 96.5; DB 2; Length 142;
Best Local Similarity 33.3%; Pred. No. 0.0083;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQYGHDPKASVLLAALLQIHP----DHQGRRTLLVALLKQGEAALAH 66
DB 18 EELRISGYSFLRQGHYSKAILFREALVILDPISYDHQ----TLGGLYLIQIGNSQALAV 73

QY 67 VDQLMQOGEADGPLWLCRSRACQAGRLDEARFAYQOYL 105
DB 74 LDQALRMQGDHLPTLLNKTALFCLGRIEAT-AIATYL 111

RESULT 6
H83217
Probable transcription regulator PA3420 [imported] - Pseudomonas aeruginosa (strain PAO)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83217
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83217
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-827 <STO>
A:Cross-references: UNIPROT:Q9HYI5; UNIPARC:UPI000000C5A01; GB:AE004763; GB:AE004091; NID:G89878795; PIDN:G89878795; PMD:10871362
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3420
C:Superfamily: regulatory protein malt

Query Match 14.7%; Score 88.5; DB 2; Length 827;
Best Local Similarity 26.5%; Pred. No. 0.38; Indels 25; Gaps 5;

Qy 1 MTWLTSSQDALL-----LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLV 52
Db 354 MVLALRDLPAALLASTPRVLINAWTLLYAGRLAEADCTGQARFLPMPASRQRVLL 413
Qy 53 A-----LLKQGEAEALAH-----VDQLMQQGEADGPIWLCRSRACOLA---GRIDEA 97
Db 414 AQWQGLFGILLHCRGERGAADYLRLEALEQLPEDAWSQ--LICRSALMQLAMIEGRMDQA 471
Qy 98 RFAYQOQYLEEQNES 113
Db 472 RLIGRDALRLAREHDS 487

RESULT 7
S74806
hypothetical protein sll1628 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384 <KAN>
A;Cross-references: UNIPROT:P73719; UNIPARC:UPI00000C10C7; EMBL:D90909; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
F;266-299/Domain: tetratricopeptide repeat homology <TT1>
F;300-333/Domain: tetratricopeptide repeat homology <TT2>
F;334-367/Domain: tetratricopeptide repeat homology <TT3>

Query Match 14.4%; Score 86.5; DB 2; Length 384;
Best Local Similarity 28.1%; Pred. No. 0.27;
Matches 27; Conservative 15; Mismatches 49; Indels 5; Gaps 1;

Qy 18 WL-----QLQVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAEALAHVDQLMQ 72
Db 269 WNLGIIQQAQRGELETAISNGEAIISLPQNTSNAQNGSALGVMGKLEALANFDEALA 328

Qy 73 QGEADGPIWLCRSRACOLAGRLDEARFAYQOQYLE 108
Db 329 QNPDDAEVWLRSGLLLEAMERKEAIPSEYKALTLE 364

RESULT 8
D83063
hypothetical protein PA4667 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83063
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <STO>
A;Cross-references: UNIPROT:P42810; UNIPARC:UPI0000013A09A; GB:AE004880; GB:AE004091; NID
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4667

Query Match 14.3%; Score 86; DB 2; Length 590;
Best Local Similarity 29.1%; Pred. No. 0.48;
Matches 30; Conservative 15; Mismatches 58; Indels 0; Gaps 0;

Qy 13 LLLTGWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAEALAHVDQLMQ 72
Db 238 LLLRSRLQSMKRSDEALPLLKAGIKEHPDDKRVLYARVLLVQNRLDDAKAEFAGLVQ 297
Qy 73 QGEADGPIWLCRSRACOLAGRLDEARFAYQOQYLEEQNESTH 115
Db 298 QFPDDDDLRFLSFLAVLCLEAQAWDEARIYLELVERDHSVDAAH 340

RESULT 9
A82593
hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82593
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-698 <SIM>
A;Cross-references: UNIPROT:Q9PBH5; UNIPARC:UPI00000C2968; GB:AE004030; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kutamae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2169

Query Match 14.0%; Score 84; DB 2; Length 698;
Best Local Similarity 28.6%; Pred. No. 0.92;
Matches 26; Conservative 13; Mismatches 50; Indels 2; Gaps 1;

Qy 15 LTCWLQLOVGHDPKASVLLAALLQIHPDHQGGRTLLVALLKQGEAEALAHVDQLMQQ 74
Db 250 LTGEFELLAGHPDRALTHLRQVLATWPDPTLEALLTANKQLDMDDDARITLDAALDIK 309
Qy 75 EADGPIWLCRSRACOLAGRLDEARFAYQOQYL 105
Db 310 PRNHDLWLARLAVPVGS--DEARIVIERWL 338

RESULT 10
F83264
hypothetical protein PA3063 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83264
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83264
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1193 <STO>

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 91.1024 Seconds
(without alignments)
1177.815 Million cell updates/sec

Title: US-10-813-908A-5
Perfect score: 602
Sequence: 1 MTWVLTSSQDDALLLTGWLQ.....ARFAYQOYLEEQNESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602	100.0	116	2	Q8GA92 aeromonas s
2	547	90.9	116	2	Q5CCAL aeromonas s
3	537	89.2	116	2	Q699R4 aeromonas h
4	483	80.2	116	2	Q6TLM6 aeromonas h
5	467	77.6	116	2	Q5XL08 aeromonas h
6	338	56.1	109	2	Q84GV9 photorhabdu
7	324	53.8	109	2	Q7N0W7 photorhabdu
8	285	47.3	114	1	Q93KU0 yersinia en
9	285	47.3	114	1	P61417 yersinia pe
10	285	47.3	114	2	Q663K5 yersinia ps
11	270	44.9	109	2	Q30535 pseudomonas
12	264	43.9	109	2	Q91328 pseudomonas
13	156.5	26.0	112	2	Q6QVR8 vibrio harv
14	148.5	24.7	108	2	Q66PT9 pasteurella
15	140.5	23.3	112	2	Q48IR6 pseudomonas
16	138.5	23.0	114	2	Q87P55 vibrio para
17	126	20.9	700	2	Q2JHG5 cyanobacter
18	118	19.6	798	2	Q2W4R4 magnetospi
19	116	19.3	788	2	Q31890 synecococc
20	116	19.3	788	2	Q5N228 synecococc
21	114.5	19.0	142	2	Q9AN16 bradyrhizob
22	107.5	17.9	467	2	Q5LTY9 silicibacte
23	107	17.8	955	2	Q34XX4 alkalilimni
24	105.5	17.5	192	2	Q34XH6 alkalilimni
25	105	17.4	1837	2	Q2RRU7 rhodospiril
26	104	17.3	313	2	Q39ZX0 pelobacter
27	99.5	16.5	530	2	Q4C0T9 crocospaer
28	99	16.4	626	2	Q7W184 bordetella
29	99	16.4	628	2	Q7VUG8 bordetella
30	99	16.4	628	2	Q7WNY7 bordetella
31	98	16.3	422	2	Q67NN9 symbiobacte

32	97	16.1	443	2	Q40MR2 desulfuromo
33	96.5	16.0	142	2	Q9Z8C0 chlamydia p
34	95	15.8	774	2	Q2JSZ1 cyanobacter
35	94	15.6	582	2	Q5LPE5 silicibacte
36	93.5	15.5	560	2	Q2ND56 erythroba
37	93	15.4	1138	2	Q46GI8 methanosarc
38	93	15.4	1349	2	Q9L096 streptomyce
39	92.5	15.4	161	2	Q3QHM9 shewanella
40	92.5	15.4	652	2	Q399P6 burkholderi
41	92	15.3	718	2	Q2IFU6 anaeromyxob
42	91	15.1	700	2	Q3X9C2 methylobaci
43	91	15.1	1198	2	Q4KCF4 pseudomonas
44	90	15.0	547	2	Q9X3W6 zymomonas m
45	90	15.0	1129	2	Q8PTJ5 methanosarc

ALIGNMENTS

RESULT 1

Q8GA92_AERSA
ID Q8GA92_AERSA PRELIMINARY; PRT; 116 AA.
AC Q8GA92
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Ascy protein.
GN Name=ascy;
OS Aeromonas salmonicida subsp. salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RX MEDLINE=22626111; PubMed=12374830;
RX DOI=10.1128/JB.184.21.5966-5970.2002;
RA Burr S.E., Stuber K., Wahli T., Frey J.;
RT "Evidence for a type III secretion system in Aeromonas salmonicida
subsp. salmonicida.";
RL J. Bacteriol. 184:5966-5970(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida
type -III secretion mutant in a rainbow trout model.";
RL Microbiol. 151:2111-2118(2005).
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CC -----
CC EMBL; AJ458292; CAD30217.1; -; Genomic_DNA.
CC EMBL; AJ616218; CAE83104.1; -; Genomic_DNA.
CC GO; GO:0005488; F:binding; IEA.
CC InterPro; IPR011990; TPR-like_helical.
CC InterPro; IPR013105; TPR_2.
CC InterPro; IPR013026; TPR_region.
CC PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 116 AA; 12945 MW; AC1273193B180CB1 CRC64;

Query Match	100.0%;	Score 602;	DB 2;	Length 116;
Best Local Similarity	100.0%;	Pred. No. 4.5e-51;		
Matches 116;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTWVLTSSQDDALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQEG	60	
Db	1	MTWVLTSSQDDALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQEG	60	
QY	61	EAALAHVDQMQOGEADGPLWLCRSRACLAGRLDEARFAYQOYLEEQNESTHP	116	
Db	61	EAALAHVDQMQOGEADGPLWLCRSRACLAGRLDEARFAYQOYLEEQNESTHP	116	

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RESULT 2
OSCCAL_AERSO PRELIMINARY; PRT; 116 AA.
ID Q5CCAL;
AC Q5CCAL;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acyl protein.
GN Name=acy;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca fluviatilis."
RL J. Fish Dis. 28:141-150(2005).
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CC -----
DR EMBL; AJ749609; CAG44554.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013105; TPR 2.
SQ SEQUENCE 116 AA; 13033 MW; ECD5E1A55569E48A CRC64;

Query Match 90.9%; Score 547; DB 2; Length 116;
Best Local Similarity 92.2%; Pred. No. 1.1e-45;
Matches 107; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTWVLTSSQODALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQGG 60
Db 1 MTWVLTSSQODALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQGG 60

QY 61 EAALAHVDQLMOQGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116
Db 61 EAALAHVDQLMOQGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116

RESULT 3
Q699R4_AERHY PRELIMINARY; PRT; 116 AA.
ID Q699R4;
AC Q699R4;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Acyl.
GN Name=acy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Marino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas hydrophila strain."
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
DR EMBL; AY528667; AAS91815.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.

DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013105; TPR 2.
SQ SEQUENCE 116 AA; 13140 MW; FF798C42C5A104E9 CRC64;

Query Match 89.2%; Score 537; DB 2; Length 116;
Best Local Similarity 90.5%; Pred. No. 1.1e-44;
Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTWVLTSSQODALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQGG 60
Db 1 MTWVLTSSQODALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQGG 60

QY 61 EAALAHVDQLMOQGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116
Db 61 EAALAHVDQLMOQGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116

RESULT 4
Q6TLM6_AERHY PRELIMINARY; PRT; 116 AA.
ID Q6TLM6;
AC Q6TLM6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Acyl.
GN Name=acy;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1 pathogenesis."
RL Infect. Immun. 72:1248-1256(2004).
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CC -----
DR EMBL; AY394563; AAR26335.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR005158; BTAD.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF03704; BTAD; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 116 AA; 13174 MW; C8CBF54A5459863D CRC64;

Query Match 80.2%; Score 483; DB 2; Length 116;
Best Local Similarity 79.3%; Pred. No. 2.2e-39;
Matches 92; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 MTWVLTSSQODALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQGG 60
Db 1 MTWVLTSSQODALLLTGWLQYGHDPKASVLLAALLQIHPDHQGGRRLLVALLKQGG 60

QY 61 EAALAHVDQLMOQGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116
Db 61 EAALAHVDQLMOQGEADGFWLWLCRSRACQAGRLDEARFAYQYQYLEEQNESTHP 116

RESULT 5
Q5XL08_AERHY PRELIMINARY; PRT; 116 AA.
ID Q5XL08;
AC Q5XL08;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acyl.
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GN Name=ascv;
 OS Aeromonas hydrophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OX NCBI_TaxID=644;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SSU;
 RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
 RA Sha J., Pillai L., Padl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
 RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
 RT Virulence of Aeromonas hydrophila.";
 RL Infect. Immun. 73:6446-6457(2005).
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 CC -----
 CC EMBL: AY763611; AAU30229.1; -; Genomic_DNA.
 DR GO: GO:0005488; F:binding; IEA.
 DR InterPro: IPR011990; TPR-like_helical.
 DR InterPro: IPR013105; TPR 2.
 DR InterPro: IPR013026; TPR region.
 DR PROSITE: PS0293; TPR_REGION; 1.
 SQ SEQUENCE 116 AA; 12997 MW; 48E0C804287AB265 CRC64;
 CC -----
 CC Query Match 77.6%; Score 467; DB 2; Length 116;
 CC Best Local Similarity 78.1%; Pred. No. 8.2e-38;
 CC Matches 89; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 CC -----
 QY 1 MTWVLTSQQODALLLTGWLQLOYGHDPKASVLLAALLQIHPDHOGGRRTLLVALLKQEG 60
 Db 1 MTWVLTSQQODALLLTGWLQLOYGHDPKASVLLAALLQIHPDHOGGRRTLLVALLKQEG 60
 QY 61 EALAHVDLMQOGEADGPIWLCRSRACLAGRLDEARFAQQVLELEEQNEST 114
 Db 61 EALAHVQLVAEAGDALWLCRSRACQLAGRLDEARFAQVHYLEEQNEPT 114
 CC -----
 RESULT 6
 ID Q84GY9 PHOLU PRELIMINARY; PRT; 109 AA.
 AC Q84GY9;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE LscC.
 GN Name=lscC;
 OS Photorhabdus luminescens (Xenorhabdus luminescens).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 OX NCBI_TaxID=29488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=W14;
 RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
 RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
 RT "Genomic islands in Photorhabdus.";
 RL Trends Microbiol. 10:541-545(2002).
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 CC -----
 CC EMBL: AY144116; AAO18049.1; -; Genomic_DNA.
 DR GO: GO:0005488; F:binding; IEA.
 DR InterPro: IPR011990; TPR-like_helical.
 SQ SEQUENCE 109 AA; 12103 MW; 3D6DE6BD1BE4FD2 CRC64;
 CC -----
 CC Query Match 56.1%; Score 338; DB 2; Length 109;
 CC Best Local Similarity 63.1%; Pred. No. 3.5e-25;
 CC Matches 65; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
 CC -----
 QY 3 MVLTSQQODALLLTGWLQLOYGHDPKASVLLAALLQIHPDHOGGRRTLLVALLKQEGEA 62

Db 1 MTL5AKQSQSALLLLGWLQYQYGHPPDRARILLDALLALHPEHQEGRRALVSLKLQKQSGA 60

Qy 63 ALAHVDQLMQOGEADGFLWLCRSRACQLAGRLDEARFAYQOYVL 105

Db 61 AKEHCSLLQOGEQSAALWLCVSRACQOEGNLEARSAYQYVL 103

RESULT 7

Q7NOW7_PHOLL PRELIMINARY; PRT; 109 AA.

AC Q7NOW7

DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.

DT 15-DEC-2003, sequence version 1.

DT 07-FEB-2006, entry version 10.

DE Type III secretion protein SctY.

GN Names: sctY; OrderedLocNames=plu3762;

OS Photorhabdus luminescens subsp. laumondii.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Photorhabdus.

OX NCBI_TaxID=141679;

FN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=TT01.

RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;

RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,

RA Taourit S., Bocs S., Boursau-Eude C., Chandler M., Charles J.-F.,

RA Dassa E., Derose R., Dersaule S., Freyssinet G., Gaudriault S.,

RA Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V.,

RA Zouine M., Glaser P., Bomare N., Danchin A., Kunst F.,

RT "The genome sequence of the non-pathogenic bacterium Photorhabdus

RT luminescens.";

RL Nat. Biotechnol. 21:1307-1313(2003).

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CC -----

DR EMBL; BX571871; CAE16134.1; -; Genomic DNA.

DR Photolista; plu3762; -.

DR BioCyc; PLUM243265; PLU3762-MONOMER; -.

DR GO; GO:0005488; F.binding; IEA.

DR InterPro; IPR011990; TPR-like_helical.

KW Complete proteome.

SQ SEQUENCE 109 AA; 12176 MW; 516493CE4A65312D CRC64;

Query Match 53.8%; Score 324; DB 2; Length 109;

Best Local Similarity 60.2%; Pred. No. 8 4e-24;

Matches 62; Conservative 14; Mismatches 27; Indels 0; Gaps

Qy 3 MVLTSQQDALLLTGWLQYQYGHPPDKASVLLAALLQIHPDHQGGRRLLVALLKQGEA 62

Db 1 MTL5AKQSQSALLLLGWLQYQYGHPPDRARILLDALLALHPEHQEGRRALVSLKLQKQSGM 60

Qy 63 ALAHVDQLMQOGEADGFLWLCRSRACQLAGRLDEARFAYQOYVL 105

Db 61 AKEHCTLLQOGEQSAALWLCVSRACQOEGNLEARSAYQYVL 103

RESULT 8

YSCY_YEREN STANDARD; PRT; 114 AA.

ID YSCY_YEREN

AC Q93KU0; P21209;

DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.

DT 24-MAY-2004, sequence version 2.

DT 07-MAR-2006, entry version 17.

DE Chaperone protein yscY (Yop proteins translocation protein Y).

GN Name=yscY;

OS Yersinia enterocolitica.

OC Gram negative bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Gram negative bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Gram negative bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Gram negative bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OX NCBI_TaxID=630;

FN [1]

GN Name=ascv;
 OS Aeromonas hydrophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OX NCBI_TaxID=644;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SSU;
 RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
 RA Sha J., Pillai L., Padl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
 RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
 RT Virulence of Aeromonas hydrophila.";
 RL Infect. Immun. 73:6446-6457(2005).
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 CC -----
 CC EMBL: AY763611; AAU30229.1; -; Genomic_DNA.
 DR GO: GO:0005488; F:binding; IEA.
 DR InterPro: IPR011990; TPR-like_helical.
 DR InterPro: IPR013105; TPR 2.
 DR InterPro: IPR013026; TPR region.
 DR PROSITE: PS0293; TPR_REGION; 1.
 SQ SEQUENCE 116 AA; 12997 MW; 48E0C804287AB265 CRC64;
 CC -----
 CC Query Match 77.6%; Score 467; DB 2; Length 116;
 CC Best Local Similarity 78.1%; Pred. No. 8.2e-38;
 CC Matches 89; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
 CC -----
 QY 1 MTWVLTSQQODALLLTGWLQLOYGHDPKASVLLAALLQIHPDHOGGRRTLLVALLKQEG 60
 Db 1 MTWILSSQQODLLLTGWLHLOYGHADRTATLLGALLQLYPAHQGRMLLVSLKLGRG 60
 QY 61 EALAHVDLMQOGEADGPIWLCRSRACLAGRLDEARFAQQVLELEEQNEST 114
 Db 61 EELAHVQLVAEGADGALWLCRSRACQLAGRLDEARFAQHYLELEEQNEPT 114
 CC -----
 RESULT 6
 ID Q84GY9 PHOLU PRELIMINARY; PRT; 109 AA.
 AC Q84GY9;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE LscC.
 GN Name=lscC;
 OS Photorhabdus luminescens (Xenorhabdus luminescens).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 OX NCBI_TaxID=29488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=W14;
 RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
 RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
 RT "Genomic islands in Photorhabdus.";
 RL Trends Microbiol. 10:541-545(2002).
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 CC -----
 CC EMBL: AY144116; AAO18049.1; -; Genomic_DNA.
 DR GO: GO:0005488; F:binding; IEA.
 DR InterPro: IPR011990; TPR-like_helical.
 SQ SEQUENCE 109 AA; 12103 MW; 3D6DE6BD1BE4FD2 CRC64;
 CC -----
 CC Query Match 56.1%; Score 338; DB 2; Length 109;
 CC Best Local Similarity 63.1%; Pred. No. 3.5e-25;
 CC Matches 65; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
 CC -----
 QY 3 MVLTSQQODALLLTGWLQLOYGHDPKASVLLAALLQIHPDHOGGRRTLLVALLKQEGEA 62

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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND INDUCTION.
RC STRAIN=serotype O:3; PLASMID=pYV;
RX MEDLINE=90264308; PubMed=2160939;
RA Viitanen A.-M., Toivanen P., Skurnik M.;
RT "The lcrE gene is part of an operon in the lcr region of Yersinia
RL enterocolitica O:3.";
RL J. Bacteriol. 172:3152-3162(1990).
RN [2]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=M22703 / Serotype O:9 / Biotype 2; PLASMID=pYve227;
RA Iriarte M., Lambert M., Kerbourn C., Cornelis G.R.;
RT "Detailed genetic map of the pYve227 plasmid of Yersinia
RL enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=6081 / Serotype O:8 / Biotype 1B; PLASMID=pYve8081;
RX MEDLINE=21295118; PubMed=11402007;
RX DOI=10.1128/JAI.69.7.4627-4638.2001;
RA Snellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype O:8 low-
RL calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
RN [4]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=A127/90 / Serotype O:8 / Biotype 1B; PLASMID=pYval27/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foultier B., Cornelis G.R.;
RT "DNA sequence and analysis of the pYval27/90 virulence plasmid of
RL Yersinia enterocolitica strain A127/90.";
RL Res. Microbiol. 154:553-557(2003).
RN [5]
RN PLASMID=pYV;
RC MEDLINE=99102236; PubMed=9882687;
RX Iriarte M., Cornelis G.R.;
RA "Identification of SyncN, YscX, and YscY, three new elements of the
RT Yersinia Yop virulon.";
RL J. Bacteriol. 181:675-680(1999).
CC -!- FUNCTION: Required for Yop secretion. Functions probably as a
CC chaperone which stabilizes yscX within the cell, before its
CC secretion (By similarity).
CC -!- SUBUNIT: Binds to yscX (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -!- INDUCTION: Temperature seems to play the major role in regulation
CC of transcription of the lcrE-containing operon of pYV, whereas
CC Ca(2+) concentration has only a moderate effect at 37 degrees
CC Celsius, and no effect at room temperature.
CC -----
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CC -----
CC EMBL: M22097; AAA98432.1; -; Genomic DNA.
CC EMBL: AF102990; AAD16819.1; -; Genomic DNA.
CC EMBL: AF363909; AAK69217.1; -; Genomic DNA.
CC EMBL: AV150843; AAN37530.1; -; Genomic DNA.
CC FTR: E35392; E35392.
CC InterPro: IPR011990; TPR-like_helical.
CC Chapterone; Plasmid.
FT CHAIN 1 114 Chapterone protein yscY.
FT VARIANT 38 38 /FTId=PRO_0000066501.
FT VARIANT 114 114 T -> M (in plasmid pYve8081).
FT SEQUENCE 114 AA; 13117 MW; 2DB6D1586B5E124E CRC64;
Query Match 47.3%; Score 285; DB 1; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
QY 1 MTWVLTQQDALLTGWLQYGHDPKASVLLAALQTHPDHGGRTLLVALLKQGG 60
DB 1 MNITLTKROQEFLLNGWLQYGHGAERACILLDALLTLNPHLAGRCRLVALLNNQ 60
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QY 61 EAALAHVDLMQGGADGFLWLCRSACOLAGRLDEARFAYQOYLYLEBONES 113
DB 61 ERAEKEAQWLISHDPLQAGNWLCSLRAQQLNGDLDRARHAYQHYLELKHNES 113
RESULT 9
YSCY YERPE
ID YSCY YERPE STANDARD; PRT; 114 AA.
AC P61417; P21209;
DT 24-MAY-2004, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 1.
DT 07-MAR-2006, entry version 16.
DE Chapterone protein yscY [Yop proteins translocation protein Y].
GN Name=yscY; OrderedLocusNames=YPCD1.35c, Y5043, Y0046, pCD48;
OS Yersinia pestis.
OC Plasmid pCD1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]_TaxID=632;
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RL Yersinia pestis KIM5.";
RN [2]
RN Infect. Immun. 66:4611-4623(1998).
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
RL pestis.";
RN [3]
RN J. Bacteriol. 180:5192-5202(1998).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=201470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebatia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Felwell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [4]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RL avirulent to humans.";
RL DNA Res. 11:179-197(2004).
RN [5]
RN FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RC STRAIN=KIM8;
RX PubMed=10714987; DOI=10.1128/JB.182.7.1834-1843.2000;
RA Day J.B., Plano G.V.;
RT "The Yersinia pestis yscY protein directly binds YscX, a secreted
RL component of the type III secretion machinery.";
RL J. Bacteriol. 182:1834-1843(2000).
CC -!- FUNCTION: Required for Yop secretion. Functions probably as a
CC chaperone which stabilizes yscX within the cell, before its
CC secretion.
```

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CC -!- SUBUNIT: Binds to yscY.
CC -!- SUBCELLULAR LOCATION: Cytoplasm.
CC -----
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CC -----
DR EMBL; AF074612; AAC69796.1; -; Genomic_DNA.
DR EMBL; AF053946; AAC82570.1; -; Genomic_DNA.
DR EMBL; AL117189; CAB54912.1; -; Genomic_DNA.
DR EMBL; AE017043; AAS58567.1; -; Genomic_DNA.
DR PIR; T43590; T43590.
DR GenomeReviews; AE017043 GR; pCD48.
DR GenomeReviews; AL117189 GR; YPCD1.35c.
DR BioCyc; YPES229193:PCD48-MONOMER; -.
DR InterPro; IPR011990; TPR-like_helical.
DR Complete proteome; Plasmid.
KW CHAIN 1
FT CHAIN 114
FT SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;
Query Match 47.3%; Score 285; DB 1; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
Qy 1 MTWVLTQQDALLTGWLQYGHDPKASVLLAALLQIHPDHOGGRTLLVALLKQEG 60
Db 1 MNITLTTRQQBFLLNGWLQCCGHAERACILLDALLTLNPEHLAAGRCRLVALLNNQG 60
Qy 61 EAALAHVDQLMQQGEADGPLWLCRSRACQLAGRLDEARFAYQOYLEEQNES 113
Db 61 ERAEKEAQLWLSHPDPLQAGNWLCLSRQAQLNGDLDKARHAYQHYLELKHNES 113
RESULT 10
ID Q663K5 YERPS PRELIMINARY; PRT; 114 AA.
AC Q663K5
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 9.
DE yscY; putative type III secretion protein.
GN OrderedLocusNames=pYV0061;
OS Versinia pseudotuberculosis.
OC Plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Versinia pestis through whole-genome
RT comparison with Versinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
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CC -----
DR EMBL; BX936399; CAF25404.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
KW Complete proteome; Plasmid.
FT SEQUENCE 114 AA; 13117 MW; 2DB6D15868E5124E CRC64;
Query Match 47.3%; Score 285; DB 2; Length 114;
Best Local Similarity 52.2%; Pred. No. 5.9e-20;
Matches 59; Conservative 14; Mismatches 40; Indels 0; Gaps 0;
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Qy 1 MTWVLTQQDALLTGWLQYGHDPKASVLLAALLQIHPDHOGGRTLLVALLKQEG 60
Db 1 MNITLTTRQQBFLLNGWLQCCGHAERACILLDALLTLNPEHLAAGRCRLVALLNNQG 60
Qy 61 EAALAHVDQLMQQGEADGPLWLCRSRACQLAGRLDEARFAYQOYLEEQNES 113
Db 61 ERAEKEAQLWLSHPDPLQAGNWLCLSRQAQLNGDLDKARHAYQHYLELKHNES 113
RESULT 11
ID O30535 PSEAE PRELIMINARY; PRT; 109 AA.
AC O30535;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Pcr4.
GN Name=pCr4;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=388;
RX MEDLINE=98037517; PubMed=9371466;
RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7165-7168(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX PubMed=16267298; DOI=10.1128/JB.187.22.7738-7752.2005;
RA Broms J.E., Edqvist P.J., Carlsson K.E., Forsberg A., Francis M.S.;
RT "Mapping of a YscY Binding Domain within the LcrH Chaperone That Is
RT Required for Regulation of Yersinia Type III Secretion.";
RL J. Bacteriol. 187:7738-7752(2005).
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CC -----
DR EMBL; AF010150; AAC45943.1; -; Genomic_DNA.
DR EMBL; DQ000666; AAY17110.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013026; TPR region.
DR PROSITE; PS02993; TPR_REGION; 1.
SQ SEQUENCE 109 AA; 12222 MW; 3C3F19535EB038C9 CRC64;
Query Match 44.9%; Score 270; DB 2; Length 109;
Best Local Similarity 55.7%; Pred. No. 1.7e-18;
Matches 59; Conservative 12; Mismatches 35; Indels 0; Gaps 0;
Qy 3 MVLTSQQDALLTGWLQYGHDPKASVLLAALLQIHPDHOGGRTLLVALLKQGEA 62
Db 1 MTLKPTQORLLMLGWLHLQCGQPRRAQVLLALLSVAPERRDRALLALLQOGLGEP 60
Qy 63 ALAHVDQLMQQGEADGPLWLCRSRACQLAGRLDEARFAYQOYLELE 108
Db 61 AVRLCRLQDGEPEGPGIWLCLSRQAQLNGDLDKARHAYQHYLELKHNALELE 106
RESULT 12
ID Q91328 PSEAE PRELIMINARY; PRT; 109 AA.
AC Q91328;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein.
GN OrderedLocusNames=PA1702;
OS Pseudomonas aeruginosa.
```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Coltray L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
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 CC -----
 CC EMBL; AE004597; AAG05091.1; -; Genomic_DNA.
 DR PIR; C83432; C83432.
 DR BLOSCY; FAER287:PA1702-MONOMER; -.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like helical.
 DR InterPro; IPR013026; TPR region.
 DR PROSITE; PS50293; TPR REGION; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 109 AA; 12265 MW; 3C3F19535EAFD937 CRC64;
 Query Match 43.9%; Score 264; DB 2; Length 109;
 Best Local Similarity 54.7%; Pred. No. 6.5e-18;
 Matches 58; Conservative 12; Mismatches 36; Indels 0; Gaps 0;
 QY 3 MVLTSQQDALLTGWLQYHPDKASVLLAALLQHPDQGRRTLLVALLKQGEAA 62
 DB 1 MTLKPTQORLLMLGWLHLCQGPRAQVLLLEALLSVAPRRDGRALLLALQQLGEP 60
 QY 63 ALAHVDOLMQGGADGFWLCSRACQLAGRLDEARFAYQOYLE 108
 DB 61 AVRLCRLQDGGEEPGFWLCSRACQLAGRLDEARFAYQOYLE 106
 RESULT 13
 Q6QVR8_VIBHA PRELIMINARY; PRT; 112 AA.
 ID Q6QVR8_VIBHA
 AC Q6QVR8_VIBHA
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE VscY.
 GN Name=vscY;
 OS Vibrio harveyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=569;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Henke J.M., Bassler B.L.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; AY524044; AAS1313.1; -; Genomic_DNA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like helical.
 DR InterPro; IPR013026; TPR region.
 DR PROSITE; PS50293; TPR REGION; 1.
 SQ SEQUENCE 112 AA; 12913 MW; BAB232661790D401 CRC64;
 Query Match 26.0%; Score 156.5; DB 2; Length 112;
 Best Local Similarity 36.3%; Pred. No. 2.4e-07;

Matches 41; Conservative 22; Mismatches 45; Indels 5; Gaps 3;
 QY 4 VLTSSQQDALLTGWLQYHPDKASVLLAALLQHPDQGRRTLLVALLKQGEAA 63
 DB 1 MLQSKDVELLLVHAALQVQKPEQAITLLDALLEPQHQEQVROTFLAVACLSNGRYTRS 60
 QY 64 LAHVDDOLM--QQGEADGFWLCSRACQLAGRLDEARFAYQOYLE--EEQNE 112
 DB 61 IELCESLLKTEHSNKEG-LWFCLSQARWKQODVEGARHARRHYLQSLNESNE 112
 RESULT 14
 Q66PT9_PASPI PRELIMINARY; PRT; 108 AA.
 ID Q66PT9_PASPI
 AC Q66PT9_PASPI
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Putative TTSS protein Y.
 OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Photobacterium.
 OX NCBI_TaxID=38294;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
 RT "Photobacterium damsela subsp. piscicida encodes a functional type
 RT three secretion system (TTSS) that is involved in pathogenesis.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 CC EMBL; AY647223; AAU11477.1; -; Genomic_DNA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like helical.
 DR InterPro; IPR013026; TPR region.
 DR PROSITE; PS50293; TPR REGION; 1.
 SQ SEQUENCE 108 AA; 12478 MW; 75C85FDF70C1470C CRC64;
 Query Match 24.7%; Score 148.5; DB 2; Length 108;
 Best Local Similarity 34.6%; Pred. No. 1.4e-06;
 Matches 36; Conservative 24; Mismatches 43; Indels 1; Gaps 1;
 QY 4 VLTSSQQDALLTGWLQYHPDKASVLLAALLQHPDQGRRTLLVALLKQGEAA 63
 DB 1 MLQTKDVELLLVHAALQVQKPEQAITLLDALLEPQHQEQVROTFLAVACLSNGRYTRS 60
 QY 64 LAHVDDOLMQGGADGFWLCSRACQLAGRLDEARFAYQOYLE 106
 DB 61 IELCESLLKTEHSNKEG-LWFCLSQARWKQODVEGARHARRHYLQ 104
 RESULT 15
 Q48IR6_PSE14 PRELIMINARY; PRT; 112 AA.
 ID Q48IR6_PSE14
 AC Q48IR6_PSE14
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 21-FEB-2006, entry version 7.
 DE Type III secretion component, putative (EC 2.4.1.-).
 GN OrderedLocNames=PSPPH_2519;
 OS Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=264730;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=16159782; DOI=10.1128/JB.187.18.6488-6498.2005;
 RA Joardar V., Lindeberg M., Jackson R., Selengut J., Dodson R.,
 RA Brinkar L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Winn Giglio M., Madupu R., Nelson W.C., Rosovitz M.J., Sullivan S.A.,
 RA Crabtree J., Creasy T., Davidsen T.M., Haft D.H., Zafar L., Zhou L.,

RA Halpin R., Holley T., Khouri H.M., Feldblyum T.V., White O.,
RA Fraser C.M., Chatterjee A.K., Cartinhour S., Schneider D.,
RA Mansfield J., Collmer A., Buell R.;
RT "Whole-genome sequence analysis of *Pseudomonas syringae* pv.
RT phaseolicola 1448A reveals divergence among pathovars in genes
RT involved in virulence and transposition.";
RL J. Bacteriol. 187:6488-6498(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000058; AA234406.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07721; TPR_4; 1.
DR SMART; SM00028; TPR; 1.
DR PROSITE; PS50005; TPR; 2.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 112 AA; 12534 MW; 1DACD78D6FAE2C59 CRC64;

Query Match 23.3%; Score 140.5; DB 2; Length 112;
Best Local Similarity 34.0%; Pred. No. 9e-06;
Matches 35; Conservative 23; Mismatches 42; Indels 3; Gaps 1;

Qy 7 SQQQDALL--TCWLQYGHDPKASVLLAALLQIHDPHQGRRTLLVALLKQEGEAA 63
| | : : | | : : | | : : | | : : | | : : | | : : | | : : |
Db 4 SQDRECIELHGMGDLVRRSQPQKALVMLLIAIQLAPTSALLHSLVLAFTDSGDTTRA 63
| | : : | | : : | | : : | | : : | | : : | | : : | | : : |

Qy 64 LAHVQDLMOQGEADGPIWLCESRACQLAGRLDEARFAYQOYLE 106
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 IALDLRIVEQQGESALLLLRSRALWKAGRKDDARQCRRYLE 106
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: June 16, 2006, 19:22:56
Job time : 94.1024 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 21.4081 Seconds
(without alignments)
474.285 Million cell updates/sec

Title: US-10-813-908A-5
Perfect score: 602
Sequence: 1 MTWLTQQQDALLTGWLQ.....ARFAYQQYLEEONESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /EMC_Celerra_SID3S/ptodata/2/iaa/5_COMB.pep.*
 - 2: /EMC_Celerra_SID3S/ptodata/2/iaa/6_COMB.pep.*
 - 3: /EMC_Celerra_SID3S/ptodata/2/iaa/7_COMB.pep.*
 - 4: /EMC_Celerra_SID3S/ptodata/2/iaa/H_COMB.pep.*
 - 5: /EMC_Celerra_SID3S/ptodata/2/iaa/PCUTUS_COMB.pep.*
 - 6: /EMC_Celerra_SID3S/ptodata/2/iaa/RE_COMB.pep.*
 - 7: /EMC_Celerra_SID3S/ptodata/2/iaa/backfilesl.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	45.2	231	2	US-09-252-991A-29962
2	111.5	18.5	470	2	US-09-902-540-12418
3	96.5	16.0	143	2	US-09-198-452A-442
4	96.5	16.0	143	2	US-09-438-185A-425
5	88.5	14.7	870	2	US-09-252-991A-28407
6	83	13.8	1219	2	US-09-252-991A-28840
7	81	13.5	953	2	US-09-902-540-14681
8	80	13.3	368	2	US-09-252-991A-30717
9	79.5	13.2	956	2	US-09-902-540-10395
10	78.5	13.0	169	2	US-08-833-167-58
11	78.5	13.0	169	2	US-09-344-837A-58
12	78	13.0	325	2	US-09-510-238A-273
13	78	13.0	390	2	US-09-902-540-16621
14	77.5	12.9	171	2	US-08-833-167-44
15	77.5	12.9	171	2	US-08-833-167-45
16	77.5	12.9	171	2	US-08-833-167-47
17	77.5	12.9	171	2	US-08-833-167-57
18	77.5	12.9	171	2	US-08-833-167-59
19	77.5	12.9	171	2	US-08-833-167-60
20	77.5	12.9	171	2	US-09-344-837A-44
21	77.5	12.9	171	2	US-09-344-837A-45
22	77.5	12.9	171	2	US-09-344-837A-47
23	77.5	12.9	171	2	US-09-344-837A-57
24	77.5	12.9	171	2	US-09-344-837A-59
25	77.5	12.9	171	2	US-09-344-837A-60
26	77.5	12.9	299	2	US-09-510-238A-193

27	77.5	12.9	302	2	US-09-510-238A-168	Sequence 168, App
28	77.5	12.9	302	2	US-09-510-238A-170	Sequence 170, App
29	77.5	12.9	302	2	US-09-510-238A-172	Sequence 172, App
30	77.5	12.9	302	2	US-09-510-238A-174	Sequence 174, App
31	77.5	12.9	302	2	US-08-957-610A-474	Sequence 474, App
32	77.5	12.9	302	2	US-08-957-610A-476	Sequence 476, App
33	77.5	12.9	302	2	US-08-957-610A-478	Sequence 478, App
34	77.5	12.9	302	2	US-08-957-610A-480	Sequence 480, App
35	77.5	12.9	317	2	US-09-510-238A-169	Sequence 169, App
36	77.5	12.9	317	2	US-09-510-238A-171	Sequence 171, App
37	77.5	12.9	317	2	US-09-510-238A-173	Sequence 173, App
38	77.5	12.9	317	2	US-09-510-238A-175	Sequence 175, App
39	77.5	12.9	317	2	US-08-957-610A-475	Sequence 475, App
40	77.5	12.9	317	2	US-08-957-610A-477	Sequence 477, App
41	77.5	12.9	317	2	US-08-957-610A-479	Sequence 479, App
42	77.5	12.9	317	2	US-08-957-610A-481	Sequence 481, App
43	77.5	12.9	319	2	US-09-510-238A-199	Sequence 199, App
44	77.5	12.9	319	2	US-09-510-238A-201	Sequence 201, App
45	77.5	12.9	319	2	US-08-957-610A-505	Sequence 505, App

ALIGNMENTS

RESULT 1
US-09-252-991A-29962
; Sequence 29962, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29962
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29962

Query Match 45.2%; Score 272; DB 2; Length 231;
Best Local Similarity 55.1%; Pred. No. 1.5e-26;
Matches 59; Conservative 13; Mismatches 35; Indels 0; Gaps 0;
Qy 2 TWVLTQQQDALLTGWLQYGHDPKASVLLAALLQIHDPHQGGRETLVALLKQGE 61
Db 122 SMTLKQTQORLLMLGWLHLCQCPRAQVLLLEALLSVAPERDRGRALLLLOQGLGE 181
Qy 62 AALAHVDQLMQQGEAGDGLMCLSRACQLAGRLDEARFAYQQVYLE 108
Db 182 PAVRLCRLQEDGEEEPGLMCLSRAEQLAGRLDARAARALELE 228

RESULT 2
US-09-902-540-12418
; Sequence 12418, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883


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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28840
; LENGTH: 1219
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28840

Query Match      13.8%; Score 83; DB 2; Length 1219;
Best Local Similarity 30.5%; Pred. No. 0.26;
Matches 25; Conservative 15; Mismatches 36; Indels 6; Gaps 2;

Qy 1 MTWLTSSQQDALLTGWLQYGHDPKASVLLA-ALLQIHPDHQGGRTLLVALLKQGE 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 56 LVLLWLTNSEEVFMPSG-----DGEFDAVSVNYAELLQAHPENDALRLTLIDLVLKIGD 110

Qy 60 GEAAALHVDQLMQQGEADGPLW 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 FEQARHLLARLURGDKRLATPPY 132

RESULT 7
US-09-902-540-14681
; Sequence 14681, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14681
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14681

Query Match      13.5%; Score 81; DB 2; Length 953;
Best Local Similarity 36.9%; Pred. No. 0.33;
Matches 31; Conservative 12; Mismatches 33; Indels 8; Gaps 5;

Qy 26 PDKASVLLAALLQIHPDHQGGRTLLVALLKQGEAALAHVDQLMQQGE-ADGPLWLCR 84
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 425 PERAERLLPALLN-HPD-VGURCAAGALVKSTGSAVALDALRAMLSRGEGAPVPE---R 479

Qy 85 SRACQLAGRLEARFA--YQOYLE 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 480 REVARLLGRIGNSRFAEPLARYLE 503

RESULT 8
US-09-252-991A-30717
; Sequence 30717, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; SEQ ID NO 30717
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30717

Query Match      13.3%; Score 80; DB 2; Length 368;
Best Local Similarity 29.2%; Pred. No. 0.12;
Matches 26; Conservative 14; Mismatches 49; Indels 0; Gaps 0;

Qy 27 DKASVLLAALLQIHPDHQGGRTLLVALLKQGEAALAHVDQLMQQGEADGPLWLCRSR 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 30 DDALPLKAGIKKEHPDDKRVRLAYARLLVBNQLRDDAKAEFAGLVQQQFPDDDDDLRFLSAL 89

Qy 87 ACQAGLRLEARFAYQOYLEEQNESTH 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 90 VCLEAQAWDEARIYLEELVERDSHVDAAH 118

RESULT 9
US-09-902-540-10395
; Sequence 10395, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10395
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10395

Query Match      13.2%; Score 79.5; DB 2; Length 956;
Best Local Similarity 33.8%; Pred. No. 0.52;
Matches 27; Conservative 10; Mismatches 24; Indels 19; Gaps 4;

Qy 21 LOYGHDPKASVLLAALLQIHPDH---QGRR-----TLVV-----ALLKQGE---GE 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 LEQGHPEQALLIDGVLRQAPHAQAQWNALVLRMGLTLLAAAEAFDAVVYKRGEGPWSE 234

Qy 62 AALAHVDQLMQQGEADGPLW 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 EARIRARALRQQTQARGRAW 254

RESULT 10
US-08-833-167-58
; Sequence 58, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIONG
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
```



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;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15774
; FILING DATE: 06-OCT-1996
; APPLICATION NUMBER: US 60/004,834
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: 2910/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 273:
US-09-510-238A-273

Query Match      13.0%; Score 78; DB 2; Length 325;
Best Local Similarity 28.2%; Pred. No. 0.18; Indels 24; Gaps 4;
Matches 31; Conservative 15; Mismatches 40;

Qy 24 GHPDKASVLLAALQIHPDHQGGRTLLVALLK-----QGGEA-----ALAH 66
Db 120 GSPGEPSPITINPSPSKESHKSPNNAFLKLSLEQVRKIQDGAALQEKLCATYKLC 179

Qy 67 VDQLMQQGEADG----PLWLCRSACQIAG---RLDEARFAYQVYLEEE 109
Db 180 PEELVLLHSLGIPWAPLSSCPSQLAGLQAGLSQLHSLGLYQGLLQALE 229

RESULT 13
US-09-902-540-16621
; Sequence 16621, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16621
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16621

Query Match      13.0%; Score 78; DB 2; Length 390;
Best Local Similarity 27.3%; Pred. No. 0.23; Indels 42; Gaps 8;
Matches 39; Conservative 17; Mismatches 45;

Qy 10 QDALLTGWLQYGHDPK--ASVLLAALQIHPDH-----QGRR--TILV 52
Db 35 KDASALLGLRLAQHDETAARAVLQRLVALHPHPPEALSHLARLDAEKGDARQLDLA 94

Qy 53 ALLKQ-----GEGEAAALAH-----VDQL-----MQGEADGPLWLCSRACQIAG 92
Db 95 ALAAQPKAGFFEVINHGSGALLGHDRYAAAIPERALALQPGNAQTLYL--GMAIQGDK 152

Qy 93 RLDEARFAYQVYLEEENQESTH 115
Db 153 QLDR---ALRRYLEAAEANKTEH 172
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RESULT 14
US-08-833-167-44
; Sequence 44, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: PENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/833,167
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-167-44

Query Match      12.9%; Score 77.5; DB 2; Length 171;
Best Local Similarity 32.6%; Pred. No. 0.088;
Matches 28; Conservative 12; Mismatches 25; Indels 21; Gaps 4;

Qy 45 GGRRTLLVALLK-----QGGEA-----ALAHVDQLMQQGEADG---PLWLCPSR 86
Db 83 GGSQFLKLSLEQVRKIQDGAALQEKLCATYKLCHEELVLLHSLGIPWAPLSSCP 142

Qy 87 ACQIAG---RLDEARFAYQVYLEEE 109
Db 143 ALQAGCLSQLHSLGLYQGLLQALE 168

RESULT 15
US-08-833-167-45
; Sequence 45, Application US/08833167
; Patent No. 6100070
; GENERAL INFORMATION:
; APPLICANT: ZURFLUH, LINDA L
```

```

; APPLICANT: MCWHERTER, CHARLES A
; APPLICANT: MCKEARN, JOHN P
; APPLICANT: KLEIN, BARBARA K
; APPLICANT: FENG, YIQING
; APPLICANT: BRAFORD-GOLDBERG, SARAH R
; APPLICANT: LEE, STEPHEN C
; TITLE OF INVENTION: G-CSF RECEPTOR AGONISTS
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DENNIS A BENNETT, G.D. SEARLE & CO.,
; ADDRESSEE: CORPORATE PATENT DEPT.
; STREET: P.O. BOX 5110
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,167
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US 96/15935
; FILING DATE: 04-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,382
; FILING DATE: 05-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENNETT, DENNIS A
; REFERENCE/DOCKET NUMBER: 2907/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-5402
; TELEFAX: 314-694-9095
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-167-45

```

```

Query Match      12.9%; Score 77.5; DB 2; Length 171;
Best Local Similarity 32.6%; Pred. No. 0.088;
Matches 28; Conservative 12; Mismatches 25; Indels 21; Gaps 4;

QY      45  GGRRTLLVALLK-----QGGEA-----ALAHVDOLMOQGEADG-----PLWLCSR 86
Db      47  GGSQSFLLKLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAPLSSCP 106

QY      87  ACQLAG---RLDEARFAYQQYLEEE 109
Db     107  ALQLAGCLSQLHSGFLYQGLQALE 132

```

Search completed: June 16, 2006, 19:28:55
Job time : 21.4081 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 64.8846 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-5
Perfect score: 602
Sequence: 1 MTWVLTSSQDDALLLTGWLQ.....ARFAYQYLEEQNESTHP 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	100.0	116	5	US-10-813-908-4
2	141.5	23.5	113	6	US-11-098-686-10792
3	99	16.4	619	4	US-10-282-122A-50903
4	96.5	16.0	143	4	US-10-289-762-442
5	86.5	14.4	713	4	US-10-425-115-201172
6	86.5	14.4	719	4	US-10-425-114-51666
7	84.5	14.0	643	4	US-10-425-115-201174
8	84.5	14.0	737	4	US-10-425-114-57283
9	83	13.8	1586	4	US-10-282-122A-49391
10	83	13.8	1864	5	US-10-732-923-2391
11	79.5	13.2	1743	5	US-10-732-923-18400
12	79	13.1	107	6	US-11-096-568A-26392
13	79	13.1	108	6	US-11-096-568A-26392
14	79	13.1	124	6	US-11-096-568A-26391
15	78.5	13.0	1234	6	US-11-097-143-32322
16	78	13.0	325	4	US-10-695-584A-273
17	77.5	12.9	238	3	US-09-920-552-3
18	77.5	12.9	299	4	US-10-695-584A-193
19	77.5	12.9	302	4	US-10-695-584A-168
20	77.5	12.9	302	4	US-10-695-584A-170
21	77.5	12.9	302	4	US-10-695-584A-172
22	77.5	12.9	302	4	US-10-695-584A-174
23	77.5	12.9	317	4	US-10-695-584A-169
24	77.5	12.9	317	4	US-10-695-584A-171
25	77.5	12.9	317	4	US-10-695-584A-173
26	77.5	12.9	317	4	US-10-695-584A-175
27	77.5	12.9	319	4	US-10-695-584A-199

28	77.5	12.9	319	4	US-10-695-584A-201	Sequence 201, App
29	77.5	12.9	321	4	US-10-695-584A-186	Sequence 186, App
30	77.5	12.9	321	4	US-10-695-584A-187	Sequence 187, App
31	77.5	12.9	321	4	US-10-695-584A-188	Sequence 188, App
32	77.5	12.9	321	4	US-10-695-584A-189	Sequence 189, App
33	77.5	12.9	329	3	US-09-920-552-9	Sequence 9, Appli
34	77.5	12.9	329	4	US-10-695-584A-190	Sequence 190, App
35	77.5	12.9	329	4	US-10-695-584A-191	Sequence 191, App
36	77.5	12.9	329	4	US-10-695-584A-192	Sequence 192, App
37	77.5	12.9	332	3	US-09-920-552-17	Sequence 17, Appl
38	77.5	12.9	352	5	US-10-481-935A-219	Sequence 219, App
39	77.5	12.9	367	5	US-10-481-935A-220	Sequence 220, App
40	77.5	12.9	1814	3	US-09-920-552-103	Sequence 103, App
41	77	12.8	233	4	US-10-369-493-11128	Sequence 11128, A
42	77	12.8	518	4	US-10-193-295-5	Sequence 5, Appli
43	77	12.8	518	4	US-10-622-516-5	Sequence 5, Appli
44	77	12.8	518	5	US-10-971-001A-5	Sequence 5, Appli
45	77	12.8	520	5	US-10-732-923-19653	Sequence 19653, A

ALIGNMENTS

RESULT 1

US-10-813-908-4
; Sequence 4, Application US/10813908
; Publication No. US20050058662A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and r
; FILE REFERENCE: MIC01/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813,908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
; US-10-813-908-4

Query Match

Best Local Similarity 100.0%; Score 602; DB 5; Length 116;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTWVLTSSQDDALLLTGWLQYGHDPKASVLLAALQIHPDHQGRRTLLVALLKQEG 60
Db 1 MTWVLTSSQDDALLLTGWLQYGHDPKASVLLAALQIHPDHQGRRTLLVALLKQEG 60
Qy 61 EALAHVDQLMQQEGADGPLWLCRSRACOLAGRLDEARFAYQYLEEQNESTHP 116
Db 61 EALAHVDQLMQQEGADGPLWLCRSRACOLAGRLDEARFAYQYLEEQNESTHP 116

RESULT 2

US-11-098-686-10792
; Sequence 10792, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04

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; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10792
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10792

Query Match      23.5%; Score 141.5; DB 6; Length 113;
Best Local Similarity 30.3%; Pred. No. 3.4e-08;
Matches 33; Conservative 28; Mismatches 43; Indels 5; Gaps 2;

QY 3 MVLTSQDQDALLTGWLQVGHDPDKASVLLAALLQIHPDHQGGRRRTLLVALLKQSGEA 62
Db 1 MLTSEQRTYLILGYLYIRGLNDSAEERLFKTLISLFPEDKWSHSLAVIAWRKGDSS 60

QY 63 ALAHVDQLMOQGE-----ADGPLWLCRSRACQLAGRLDEARFAYQVYLEL 107
Db 61 CLAHYKAV-AGEHSIVKHAPLLLLQALWNLGRYSERSTSIQNVIKI 108

RESULT 3
US-10-282-122A-50903
; Sequence 50903, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsythe, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITPA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50903
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-10-282-122A-50903

Query Match      16.4%; Score 99; DB 4; Length 619;
Best Local Similarity 29.0%; Pred. No. 0.022;
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Matches 29; Conservative 21; Mismatches 46; Indels 4; Gaps 2;

QY 21 LOYG---HPDKASVLLAALLQIHPDHQGGRRRTLLVALLKQSGEAAALAHVDQLMQQGEAD 77
Db 259 LEYGAKVDAATRAQHQARAFINRNPDKRLMLAGQIADGGDYDGAALAEQLQAMSRSPED 318

QY 78 GPIWLCSRACQLAGRLDEARFAYQVYLEEEQNE-STHP 116
Db 319 FDLMFQQAQLAYKAGRLDQARGYLQOYLDVQNRQMATA 358

RESULT 4
US-10-289-762-442
; Sequence 442, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 442
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-442

Query Match      16.0%; Score 96.5; DB 4; Length 143;
Best Local Similarity 33.3%; Pred. No. 0.0073;
Matches 33; Conservative 17; Mismatches 40; Indels 9; Gaps 3;

QY 11 DALLLTGWLQVGHDPDKASVLLAALLQIHP-----DHQGGRRRTLLVALLKQSGEAAALAH 66
Db 19 EELRISGYSFLRQGHYSKAILFFELVILDPISYDHQ----TLGGYLQIGENSQALAV 74

QY 67 VQVLMQQGEADGPLWLCRSRACQLAGRLDEARFAYQVYL 105
Db 75 LPQALRMQGDHLPTLLNKTKALFCLGRIEAT-AIATYL 112

RESULT 5
US-10-425-115-201172
; Sequence 201172, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201172
; LENGTH: 713
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115054C.1.pep
US-10-425-115-201172

Query Match      14.4%; Score 86.5; DB 4; Length 713;
Best Local Similarity 29.8%; Pred. No. 0.72;
Matches 34; Conservative 15; Mismatches 42; Indels 23; Gaps 4;

QY 19 LQVGHDPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQSGEAAALAHVDQL 70
Db 350 LQL-----DEAQLCQIALDIHREHTASLEETADRRRLMGLICDTKGDHEAALEHVA 404
```

Db 350 LQL-----DEAQRLCQIALDIHREHGGTASLEETADRRMLGLIYDTKGDHEAALEHLVMA 404

Qy 71 MQQGEADGPLWLCSSRACOLA-----GRLDEARFAYQOYLEL-----EQNEST 114

Db 405 GTAMIANGQETEVASVDCSIGDIYLSLGRYDEAVFAYQKALTVPFKTSKGENHAT 458

RESULT 8

US-10-425-114-57283

; Sequence 57283, Application US/10425114

; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 57283

; LENGTH: 737

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLMO17278G10_FLI.pep

US-10-425-114-57283

Query Match 14.0%; Score 84.5; DB 4; Length 737;

Best Local Similarity 30.7%; Pred. No. 1.3;

Matches 35; Conservative 14; Mismatches 42; Indels 23; Gaps 4;

Qy 19 LQLOYGHPDKASVLLAALLQHPDQ-----GRTLVALLKQGEBAALAHVDOL 70

Db 444 LQL-----DEAQRLCQIALDIHREHGGTASLEETADRRMLGLIYDTKGDHEAALEHLVMA 498

Qy 71 MQQGEADGPLWLCSSRACOLA-----GRLDEARFAYQOYLEL-----EQNEST 114

Db 499 GTAMIANGQETEVASVDCSIGDIYLSLGRYDEAVFAYQKALTVPFKTSKGENHAT 552

RESULT 9

US-10-282-122A-49391

; Sequence 49391, Application US/10282122A

; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49391
; LENGTH: 1586
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49391
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Query Match 13.8%; Score 83; DB 4; Length 1586;
Best Local Similarity 28.8%; Pred. No. 4.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;

QY 3 MVLTSQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRRTLVLALLKQGEA 62
Db 391 IALNPSDVTQVLLGEMLLANGDPVGAEQAYRMALRRQADNPDAVRGLVGALAAQGRGDE 450
QY 63 ALAHVDQL--MQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 451 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAARAGDLGARSJLFEDAL 501
```

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RESULT 10
US-10-732-923-2391
; Sequence 2391, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 2391
; LENGTH: 1864
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-732-923-2391
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Query Match 13.8%; Score 83; DB 5; Length 1864;
Best Local Similarity 28.8%; Pred. No. 5.8;
Matches 32; Conservative 14; Mismatches 57; Indels 8; Gaps 2;

QY 3 MVLTSQQDALLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRRRTLVLALLKQGEA 62
Db 669 IALNPSDVTQVLLGEMLLANGDPVGAEQAYRMALRRQADNPDAVRGLVGALAAQGRGDE 728
QY 63 ALAHVDQL--MQGEAD-----GPLWLCRSRACQLAGRLDEARFAYQQYL 105
Db 729 ALQFANQLNAEQSKAGGINRLRGEAQAAQARAARAGDLGARSJLFEDAL 779
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RESULT 11
US-10-732-923-18400
; Sequence 18400, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
```

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; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18400
; LENGTH: 1743
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-732-923-18400
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Query Match 13.2%; Score 79.5; DB 5; Length 1743;
Best Local Similarity 23.8%; Pred. No. 14;
Matches 25; Conservative 21; Mismatches 40; Indels 19; Gaps 3;

QY 9 QQDALLTGWLQYGHDP--KASVLLAALLQIHPDHQGGRRRTLVLALLKQGEAALAH 66
Db 1627 QCHVQLISKFAQLFEFKHGDAERGRITLLEGLVTAHPKKTDLWLVAEAVLK---HLGIEH 1682
QY 67 VQOLMOQGEADGPLWLCRSRACQLAGRLDEARFAYQQYLELEBQN 111
Db 1683 ARKVLK-----RACNLGFSIHKMRPLYKKWLEMESKH 1714
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RESULT 12
US-11-096-568A-26393
; Sequence 26393, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26393
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(107)
; OTHER INFORMATION: Ceres Seq. ID no. 13564029
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (93)..(93)
; OTHER INFORMATION: Xaa is any aa, unknown or other
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (97)..(97)
; OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-26393
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Query Match 13.1%; Score 79; DB 6; Length 107;
Best Local Similarity 35.7%; Pred. No. 0.55;
Matches 25; Conservative 8; Mismatches 27; Indels 10; Gaps 3;

QY 49 TLLVALLKQGEAALAHVDQLMQ--QGEADGPLWLCRSRACQLAGRLDEARFAYQQYLE 106
Db 11 TTISGLAMHGHQPQEAL----DLFORMQDRPDGATLLAVLRACSLAGRIDDARW----YFE 62
QY 107 LEEQNESTHP 116
Db 63 SMERVYGINP 72
```

```
RESULT 13
US-11-096-568A-26392
; Sequence 26392, Application US/11096568A
; Publication No. US20060048240A1
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: June 16, 2006, 20:13:41 ; Search time 4.99837 Seconds
(without alignments)
523.484 Million cell updates/sec
Title: US-10-813-908A-5
Perfect score: 602
Sequence: 1 MTWLTSSQDALLTGWLQ.....ARFAYQVLELEQNETHP 116
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 96747 seqs, 22556637 residues
Total number of hits satisfying chosen parameters: 96747
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA New:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pap:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pap:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pap:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pap:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pap:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pap:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pap:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	13.0	737	6	US-10-449-902-53938
2	74	12.3	599	6	US-10-449-902-47030
3	73.5	12.2	711	6	US-10-449-902-46399
4	73	12.1	457	7	US-11-221-332-32
5	71.5	11.9	570	6	US-10-953-349-4630
6	71.5	11.9	772	6	US-10-953-349-4629
7	71.5	11.9	802	6	US-10-953-349-4628
8	71	11.8	495	6	US-10-953-349-31757
9	71	11.8	530	6	US-10-953-349-31756
10	71	11.8	610	6	US-10-953-349-31755
11	70.5	11.7	228	7	US-11-289-102-381
12	70.5	11.7	804	6	US-10-449-902-38463
13	70	11.6	174	7	US-11-183-218-2
14	70	11.6	177	7	US-11-330-353-14
15	70	11.6	204	6	US-10-511-937-2461
16	70	11.6	787	7	US-11-330-353-16
17	69.5	11.5	599	6	US-10-449-902-53783
18	67	11.1	840	6	US-10-449-902-41113
19	66.5	11.0	469	6	US-10-953-349-241172
20	66.5	11.0	473	6	US-10-449-902-47334
21	66.5	11.0	876	6	US-10-449-902-44948
22	66	11.0	525	6	US-10-953-349-34744
23	66	11.0	699	6	US-10-449-902-45095
24	65	10.8	622	6	US-10-505-928-735
25	64.5	10.7	330	6	US-10-449-902-30918

26	64.5	10.7	626	6	US-10-449-902-46528	Sequence 46528, A
27	64.5	10.7	690	6	US-10-449-902-41502	Sequence 41502, A
28	64	10.6	272	6	US-10-449-902-37122	Sequence 37122, A
29	64	10.6	272	6	US-10-449-902-48530	Sequence 48530, A
30	64	10.6	711	6	US-10-449-902-48230	Sequence 48230, A
31	63.5	10.5	519	7	US-11-293-697-4747	Sequence 4747, Ap
32	63.5	10.5	842	7	US-11-266-446-68	Sequence 68, Appl
33	63.5	10.5	2364	7	US-11-289-102-242	Sequence 242, App
34	63	10.5	325	6	US-10-953-349-35099	Sequence 35099, A
35	63	10.5	515	6	US-10-449-902-37134	Sequence 37134, A
36	63	10.5	1011	6	US-10-449-902-36207	Sequence 36207, A
37	62.5	10.4	440	7	US-11-122-986-266	Sequence 266, App
38	62.5	10.4	440	7	US-11-122-986-268	Sequence 268, App
39	62.5	10.4	507	6	US-10-449-902-39176	Sequence 39176, A
40	62.5	10.4	794	6	US-10-449-902-42587	Sequence 42587, A
41	62.5	10.4	972	6	US-10-449-902-41157	Sequence 41157, A
42	62	10.3	236	6	US-10-449-902-34843	Sequence 34843, A
43	62	10.3	408	6	US-10-449-902-46992	Sequence 46992, A
44	62	10.3	587	6	US-10-449-902-40565	Sequence 40565, A
45	62	10.3	623	6	US-10-449-902-47699	Sequence 47699, A

ALIGNMENTS

RESULT 1
US-10-449-902-53938
; Sequence 53938, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53938
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53938
Query Match 13.0%; Score 78; DB 6; Length 737;
Best Local Similarity 34.7%; Pred. No. 0.81;
Matches 26; Conservative 17; Mismatches 20; Indels 12; Gaps 5;
Qy 28 KASVLAALLQIHPDHQGGRTLLVALLKQGEAALAHVDQLMQGEADGP----LWLC 83
Db 289 KARLLKSVITQTPKPPG--WIAAARLBVEAGKLQVA--QLIQRCGECPTNEDVWL- 343
Qy 84 RSPACOLAGRLDEAR 98
Db 344 --KACRLASP-DEAK 355
RESULT 2
US-10-449-902-47030
; Sequence 47030, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF


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; SEQ ID NO 4629
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4629

Query Match
Best Local Similarity 11.9%; Score 71.5; DB 6; Length 772;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 378 DALYNLGGLYMDLGRFORASEMYTRVLAVPNHRAQLNKAVSLLGAGETEAKRALKEA 437
Qy 63 -----ALAHVDQLMQ-----GEADGPLWLCRSRACQLAG 92
Db 438 LKMTNRVELHDVASHLKQLQKKKKVKKGNSANESEGGPFIVVSSKFKTVG 486

RESULT 7
US-10-953-349-4628
; Sequence 4628, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4628
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4628

Query Match
Best Local Similarity 11.9%; Score 71.5; DB 6; Length 802;
Matches 25; Conservative 16; Mismatches 41; Indels 27; Gaps 2;

Qy 11 DALLLTGWLQYGHDPDKASVLLAALLQIHPDHQGGRTLLVALLKQGEA-----62
Db 408 DALYNLGGLYMDLGRFORASEMYTRVLAVPNHRAQLNKAVSLLGAGETEAKRALKEA 467
Qy 63 -----ALAHVDQLMQ-----GEADGPLWLCRSRACQLAG 92
Db 468 LKMTNRVELHDVASHLKQLQKKKKVKKGNSANESEGGPFIVVSSKFKTVG 516

RESULT 8
US-10-953-349-31757
; Sequence 31757, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31757
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31757

Query Match
Best Local Similarity 11.8%; Score 71; DB 6; Length 495;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;
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Qy 21 LOYGHDPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 121 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 177
Qy 73 QGEADGPLWLCRSRACOLA-----GRLEDEARFAYQOYLE-LEEQNESTHP 116
Db 178 TWVANG-----RDVEVATIDVAIGNTYLALARFDESFSYQKALTVLKSARGDDHP 228

RESULT 9
US-10-953-349-31756
; Sequence 31756, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31756
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31756

Query Match
Best Local Similarity 11.8%; Score 71; DB 6; Length 530;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYGHDPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 156 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 212
Qy 73 QGEADGPLWLCRSRACOLA-----GRLEDEARFAYQOYLE-LEEQNESTHP 116
Db 213 TWVANG-----RDVEVATIDVAIGNTYLALARFDESFSYQKALTVLKSARGDDHP 263

RESULT 10
US-10-953-349-31755
; Sequence 31755, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31755
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31755

Query Match
Best Local Similarity 11.8%; Score 71; DB 6; Length 610;
Matches 30; Conservative 17; Mismatches 39; Indels 32; Gaps 5;

Qy 21 LOYGHDPDKASVLLAALLQIHPDHQ-----GGRRTLLVALLKQGEAALAHVDQLMQ 72
Db 236 LQF---DEAEKLCRKALEIHRHSAPASLEASDRRLMALILDAGDYDGALEHLVLASM 292
Qy 73 QGEADGPLWLCRSRACOLA-----GRLEDEARFAYQOYLE-LEEQNESTHP 116
Db 293 TWVANG-----RDVEVATIDVAIGNTYLALARFDESFSYQKALTVLKSARGDDHP 343
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STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/330,353
FILING DATE: 12-Jan-2006
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
FILING DATE: 10-Sep-2002
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-330-353-14

Query Match 11.6%; Score 70; DB 7; Length 177;
Best Local Similarity 34.8%; Pred. No. 1.2;
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;
Qy 57 QGGEA-----ALAHVDQLMQQGEADG-----PLWLCSRACQLAG---RLDEARFA 100
Db 28 QGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAPLSSCPQALQLAGCLSLHSGFL 87
Qy 101 YQYVLEEE 109
Db 88 YQGLQALE 96

RESULT 15
US-10-511-937-2461
Sequence 2461, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2461
LENGTH: 204
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2461

Query Match 11.6%; Score 70; DB 6; Length 204;
Best Local Similarity 34.8%; Pred. No. 1.4;
Matches 24; Conservative 8; Mismatches 21; Indels 16; Gaps 3;
Qy 57 QGGEA-----ALAHVDQLMQQGEADG-----PLWLCSRACQLAG---RLDEARFA 100
Db 55 QGDGAALQEKLCATYKLCHPPELVLLGHSIGIPWAPLSSCPQALQLAGCLSLHSGFL 114
Qy 101 YQYVLEEE 109
Db 115 YQGLQALE 123

Search completed: June 16, 2006, 20:25:52
Job time : 4.99837 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 61.622 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-6
Perfect score: 483
Sequence: 1 MLVRRGERAGLANPFAALY.....ATEQVCLRDMDKQKHGLA 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 8:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	93	5 ABB80774	Abb80774 A. salmon
2	258	53.4	875	7 ABO81310	AbO81310 Pseudomon
3	72	14.9	929	4 ABG05766	Abg05766 Novel hum
4	72	14.9	2301	6 ABUS2379	Abu52379 Human GPC
5	72	14.9	2301	8 ADL24093	Adl24093 Human NOV
6	71	14.7	298	7 ADM66546	Adm26546 Hyperther
7	70.5	14.6	240	2 AAY35351	Aay35351 Amino aci
8	70	14.5	211	7 ABO74225	AbO74225 Pseudomon
9	69	14.3	236	7 ABM86863	Abm86863 Rice abio
10	69	14.3	441	6 ABM69700	Abm69700 Photorhab
11	68	14.1	76	4 AAM81462	Aam81462 Human hae
12	67.5	14.0	168	6 ABR43312	AbR43312 Human lip
13	67	13.9	378	7 ABO78198	AbO78198 Pseudomon
14	67	13.9	381	4 AAU33703	Aau33703 Pseudomon
15	67	13.9	381	6 ABUI5637	Abui5637 Protein e
16	67	13.9	395	7 ABM88963	Abm88963 Rice abio
17	66.5	13.8	369	7 ADD14092	Add14092 Human src
18	66.5	13.8	427	5 ABP63531	Abp63531 KRAA 0751
19	66.5	13.8	427	7 ADD12210	Add12210 PBZ domai
20	66.5	13.8	1201	8 ADN21296	Adn21296 Bacterial
21	66.5	13.8	1333	6 ABO07123	AbO07123 Novel hum
22	66	13.7	374	8 ADX93170	Adx93170 Plant hum
23	65.5	13.6	202	2 AAU09385	Aau09385 S-recepto

24	65.5	13.6	375	6 ADA34975	Ada34975 Acinetoba
25	65.5	13.6	433	2 AAU09384	Aau09384 S-sugar p
26	65.5	13.6	1590	4 AAB73488	Aab73488 Mouse Rim
27	65	13.5	378	6 ABU49755	Abu49755 Protein e
28	65	13.5	2023	8 ABM84980	Abm84980 Human dia
29	64.5	13.4	197	8 ADX5891	Adx5891 Plant ful
30	64.5	13.4	468	8 ADN24975	Adn24975 Bacterial
31	64.5	13.4	468	8 ADN22215	Adn22215 Bacterial
32	64.5	13.4	469	6 ABU21852	Abu21852 Protein e
33	64	13.3	440	9 ABM96571	Abm96571 M. xanthu
34	63.5	13.1	133	4 ABG05180	Abg05180 Novel hum
35	63.5	13.1	420	2 AAW20266	Aaw20266 H. pylori
36	63.5	13.1	424	2 AAW20977	Aaw20977 H. pylori
37	63	13.0	472	8 AED27779	Aed27779 Bacterial
38	63	13.0	475	5 AED28479	Aed28479 Phospholi
39	62.5	12.9	57	5 ABP06256	Abp06256 Human ORF
40	62.5	12.9	220	7 ABO81436	AbO81436 Pseudomon
41	62.5	12.9	252	3 AAG07105	Aag07105 Arabidops
42	62.5	12.9	316	8 ADR09962	Adr09962 Human pro
43	62.5	12.9	391	3 AAG20311	Aag20311 Arabidops
44	62.5	12.9	391	3 AAG61061	Aag61061 Arabidops
45	62.5	12.9	397	3 AAG61060	Aag61060 Arabidops

ALIGNMENTS

RESULT 1
ABB80774
ID ABB80774 standard; protein; 93 AA.
XX AC ABB80774;
XX DT 23-SEP-2002 (first entry)
XX DE A. salmonicida type III secretion protein acrR sequence.
XX KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;
XX KR acrv; acrH; antibiotic; vaccine; fish.
XX OS Aeromonas salmonicida.
XX DN WO2002040514-A2.
XX PD 23-MAY-2002.
XX PF 15-NOV-2001; 2001WO-CA001589.
XX PR 15-NOV-2000; 2000US-0248864P.
XX (FREY/) FREY J.
XX (STUB/) STUBER K.
XX (THOR/) THORNTON J C.
XX (KUZV/) KUZYK M A.
XX (BURI/) BURIAN J.
XX Frey J, Stuber K, Thornton JC, Kuzyk MA, Burian J;
XX WPI: 2002-537338/57.
XX N-PSDB; ABN86172.
XX Novel protein from Aeromonas salmonicida and nucleic acid encoding the
XX protein, useful for reducing susceptibility of fish to infection by a
XX virulent strain of Aeromonas salmonicida.
XX Claim 13; Page 28; 39pp; English.
XX The invention relates to A. salmonicida type III secretion genes and
XX encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.
XX A. salmonicida type III secretion apparatus is useful for producing
XX selected products, especially hexT. AcrV in vaccine, epitope or epitopic
XX region of AcrV or any other protein of A. salmonicida type III secretion
XX apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of A. salmonicida. The proteins and encoding DNA are
CC useful for manufacturing a diagnostic agent. Detecting the presence of
CC the genes of AcrD, AcrV or any other components of the A. salmonicida type
CC III secretion apparatus is useful for the production or quality control
CC or efficacy of vaccines made from A. salmonicida or its genes. The present
CC sequence represents the A. salmonicida type III secretion protein acr
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 483; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLVRRGGERAGLANPFAALYLLAEATLAVLGPCHFLYGNVDVFRSSLSSESLRGLRFLRW 60
Db 1 MLVRRGGERAGLANPFAALYLLAEATLAVLGPCHFLYGNVDVFRSSLSSESLRGLRFLRW 60

QY 61 TGASEPEPGWFMLATEQVCSLRDMRKQKHGLA 93
Db 61 TGASEPEPGWFMLATEQVCSLRDMRKQKHGLA 93

RESULT 2
ABO81310
ID ABO81310 standard; protein; 875 AA.

AC ABO81310;

XX 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #13485.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

XX 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX WPI; 2003-615309/58.

XX N-PSDB; ABD14881.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, of
XX useful as molecular targets for diagnostics, prophylaxis and treatment of
XX pathological conditions resulting from bacterial infection.

XX Disclosure; SEQ ID NO 30056; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX polynucleotides encoding them. The sequences are useful in diagnosis and
XX therapy of pathological conditions, as molecular targets for diagnostics,
XX prophylaxis and treatment of pathological conditions resulting from a
XX bacterial infection, for evaluating a compound, such as a polypeptide,
XX for the ability to bind a P. aeruginosa nucleic acid, as components of
XX effective antibacterial targets, as targets for antibacterial drugs,
XX including anti-P. aeruginosa drugs, as templates for recombinant
XX production of P. aeruginosa-derived peptides or polypeptides, as target
XX components for diagnosis and/or treatment of P. aeruginosa-caused
XX infection, and in detection of P. aeruginosa sequences or other sequences
XX of Pseudomonas species using biochip technology. Sequences ABO67826-
XX ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
XX sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 875 AA;

Query Match 53.4%; Score 258; DB 7; Length 875;
Best Local Similarity 58.4%; Pred. No. 6.6e-24;
Matches 52; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 1 MLVRRGGERAGLANPFAALYLLAEATLAVLGPCHFLYGNVDVFRSSLSSESLRGLRFLRW 60
Db 783 VMLRRRQARSGLANPFAALYLLAEATLDTLGPQRQLYKVLALAGSPLFGEMARFYRRW 842

QY 61 TGASEPEPGWFMLATEQVCSLRDMRKROK 89
Db 843 TGAEPADGWFELEAGRVTQSLRKROK 871

RESULT 3
ABG05766
ID ABG05766 standard; protein; 929 AA.

XX AC ABG05766;

XX 13-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #5757.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS69953.

XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.

XX Claim 20; SEQ ID NO 36125; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 929 AA;

Query Match 14.9%; Score 72; DB 4; Length 929;
Best Local Similarity 36.7%; Pred. No. 10;
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;

Oy 17 AALYLLAEATLAVLPGHFYGNV--DVFRRSSLSRLG--RFYLWWTGASEPEPGWEM 72
Db 128 AGYIFLQEASL-----FQHLYAVVIDTGFAPASAPQLGLRLKIRLWHDGRGSPGWFI 183

RESULT 4
ABU52379
ID ABU52379 standard; protein; 2301 AA.

AC ABU52379;
XX
DT 03-MAR-2003 (first entry)
XX
DE Human GPCR related protein NOV29a.
XX
KW Human; NOVX; G-protein coupled receptor; GPCR; cancer; cytostatic.

XX Homo sapiens.

XX WO200279398-A2.

XX 10-OCT-2002.

XX 08-MAR-2002; 2002WO-US007355.

XX 08-MAR-2001; 2001US-0274194P.

XX 08-MAR-2001; 2001US-0274281P.

XX 08-MAR-2001; 2001US-0274322P.

XX 09-MAR-2001; 2001US-0274849P.

XX 13-MAR-2001; 2001US-0275578P.

XX 13-MAR-2001; 2001US-0275579P.

XX 13-MAR-2001; 2001US-0275601P.

XX 14-MAR-2001; 2001US-0276000P.

XX 16-MAR-2001; 2001US-0276776P.

XX 19-MAR-2001; 2001US-0276994P.

XX 20-MAR-2001; 2001US-0277239P.

XX 20-MAR-2001; 2001US-0277327P.

XX 20-MAR-2001; 2001US-0277338P.

XX 21-MAR-2001; 2001US-0277791P.

XX 22-MAR-2001; 2001US-0277833P.

XX 23-MAR-2001; 2001US-0278152P.

XX 26-MAR-2001; 2001US-0278894P.

XX 27-MAR-2001; 2001US-0278999P.

XX 27-MAR-2001; 2001US-0279036P.

XX 30-MAR-2001; 2001US-0280233P.

XX 02-APR-2001; 2001US-0280802P.

XX 02-MAY-2001; 2001US-0288052P.

XX 02-MAY-2001; 2001US-0288056P.

XX 02-MAY-2001; 2001US-0288228P.

XX 17-MAY-2001; 2001US-0291766P.

XX 07-JUN-2001; 2001US-0296693P.

XX 08-JUN-2001; 2001US-0296856P.

XX 05-JUL-2001; 2001US-0303230P.

XX 05-JUL-2001; 2001US-0303237P.

XX 08-AUG-2001; 2001US-0310913P.

XX 13-AUG-2001; 2001US-0311978P.

XX 14-AUG-2001; 2001US-0312191P.

XX 16-AUG-2001; 2001US-0312916P.

XX 17-AUG-2001; 2001US-0313182P.

XX 20-AUG-2001; 2001US-0313626P.

XX 21-AUG-2001; 2001US-0314018P.

XX 27-AUG-2001; 2001US-0315227P.

XX 10-SEP-2001; 2001US-0318403P.

PR 10-SEP-2001; 2001US-0318510P.
PR 14-SEP-2001; 2001US-032296P.
PR 14-SEP-2001; 2001US-0322360P.
PR 27-SEP-2001; 2001US-0325378P.
PR 09-NOV-2001; 2001US-0332486P.
PR 09-NOV-2001; 2001US-0345399P.
PR 07-MAR-2002; 2002US-00094886.
XX
XX (CURA-) CURAGEN CORP.

XX Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;
PI Burgess CE, Vernet CM, Gorman L, Malyanar UM, Boldog FL;
PI Guo X, Shenoy SG, Padigaru M, Taupier RJ, Miller CE, Casman SJ;
PI Pena CE, Gangolli EA, Gusev V, Smithson G, Zerhusen BD, Gerlach V;
PI Pocharat PF, Fernandes ER, Shinkets RA, Rastelli L, Spaderna SK;
PI Larochelle WJ, Zhong M, Khrantsov NV, Voss EZ, Herrmann JL;
XX

XX WPI; 2003-058423/05.

XX N-PSDB; ABX70470.

XX NOVX polypeptides and polynucleotides, useful for treating a syndrome
PT related to a human disease associated with the NOVX polypeptide e.g.,
PT cancer.

XX Claim 1; Page 182-183; 413pp; English.

XX The present invention relates to the isolation of novel human
CC polypeptides referred to as NOVX (NOV1-NOV44), variants of these
CC proteins, and the polynucleotide sequences encoding them. The NOVX
CC proteins of the invention are G-protein coupled receptor (GPCR) related
CC proteins. The sequences of the invention are useful in the manufacture
CC of a medicament for treating a syndrome related to a human disease
CC associated with the polypeptides e.g. cancer. ABU52311-ABU52408 represent
CC the human NOVX proteins of the invention

XX SQ Sequence 2301 AA;

Query Match 14.9%; Score 72; DB 6; Length 2301;
Best Local Similarity 36.7%; Pred. No. 33;
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;

Oy 17 AALYLLAEATLAVLPGHFYGNV--DVFRRSSLSRLG--RFYLWWTGASEPEPGWEM 72
Db 1592 AGYIFLQEASL-----FQHLYAVVIDTGFAPASAPQLGLRLKIRLWHDGRGSPGWFI 1647

RESULT 5

ADL24093

ID ADL24093 standard; protein; 2301 AA.

XX ADL24093;

XX 20-MAY-2004 (first entry)

XX Human NOVX polypeptide #69.

XX Human; NOVX; G protein-coupled receptor; GPCR; cardiomyopathy;
KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
KW atrial septal defect; ASD; atrioventricular canal defect;
KW ductus arteriosus; pulmonary stenosis; subaortic stenosis;
KW ventricular septal defect; VSD; tuberosus sclerosis; scleroderma; obesity;
KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
KW neoplasm; adenocarcinoma; lymphoma; uterine cancer; haemophilia;
KW hypercoagulability; idiopathic thrombocytopenia purpura;
KW immunodeficiency; graft-versus-host disease; AIDS; bronchial asthma;
KW Crohn's disease; multiple sclerosis;
KW Abright's hereditary osteodystrophy; diabetes; infectious diseases;
KW anorexia; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; haematopoietic disorder; metabolic disorder;
XX receptor.

XX Homo sapiens.

XX

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PN US2004002120-A1.
XX 01-JAN-2004.
XX 07-MAR-2002; 2002US-00094886.
XX 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-027676P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277327P.
PR 20-MAR-2001; 2001US-0277338P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277933P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-MAY-2001; 2001US-0288052P.
PR 02-MAY-2001; 2001US-0288066P.
PR 02-MAY-2001; 2001US-0288228P.
PR 17-MAY-2001; 2001US-0291766P.
PR 07-JUN-2001; 2001US-0296693P.
PR 08-JUN-2001; 2001US-0296856P.
PR 05-JUL-2001; 2001US-0303230P.
PR 05-JUL-2001; 2001US-0303237P.
PR 08-AUG-2001; 2001US-0310913P.
PR 13-AUG-2001; 2001US-0311978P.
PR 14-AUG-2001; 2001US-0312191P.
PR 16-AUG-2001; 2001US-0312916P.
PR 17-AUG-2001; 2001US-0313182P.
PR 20-AUG-2001; 2001US-0313626P.
PR 21-AUG-2001; 2001US-0314018P.
PR 27-AUG-2001; 2001US-0315227P.
PR 10-SEP-2001; 2001US-0318403P.
PR 10-SEP-2001; 2001US-0318510P.
PR 14-SEP-2001; 2001US-0322296P.
PR 14-SEP-2001; 2001US-0322360P.
PR 27-SEP-2001; 2001US-0325378P.
PR 09-NOV-2001; 2001US-0332486P.
PR 09-NOV-2001; 2001US-0345399P.
XX (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.
PA (CASW/) CASMAN S J.
PA (PENA/) PENNA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.

(ZERR/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
XX
PI Kekuda R, Tchernev VT, Liu X, Spytek KA, Patturajan M;
PI Burgess CE, Vernet CAM, Li L, Gorman L, Malyankar UM, Boldog FL;
PI Guo X, Shenoy SG, Padigar M, Taupier RJ, Miller CE, Casman SJ;
PI Pena CEA, Gangolli EA, Gusev VY, Smithson G, Zerhusen BD, Gerlach V;
PI Pochart PF, Fernandes ER, Shimkets R, Rastelli L, Spaderna SK;
PI Larochelle WJ, Zhong M, Khrantsov NV, Voss EZ, Herrmann JL;
XX
WPI: 2004-212692/20.
DR N-PSDB; ADL24092.
XX
Novel isolated G protein-coupled receptor polypeptides, referred as NOVX,
useful for treating scleroderma, obesity, congenital adrenal hyperplasia,
prostate cancer, hemophilia, AIDS, bronchial asthma, Crohn's disease.
XX
Claim 1; SEQ ID NO 138; 287pp; English.
XX
The invention relates to human G protein-coupled receptor-related (GPCR-
related) polypeptides (designated NOVX) and the polynucleotides encoding
them. The polypeptides and polynucleotides are useful as therapeutics in
the manufacture of medicaments for treating syndromes associated with
human diseases. The sequences are useful for treating a disorder
associated with aberrant NOVX expression or activity such as
cardiomyopathy, atherosclerosis, hypertension, congenital heart defects,
aortic stenosis, atrial septal defect (ASD), atriocentric stenosis,
defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis,
ventricular septal defect (VSD), tuberosus sclerosis, scleroderma,
obesity, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate
cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer, haemophilia,
hypercoagulability, idiopathic thrombocytopenia purpura,
immunodeficiencies, graft-versus-host disease, AIDS, bronchial asthma,
Crohn's disease, multiple sclerosis, Albright's hereditary
osteodystrophy, diabetes, infectious diseases, anorexia,
neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
immune disorders, haematopoietic disorders and metabolic disorders. This
sequence represents a human NOVX polypeptide of the invention.
XX
SQ Sequence 2301 AA;

Query Match 14.9%; Score 72; DB 8; Length 2301;
Best Local Similarity 36.7%; Pred. No. 33;
Matches 22; Conservative 7; Mismatches 23; Indels 8; Gaps 3;

QY 17 AALYLLAETATLAVLPGHFLYGNV--DVFSSSLSSERLG--RFVLRWTGASEPEPGWFM 72
Db 1592 AGVIFLQEASL---PGHQLYAVVDTGTFRAPASAPQLGLRLKIRLWHDSRGPSGWTI 1647

RESULT 6
ADM26546
ID ADM26546 standard; protein; 298 AA.
XX
AC ADM26546;
XX
XX 20-MAY-2004 (first entry)
DT
DE Hyperthermophile Methanopyrus kandleri protein #1152.
XX
XX hyperthermophile; protein stability enhancement;
XX protein activity enhancement.

```


PS Disclosure; SEQ ID NO 22971; 455pp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the

CC polynucleotides encoding them. The sequences are useful in diagnosis and

CC therapy of pathological conditions, as molecular targets for diagnostics,

CC prophylaxis and treatment of pathological conditions resulting from a

CC bacterial infection, for evaluating a compound, such as a polypeptide,

CC for the ability to bind a P. aeruginosa nucleic acid, as components of

CC effective antibacterial targets, as targets for antibacterial drugs,

CC including anti-P. aeruginosa drugs, as templates for recombinant

CC production of P. aeruginosa-derived peptides or polypeptides, as target

CC components for diagnosis and/or treatment of P. aeruginosa-caused

CC infection, and in detection of P. aeruginosa sequences or other sequences

CC of Pseudomonas species using biochip technology. Sequences ABO67826-

CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The

CC sequence data for this patent did not form part of the printed

CC specification but was obtained in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html

XX seqdata.uspto.gov/sequence.html

XX Sequence 211 AA;

Query Match 14.5%; Score 70; DB 7; Length 211;

Best Local Similarity 31.2%; Pred. No. 2.9;

Matches 24; Conservative 5; Mismatches 24; Indels 24; Gaps 3;

QY 5 REGERA-----GLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSLSSERLGRFYLR 59

Db 67 RQGERAGDPDTGRTGFGA-----LPPGQRWG-----AFAEHLRGNHSCR 107

QY 60 WTGASEPEPGWFMPLATE 76

Db 108 QPGRGVYPGWPAPARTE 124

RESULT 9

ID ABM86863

XX ABM86863 standard; protein; 236 AA.

AC ABM86863;

XX 02-JUN-2005 (first entry)

DT Rice abiotic stress responsive polypeptide SEQ ID NO:5109.

DE abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.

KW Oryza sativa.

OS

XX WO2003008540-A2.

PN 30-JAN-2003.

PD 21-JUN-2002; 2002WO-US019668.

XX 22-JUN-2001; 2001US-0300112P.

PR 24-AUG-2001; 2001US-0314662P.

PR 26-SEP-2001; 2001US-0325277P.

PR 21-NOV-2001; 2001US-0332132P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri P;

PI Moughamer T, Provart N, Ricke D, Zhu T;

XX WPI; 2003-248011/24.

XX New stress-responsive nucleic acid, useful for altering the

PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold

PT stresses, salt stress or osmotic stress.

XX Claim 1; SEQ ID NO 5109; 89pp; English.

PS The invention relates to novel abiotic stress responsive polynucleotides

CC

CC and polypeptides. Also disclosed are vectors, expression cassettes, host

CC cells, and plants containing such polynucleotides. Also disclosed are

CC methods for using the polynucleotides and polypeptides to alter the

CC responsiveness of a plant to abiotic stress. The invention is useful in

CC agriculture. The nucleic acid is useful for determining whether a test

CC plant has been exposed to an abiotic stress condition. It is also useful

CC for selecting an agent that alters abiotic stress regulated

CC polynucleotide expression in a plant cell, and to identify a homolog or

CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid

CC molecule and the polypeptide encoded by it are useful in altering the

CC responsiveness of a plant to an abiotic stress, such as cold stress, salt

CC stress, osmotic stress or any of their combinations. The present sequence

CC is used in the exemplification of the invention

XX Sequence 236 AA;

QY 15 PFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSLSSERLGRFY--LRWTGASEPEPGWFM 72

Db 9 PFTLLTLLATRLA-----YDYGVVAAATFTGFSLSQ-IFLYCFARWAGALKPGGGRGV 62

QY 73 LATEQVCSLRDMRKROKHGL 92

Db 63 VAGEPVL-----RRGVHGV 76

RESULT 10

ID ABM69700

XX ABM69700 standard; protein; 441 AA.

AC ABM69700;

XX 20-NOV-2003 (first entry)

DT Photorhabdus luminescens protein sequence #2797.

DE

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

KW detection; food; gene expression; plant; animal; microorganism; toxin;

KW antibiotic; biopesticide; virulence factor; disease model; plague;

KW whooping cough.

XX Photorhabdus luminescens.

OS

XX WO200294867-A2.

PN 28-NOV-2002.

PD 07-FEB-2002; 2002WO-IB003040.

PF 07-FEB-2001; 2001FR-00001659.

XX (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PI Buchrieser C;

XX WPI; 2003-148459/14.

DR Genomic sequence of Photorhabdus luminescens and encoded polypeptides,

XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.

PT Claim 2; SEQ ID NO 2797; 1205pp; French.

PS The invention relates to the isolation of genes and their encoded

CC proteins from Photorhabdus luminescens. The isolated sequences are

CC sources of probes and primers for detecting the genome of P. luminescens

CC and related species; to study polymorphisms; for gene analysis and for

CC detection/amplification of the genes. Antibodies (Ab) raised against the

CC polypeptides encoded by the genes are used for detection/identification

CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins
XX
SQ Sequence 441 AA;

Query Match 14.3%; Score 69; DB 6; Length 441;
Best Local Similarity 27.1%; Pred. No. 10;
Matches 29; Conservative 15; Mismatches 43; Indels 20; Gaps 4;
QY 5 REGERAGLANPFAALYLIAE-----ATLAVLPGHFLYGNVDVFRSSLSSESLGRF 56
DB 44 RIGELCHLRNPNTLSLLAEVIGFQQHQALLTPGEMFGISSNTEVSTPGAMHQVGVGDY 103
QY 57 YL-----RWGASEPEP-GWFMLEQVCSLRDMRKRQKHGLA 93
DB 104 LLQGVLDGLGNPFSGQLPEPQAVPVYRDAPAM--SRKRIEHPLS 148

RESULT 11
AAM81462
ID AAM81462 standard; protein; 76 AA.
XX
AC AAM81462;
XX
DT 13-NOV-2001 (first entry)
XX
DE Human haematological malignancy-related antigen #1160.
XX
KW Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
XX
OS Homo sapiens.
XX
PN WO200164886-A2.
XX
PD 07-SEP-2001.
XX
PF 01-MAR-2001; 2001WO-US007272.
XX
PR 01-MAR-2000; 2000US-0186126P.
PR 17-MAR-2000; 2000US-0190479P.
PR 27-APR-2000; 2000US-0200545P.
PR 28-APR-2000; 2000US-0200303P.
PR 28-APR-2000; 2000US-0200779P.
PR 01-MAY-2000; 2000US-0200999P.
PR 04-MAY-2000; 2000US-0202084P.
PR 22-MAY-2000; 2000US-0206201P.
PR 14-JUL-2000; 2000US-0218950P.
PR 03-AUG-2000; 2000US-0222903P.
PR 04-AUG-2000; 2000US-0223416P.
PR 07-AUG-2000; 2000US-0223378P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J;
XX
DR WPI; 2001-514842/56.
XX
PT Compositions and methods for the detection of hematological malignancies,

PT e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
PT Hodgkin's and T/B cell non-Hodgkin's lymphoma.
XX
PS Claim 1; Page 974; 1252pp; English.
XX
CC The present invention relates to compositions and methods for the
CC detection, diagnosis and therapy of haematological malignancies. The
CC present sequence is the protein sequence of a human haematological
CC malignancy related antigen. The methods of the present invention comprise
CC detecting the presence of haematological malignancy related antigen(s) in
CC a sample obtained from the patient (an increased level of the
CC polypeptide, compared to an unaffected individual, is indicative of an
CC increased risk). Haematological malignancies which can be treated using
CC the present invention are chronic lymphocytic leukaemia, lymphoma,
CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
CC cell non-Hodgkin's lymphoma
XX
SQ Sequence 76 AA;

Query Match 14.1%; Score 68; DB 4; Length 76;
Best Local Similarity 40.9%; Pred. No. 1.5;
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;
QY 16 FAALYLLAEATLAVLPGHF-----LYGNVDVFRSSLSSESLRGRFVLRWTGASEPE 67
DB 13 FVSLPTMQEASLAVLFYHYHISPCNKVLYRQVRSMLSLSLSPRL---RLRYRGNS-PV 68
QY 68 PGWFML 73
DB 69 QSLFML 74

RESULT 12
ABR43312
ID ABR43312 standard; protein; 168 AA.
XX
AC ABR43312;
XX
DT 10-JUL-2003 (first entry)
XX
DE Human lipid-associated molecule LIPAM-17 protein SEQ ID NO:17.
XX
KW Human; lipid-associated molecule; LIPAM; cytostatic; cerebroprotective;
KW antiarteriosclerotic; anti-HIV; antiallergic; antiparkinsonian; cardiant;
KW anticonvulsant; nootropic; antiinflammatory; antitumor; hepatotropic;
KW antibacterial; virucide; protozoacide; antiparasitic; antilipemic; AIDS;
KW gene therapy; cell proliferative disease; cancer; atherosclerosis; ulcer;
KW autoimmune disease; inflammatory disease; allergy; neurological disorder;
KW stroke; Parkinson's disease; epilepsy; gastrointestinal disorder;
KW cirrhosis; cardiovascular disorder; myocardial infarction; obesity;
KW metabolic disorder; developmental disorder; endocrine disorder;
KW pulmonary disorder; infection; lipid metabolism disorder.
XX
OS Homo sapiens.
XX
PN WO2003025150-A2.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-US029980.
XX
PR 21-SEP-2001; 2001US-0324039P.
PR 26-OCT-2001; 2001US-0346197P.
PR 02-NOV-2001; 2001US-0343876P.
PR 30-NOV-2001; 2001US-0334211P.
PR 14-DEC-2001; 2001US-0340223P.
PR 18-DEC-2001; 2001US-0342166P.
PR 22-JAN-2002; 2002US-0351262P.
PR 03-MAY-2002; 2002US-0377576P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Warren BA, Emerling BM, Lee EA, Chang H, Forsythe J, Griffin JA;


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PR 16-FEB-2001; 2001US-0269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX Haseelbeck R, Ohlseen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX DR N-PSDB; AAS51562.
XX
XX New polynucleotides for the identification and development of
XX PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 5199; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX CC prokaryotic cellular proliferation, their use in identifying the genes,
XX CC their use in the discovery of novel antibiotics, the essential genes,
XX CC themselves and the encoded proteins. The prokaryotes used are Escherichia
XX CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX CC useful for the identification of potential new targets for antibiotic
XX CC development. The antisense nucleic acids can also be used to identify
XX CC proteins used in proliferation, to express these proteins, and to obtain
XX CC antibodies capable of binding to the expressed proteins. The proteins can
XX CC be used to screen compounds in rational drug discovery programmes. The
XX CC antisense nucleic acid sequence is also useful to screen for homologous
XX CC nucleic acids which are required for cell proliferation in a wide variety
XX CC of organisms. The present sequence represents an essential prokaryotic
XX CC cellular proliferation protein. Note: The sequence data for this patent
XX CC did not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 381 AA;
XX
XX Query Match 13.9%; Score 67; DB 4; Length 381;
XX Best Local Similarity 26.3%; Pred. No. 15;
XX Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;
XX
XX QY 4 RREGERAGLANPFAALYLLAEA-----TLAVLGPCHFLYGNVDVFRSSLSLSERLGR 55
XX Db 164 RYRDAHSGMSGPYAAPRRILQAMTHPAWMDVGLGKPHDL-GNISAYRGNPTGLE--- 219
XX
XX QY 56 FYLRWTGAS-EPEPGW 70
XX Db 220 -YIGWLGANFDPISW 234
XX
XX RESULT 15
XX ABU15637
XX ID ABU15637 standard; protein; 381 AA.
XX XX
XX AC ABU15637;
XX
XX XX 19-JUN-2003 (first entry)
XX DT
XX DE Protein encoded by Prokaryotic essential gene #1164.
XX
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX OS Pseudomonas aeruginosa.
XX
XX PN WO200277183-A2.
XX
XX PD 03-OCT-2002.
XX
XX PF 21-MAR-2002; 2002WO-US009107.
XX
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
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PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haseelbeck R, Ohlseen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX DR N-PSDB; ACA19507.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX
XX PS Claim 25; SEQ ID NO 43561; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids
XX CC required for proliferation in cells other than S. aureus, S. typhimurium,
XX CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX CC the target prokaryotic essential genes. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 381 AA;
XX
XX Query Match 13.9%; Score 67; DB 6; Length 381;
XX Best Local Similarity 26.3%; Pred. No. 15;
XX Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;
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XX QY 4 RREGERAGLANPFAALYLLAEA-----TLAVLGPCHFLYGNVDVFRSSLSLSERLGR 55
XX Db 164 RYRDAHSGMSGPYAAPRRILQAMTHPAWMDVGLGKPHDL-GNISAYRGNPTGLE--- 219
XX
XX QY 56 FYLRWTGAS-EPEPGW 70
XX Db 220 -YIGWLGANFDPISW 234
XX
XX Search completed: June 16, 2006, 19:06:52
XX Job time : 63.622 secs
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C;Accession: H86580
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise, N.
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: H86580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <STO>
A;Cross-references: UNIPROT:Q92712; UNIPARC:UPI00000D41C4; GB:BA000008; NID:g8979095; PMID:10984043
A;Experimental source: strain J138
C;Genetics:
A;Gene: yhbG

Query Match 14.6%; Score 70.5; DB 2; Length 240;
Best Local Similarity 32.0%; Pred. No. 1.4;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

Qy 7 GERAGLANP-----FAALYLLAEATLVLGP--GHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 29 GEIVLLGPNAGAGKTTAFYL----TVGLIRPDSGKIIFKNVDVTKTMDHRRARLIGYL- 83
Qy 60 WTGASEPEPGWFMALTEQ---VCSLR---DMRKQKH 90
Db 84 -----AQEPTIFKELTVQDNLICILEIYKARKQKSH 115

RESULT 8
C72044
ABC transporter ATPase - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C;Accession: C72044
R;Kelman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: C72044
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240 <ARN>
A;Cross-references: UNIPROT:Q92712; UNIPARC:UPI00000D41C4; GB:AE001653; GB:AE001363; NID:10984043
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: yhbG
F;19-212/Domain: ATP-binding cassette homology <ABC>

Query Match 14.6%; Score 70.5; DB 2; Length 240;
Best Local Similarity 32.0%; Pred. No. 1.4;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

Qy 7 GERAGLANP-----FAALYLLAEATLVLGP--GHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 29 GEIVLLGPNAGAGKTTAFYL----TVGLIRPDSGKIIFKNVDVTKTMDHRRARLIGYL- 83
Qy 60 WTGASEPEPGWFMALTEQ---VCSLR---DMRKQKH 90
Db 84 -----AQEPTIFKELTVQDNLICILEIYKARKQKSH 115

RESULT 9
G83050
L-lactate dehydrogenase PA4771 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83050
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83050

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <STO>
A;Cross-references: UNIPROT:Q9HV37; UNIPARC:UPI00000C5DF8; GB:AE004890; GB:AE004091; NID:10382966
A;Experimental source: strain PA01
C;Genetics:
A;Gene: llbD; PA4771
C;Superfamily: alpha-hydroxy acid dehydrogenase, FMN-dependent; (S)-2-hydroxy-acid oxid

Query Match 13.9%; Score 67; DB 2; Length 381;
Best Local Similarity 26.3%; Pred. No. 5.9;
Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;

Qy 4 RREGERAGLANPFAALYLLAE-----TLAVLGGHFLYGNVDVFRSSLSLSSERLGR 55
Db 164 RYRDAHSGMSGPYAAPRRILQAMTHPAWANDVGLGKPHDL-GNISAYRGNTGLED--- 219
Qy 56 FYLRWTGAS-EPEPGW 70
Db 220 -YIGWLGANFDPISW 234

RESULT 10
E75583
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: E75583
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <WHI>
A;Cross-references: UNIPROT:Q9RYL6; UNIPARC:UPI00000C167E; GB:AE001863; GB:AE001825; NID:10382966
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0296
A;Map position: 2

Query Match 13.8%; Score 66.5; DB 2; Length 179;
Best Local Similarity 32.4%; Pred. No. 2.9;
Matches 24; Conservative 8; Mismatches 31; Indels 11; Gaps 3;

Qy 12 LANPFA-ALYLLAEATLAVLGGHFLYGNVDVFRSS-----SLSSERLGRFYLRWT 61
Db 7 LAQPLGRAAFSLSPDAEAQLLGGGALASQALASAGVTALGELLTLVPSPLPRLPWT 66
Qy 62 GASEPE-PCWFMIA 74
Db 67 LLTDEHHPGALLIA 80

RESULT 11
H72679
hypothetical protein APE0860 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H72679
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1.
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <KAW>
A;Cross-references: UNIPROT:Q9YDQ7; UNIPARC:UPI000005DCFD; DBJ:AP0000060; NID:g5104188;

A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0860
C;Superfamily: Aeropyrum pernix hypothetical protein APE0860

Query Match 13.8%; Score 66.5; DB 2; Length 338;
Best Local Similarity 35.9%; Pred. No. 5; 9;
Matches 23; Conservative 2; Mismatches 24; Indels 15; Gaps 2;

QY 12 LANPFAALYLLAEATLAVLPGHFLYGNVDVFR-----SSLSSERLGRFYLRWT 61
Db 14 LALPLLALVAGAEAPTLVGSQPF-----DVRVGEGFYVALIDDGFFDEVGRGRFYLYWA 68
QY 62 GASE 65
Db 69 GSPE 72

RESULT 12
GEB0
osteocalcin precursor - bovine
N;Alternate names: BGP; bone Gla protein; gamma-carboxyglutamic acid-containing protein
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S12653; A03303; S08693
R;Kiefer, M.C.; Saphire, A.C.S.; Bauer, D.M.; Barr, P.J.
Nucleic Acids Res. 18, 1909, 1990
A;Title: The cDNA and derived amino acid sequences of human and bovine bone Gla protein.
A;Reference number: S12652; MUID:90245603; PMID:2336375
A;Accession: S12653
A;Molecule type: mRNA
A;Residues: 1-100 <KIE>
A;Cross-references: UNIPROT:P02820; UNIPARC:UPI0000130ED9; EMBL:X53699; NID:g719; PIDN:C
A;Note: alternative splicing may produce a sequence lacking residues 33-34
R;Price, P.A.; Poser, J.W.; Raman, N.
Proc. Natl. Acad. Sci. U.S.A. 73, 3374-3375, 1976
A;Title: Primary structure of the gamma-carboxyglutamic acid-containing protein from bo
A;Reference number: A03303; MUID:77036749; PMID:1068450
A;Accession: A03303
A;Molecule type: protein
A;Residues: 52-100 <PRI>
A;Cross-references: UNIPARC:UPI0000174545
C;Comment: This protein, isolated from bone, binds strongly to apatite.
C;Superfamily: osteocalcin
C;Keywords: bone; calcium binding; carboxyglutamic acid; hydroxyproline
F;1-51/Domain: signal sequence #status predicted <SIG>
F;52-100/Product: osteocalcin #status experimental <WAT>
F;60/Modified site: 4-hydroxyproline (Pro) #status experimental
F;68,72,75/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F;74-80/Disulfide bonds: #status experimental

Query Match 13.6%; Score 65.5; DB 1; Length 100;
Best Local Similarity 36.6%; Pred. No. 2;
Matches 26; Conservative 4; Mismatches 32; Indels 9; Gaps 3;

QY 19 LYLAEATLAVLG-----PGHFLYGNVDVFRSSLSSE---RLGRFYLRWTGASEPEPCW 70
Db 7 LALLALATLCLAGRAKFDGAEKGAAFVSKQEGSEVVKRLRYLDHWLGAPAPYPD- 65
QY 71 FMLATEQVCSL 81
Db 66 PLEPKREVCEL 76

RESULT 13
T14392
S-luciferase
S-luciferase
C;Species: Braggia rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T14392
R;Watanabe, M.; Takasaki, T.; Toriyama, K.; Yamakawa, S.; Isogai, A.; Suzuki, A.; Hinata
Plant Cell Physiol. 35, 1221-1229, 1994
A;Title: A high degree of homology exists between the protein encoded by SRK in self-ind

A;Reference number: Z18026; MUID:95211381; PMID:7697295
A;Accession: T14392
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-433 <WAT>
A;Cross-references: UNIPROT:Q39282; UNIPARC:UPI00000ACE55; EMBL:D30050; NID:g633030; P1;
A;Experimental source: strain S9-homozygote; stigma
C;Superfamily: S-luciferase; S-luciferase; S-luciferase; S-luciferase; S-luciferase
C;Keywords: glycoprotein
F;38-427/Domain: S-luciferase; S-luciferase; S-luciferase; S-luciferase; S-luciferase

Query Match 13.6%; Score 65.5; DB 2; Length 433;
Best Local Similarity 28.2%; Pred. No. 10;
Matches 20; Conservative 9; Mismatches 33; Indels 9; Gaps 2;

QY 9 RAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSSERLG-----RFYLRW 60
Db 120 RENVRSPVVA-ELLANGNFVVRDPGFLWQSFYDTDTLLPMKLGYDLKTLGNRLVSW 178
QY 61 TCASEPEPCWF 71
Db 179 RSSDDPSSGDF 189

RESULT 14
T14398
S-receptor kinase (EC 2.7.1.1) - turnip
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T14398
R;Suzuki, G.; Watanabe, M.; Isogai, A.; Hinata, K.
Gene 191, 123-126, 1997
A;Title: Highly conserved 5'-flanking regions of two self-incompatibility genes, SLG9 a
A;Reference number: Z18032; MUID:97354304; PMID:9210598
A;Accession: T14398
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-841 <SUZ>
A;Cross-references: UNIPROT:Q23745; UNIPARC:UPI00000AC8A5; EMBL:D88193; NID:g2251113; P;
C;Genetics:
A;Gene: SRK9 (B.c)
A;Introns: 428/1; 471/1; 534/3; 604/1; 683/2; 730/3
C;Function:
A;Description: involved in preventing fertilization between plants having the same S-lo
C;Superfamily: S-luciferase; S-luciferase; S-luciferase; S-luciferase; S-luciferase
C;Keywords: ATP; phosphotransferase; receptor; strins/threonine-specific protein kinase
F;38-426/Domain: S-luciferase; S-luciferase; S-luciferase; S-luciferase; S-luciferase
F;516-799/Domain: protein kinase homology <KIN>

Query Match 13.6%; Score 65.5; DB 2; Length 841;
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Matches 20; Conservative 9; Mismatches 33; Indels 9; Gaps 2;

QY 9 RAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSSERLG-----RFYLRW 60
Db 120 RENVRSPVVA-ELLANGNFVVRDPGFLWQSFYDTDTLLPMKLGYDLKTLGNRLVSW 178
QY 61 TCASEPEPCWF 71
Db 179 RSSDDPSSGDF 189

RESULT 15
B82392
L-lactate dehydrogenase VCA0984 [imported] - Vibrio cholerae (strain N16961 serogroup O:
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82392
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <HEI>
A;Cross-references: UNIPROT:O9KKW6; UNIPARC:UPI00000C3700; GB:AE004425; GB:AE003853; NID
A;Experimental source: serogroup O1, strain N16961; biotype E1 Tor
C;Genetics:
A;Gene: VCA0984
A;Map position: 2
C;Superfamily: alpha-hydroxy acid dehydrogenase, FMN-dependent; (S)-2-hydroxy-acid oxidase

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Best Local Similarity 28.6%; Pred. No. 10;
Matches 20; Conservative 13; Mismatches 23; Indels 14; Gaps 4;

Qy 10 AGLAMPFAALYLLAEA-----TLAVLPGHFLYGNVDVFRSSSLSSERLGRFYLRWT 61
Db 170 SGMSGPNAMRRVLQAMAHPSWANDVGLLGKPHDL-GNISKYRGSPTKLED----YIGWL 224

Qy 62 GAS-EPEPGW 70
Db 225 GANFDPSTSW 234

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Job time : 11.4512 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 73.039 Seconds
(without alignments)
1177.815 Million cell updates/sec

Title: US-10-813-908A-6
Perfect score: 483
Sequence: 1 MLVRRGERAGLANPFAALY.....ATEQVCSLRDMRKQKHGLA 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	100.0	93	2 Q8GA90_AERSA	Q8GA90 aeromonas s
2	439	90.9	151	2 Q699R2_AERHY	Q699R2 aeromonas h
3	426	88.2	93	2 Q5CC99_AERSO	Q5CC99 aeromonas s
4	418	86.5	151	2 Q5XL06_AERHY	Q5XL06 aeromonas h
5	282	58.4	146	1 LCRR_YEREN	O68549 yersinia en
6	282	58.4	146	1 LCRR_YERPE	P69959 yersinia pe
7	282	58.4	146	1 LCRR_YERPS	P69960 yersinia ps
8	276	57.1	144	2 Q84GY7_PHOLU	Q84GY7 photorhabdu
9	275	56.9	146	2 Q6TLM4_AERHY	Q6TLM4 aeromonas h
10	264	54.7	144	2 Q7N0W9_PHOLL	O7n0w9 photorhabdu
11	258	53.4	144	2 Q30537_PSEAE	O30537 pseudomonas
12	179	37.1	137	2 Q6QV50_VIBHA	Q6qvs0 vibrio harv
13	175	36.2	137	2 Q66PT6_PASPI	Q66pt6 pasteurilla
14	164	34.0	137	2 Q87P57_VIBPA	Q87p57 vibrio para
15	76.5	15.8	1872	2 Q4Q2V5_LEIMA	Q4q2v5 leishmania
16	75.5	15.6	612	2 Q2W001_MAGSA	Q2w001 magnetospir
17	75	15.5	500	2 Q446S7_SOLUS	Q446s7 solibacter
18	74	15.3	247	2 Q415P2_KINRA	Q415f2 kinococcus
19	73.5	15.2	938	2 Q7NUX4_CHRVO	Q7nux4 chromobacte
20	73	15.1	383	1 LDDD_BARQU	Q690j2 bartonella
21	73	15.1	538	2 Q2RPL6_RHORU	Q2rpl6 rhodospiril
22	72.5	15.0	234	2 Q3X3V1_9ACTN	Q3x3v1 rubrobacter
23	72.5	15.0	595	2 Q3WZG9_9ACTN	Q3wzg9 rubrobacter
24	72.5	15.0	1189	2 Q4DH02_TRYCR	Q4dh02 trypanosoma
25	71.5	14.8	272	2 Q3JZS7_RHIET	Q3jzs7 rhizobium e
26	71	14.7	191	2 Q31171_CAEEL	Q31171 caenorhabdi
27	71	14.7	286	2 Q3J390_RHOS4	Q3j390 rhodobacter
28	71	14.7	298	2 Q8TW84_METKA	O8tw84 methanopyru
29	70.5	14.6	240	2 Q2Z712_CHLPN	Q2z712 chlamydia p
30	70.5	14.6	272	2 Q3PEU5_PARDE	Q3pel5 paracoccus
31	70.5	14.6	306	2 Q6P2G8_HUMAN	Q6p2g8 homo sapien

32	70.5	14.6	307	2 Q69YZ2_HUMAN	Q69yz2 homo sapien
33	70.5	14.6	327	2 Q6P2Q5_HUMAN	Q6p2q5 homo sapien
34	70.5	14.6	492	2 Q4NGZ7_9MICC	Q4ngz7 arthrobacte
35	70.5	14.6	901	2 Q4Q3F6_LEIMA	Q4q3f6 leishmania
36	70	14.5	372	2 Q391Z3_BURS3	Q391z3 burkholderi
37	70	14.5	377	2 Q4M1D7_9BURK	Q4m1d7 burkholderi
38	70	14.5	381	2 Q4ZZ10_PSEU2	Q4zz10 pseudomonas
39	70	14.5	469	2 Q35LP6_9BRAD	Q35lp6 bradyrhizob
40	70	14.5	909	2 Q31PL3_SYNPF	Q31pl3 synechococc
41	70	14.5	909	2 Q5N4L1_SYNPF	Q5n4l1 synechococc
42	69.5	14.4	309	2 Q72JN5_THET2	Q72jn5 thermus the
43	69.5	14.4	501	2 Q55LZ3_CRYNE	O55l23 cryptococcu
44	69.5	14.4	501	2 Q5K8S5_CRYNE	Q5k8s5 cryptococcu
45	69.5	14.4	885	2 Q4H6M1_9DEIO	Q4h6m1 deinococcus

ALIGNMENTS

RESULT 1
Q8GA90_AERSA
ID Q8GA90_AERSA PRELIMINARY; PRT; 93 AA.
AC Q8GA90;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Acrr protein.
GN Name=acrr;
OS Aeromonas salmonicida subsp. salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RX MEDLINE=2262111; PubMed=12374830;
RX DOI=10.1128/JB.184.21.5966-5970.2002;
RA Burr S.E., Stuber K., Wahli T., Frey J.;
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida."
RL J. Bacteriol. 184:5966-5970(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type =III secretion mutant in a rainbow trout model."
RL Microbiol. 151:2111-2118(2005).
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CC -----
DR EMBL; AJ458292; CAD30219.1; -; Genomic DNA.
DR EMBL; AJ616218; CAB83106.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10429 MW; 1A5C591CD0D79460 CRC64;
Query Match 100.0%; Score 483; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.2e-47;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLVRRGERAGLANPFAALYLLAEATLVLGPGHFLYGNVDVFRSSLSLSERLGRFYLW 60
Db 1 MLVRRGERAGLANPFAALYLLAEATLVLGPGHFLYGNVDVFRSSLSLSERLGRFYLW 60
Qy 61 TGASEPPGFWFLMATEQVCSLRDMRKQKHGLA 93
Db 61 TGASEPPGFWFLMATEQVCSLRDMRKQKHGLA 93
RESULT 2
Q699R2_AERHY
ID Q699R2_AERHY PRELIMINARY; PRT; 151 AA.
AC Q699R2;

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DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Acrr.
GN Name=acrr;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919 (2004).
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CC -----
DR EMBL; AY528667; AA991817.1; -; Genomic DNA.
SQ SEQUENCE 151 AA; 16928 MW; 2B28207206E1B147 CRC64;

Query Match          90.9%; Score 439; DB 2; Length 151;
Best Local Similarity 89.2%; Pred. No. 7.9e-42;
Matches 83; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLAEATLAVLPGHFLYGNVDVFRSSLSRSLGRFLRW 60
Db 59 LLVRRQGAQGLVNPFAALYLAEATLAVLPGHFLYGNVDVFRSSLSRSLGRFLRW 118
QY 61 TGASEPEPGWFMFLATEQVCSLRDMRKQKHGLA 93
Db 119 TGASEPEPGWFMFLAEQVCSLRDMRKQKHGLA 151

RESULT 3
Q5CC99 AERSO PRELIMINARY; PRT; 93 AA.
AC Q5CC99;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Acrr protein.
GN Name=acrr;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=UF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugsarkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca
RT fluviatilis.";
RL J. Fish Dis. 28:141-150 (2005).
CC -----
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CC -----
DR EMBL; AJ749609; CAG44556.1; -; Genomic DNA.
SQ SEQUENCE 93 AA; 10214 MW; D1F527554037FE6F CRC64;

Query Match          88.2%; Score 426; DB 2; Length 93;
Best Local Similarity 86.0%; Pred. No. 1.4e-40;
Matches 80; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

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Db 1 MLVRRQGAQGLVNPFAALYLAEATLAVLPGHFLYGNVDVFRSSLSRSLGRFLRW 60
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QY 61 TGASEPEPGWFMFLATEQVCSLRDMRKQKHGLA 93
Db 61 TGASEPEPGWFMFLAEQVCSLRDMRKQKHGLA 93

RESULT 4
Q5XL06 AERHY PRELIMINARY; PRT; 151 AA.
AC Q5XL06;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acrr.
GN Name=acrr;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457 (2005).
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CC -----
DR EMBL; AY763611; AAV30231.1; -; Genomic DNA.
SQ SEQUENCE 151 AA; 17032 MW; BBD211C884E20B6 CRC64;

Query Match          86.5%; Score 418; DB 2; Length 151;
Best Local Similarity 87.1%; Pred. No. 2e-39;
Matches 81; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 1 MLVRRGERAGLANPFAALYLAEATLAVLPGHFLYGNVDVFRSSLSRSLGRFLRW 60
Db 59 LLVRRHAEPLGLANPFAALYLAEATLAVLPGHFLYGNVDVFRSSLSRSLGRFLRW 118
QY 61 TGASEPEPGWFMFLATEQVCSLRDMRKQKHGLA 93
Db 119 TGASEPEPGWFMFLAEARVCSLRDMRKQKHGLA 151

RESULT 5
LCRR YEREN STANDARD; PRT; 146 AA.
AC O68549; Q93KU2;
DT 15-JUL-1999, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Low calcium response locus protein R.
GN Name=lcrr;
OS Versinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=W22703 / Serotype O:9 / Biotype 2; PLASMID=pYVe227;
RA Iriarte M., Lambrmont I., Kerbouch C., Cornelis G.R.;
RT "Detailed genetic map of the pYVe227 plasmid of Versinia
RT enterocolitica serotype O:9.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=8081 / Serotype O:8 / Biotype 1B; PLASMID=pYVe8081;
RX MEDLINE=21295118; PubMed=11402007;
DOI=10.1128/IAI.69.7.4627-4638.2001;
```

RA Snellings N.J., Popek M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype 0:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon.";
RL Infect. Immun. 69:4627-4638(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=AL27/90 / Serotype 0:8 / Biotype 1B; PLASMID=pyVal27/90;
RX MEDLINE=22890757; PubMed=14527656; DOI=10.1016/S0923-2508(03)00147-5;
RA Foulter B., Cornelis G.R.;
RT "DNA sequence and analysis of the pYVal27/90 virulence plasmid of
RT Yersinia enterocolitica strain AL27/90.";
RL Res. Microbiol. 154:553-557(2003).
RN [4]
CC -!- FUNCTION: Involved in the down-regulation of lcrGVH transcription
CC in the presence or absence of calcium and is necessary for lcrG
CC protein expression in the absence of calcium. Plays an important
CC role in the regulation of the low-calcium response (By
CC similarity).
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CC -----
CC EMBL; AF102990; AAD16817.1; -; Genomic DNA.
DR EMBL; AF336309; AAK69215.1; -; Genomic DNA.
DR EMBL; AY150843; AAN37515.1; -; Genomic DNA.
KW Calcium; Plasmid.
FT CHAIN 1 146 Low calcium response locus protein R.
FT /FTID=PRO_0000084373.
FT VARIANT 25 25 T -> A (in plasmid pYVal27/90).
FT
FT
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SQ SEQUENCE 146 AA; 16512 MW; 2C99ED0B2A289F3B CRC64;

Query Match 58.4%; Score 282; DB 1; Length 146;
Best Local Similarity 58.1%; Pred. No. 7e-24;
Matches 54; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 1 MLVREGERAGLANPFAALYLLAEATLAVLPGCHFLYGNVDVFRSSLSRSLGRFVLRW 60
Db 54 VLIQVEQRGLKNPFAALYMLAARAVLGPDYLYGNVDVLGAGSLSTQRLAHFYRRW 113

QY 61 TGASEPEPGFWMLATEQVCSLRDMRKQKHGLA 93
Db 114 TGAKELSTGWFSFKVSVITLSNKKRQNGFA 146

RESULT 6
LCRR_YERPE STANDARD; PRT; 146 AA.
AC P69959; P19393; P31488; Q663K7;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 07-MAR-2006, entry version 1.
DE Low calcium response locus protein R.
GN Name=lcrR; OrderedLocusNames=YPCD1.33c, y5045, y0048, pCD50;
OS Yersinia pestis.
OG Plasmid pCD1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=90330579; PubMed=1695896;
RA Barve S.S., Straley S.C.;
RT "lcrR, a low-Ca2(+)-response locus with dual Ca2(+)-dependent
RT functions in Yersinia pestis.";
RL J. Bacteriol. 172:4661-4671(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;

RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RT Yersinia pestis KIMS.";
RL Infect. Immun. 66:4611-4623(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCreedy P., Skowronski E., Ganes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
RT pestis.";
RL J. Bacteriol. 180:5192-5202(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC -!- FUNCTION: Involved in the down-regulation of lcrGVH transcription
CC in the presence or absence of calcium and is necessary for lcrG
CC protein expression in the absence of calcium. Plays an important
CC role in the regulation of the low-calcium response.
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CC -----
CC EMBL; M35740; AAA98219.1; ALT SEQ; Genomic DNA.
DR EMBL; AF074612; AAC69831.1; -; Genomic DNA.
DR EMBL; AF053946; AAC62572.1; -; Genomic DNA.
DR EMBL; AL117189; CAB54910.1; -; Genomic DNA.
DR EMBL; AE017043; AAS58569.1; -; Genomic DNA.
DR PIR; A37774; A37774.
DR PIR; T43592; T43592.
DR GenomeReviews; AE017043 GR; pCD50.
DR GenomeReviews; AL117189 GR; YPCD1.33c.
KW Calcium; Complete proteome; Plasmid.
FT CHAIN 1 146 Low calcium response locus protein R.
FT /FTID=PRO_0000084374.
FT CONFLICT 5 5 P -> L (in Ref. 1).
FT CONFLICT 120 120 S -> C (in Ref. 1).
SQ SEQUENCE 146 AA; 16454 MW; 611A80CB2A2FF2F9 CRC64;

Query Match 58.4%; Score 282; DB 1; Length 146;
Best Local Similarity 58.1%; Pred. No. 7e-24;
Matches 54; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 1 MLVREGERAGLANPFAALYLLAEATLAVLPGCHFLYGNVDVFRSSLSRSLGRFVLRW 60
Db 54 VLIQVEQRGLKNPFAALYMLAARAVLGPDYLYGNVDVLGAGSLSTQRLAHFYRRW 113

QY 61 TGASEPEPGFWMLATEQVCSLRDMRKQKHGLA 93
Db 114 TGAKELSTGWFSFKVSVITLSNKKRQNGFA 146

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RESULT 7
LCRR_YERPS STANDARD; PRT; 146 AA.
AC P69960; P19393; P31488; Q663K7;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 04-JAN-2005, sequence version 1.
DT 07-MAR-2006, entry version 7.
DE Low calcium response locus protein R.
GN Name=LCrR; OrderedLocusNames=pyV0059;
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1, and plasmid pyV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RA Bergman T., Forsberg A., Backman A., Wolf-Watz H.;
RT "The LcrD protein of Yersinia pseudotuberculosis belongs to a novel
RT protein family involved in surface presentation of virulence
RT determinants.";
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I; PLASMID=pyV;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lemerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 88-146.
RC STRAIN=YPIII / Serotype O:3; PLASMID=pIB1;
RX MEDLINE=91154114; PubMed=1705541;
RA Bergman T., Haakanson S., Forsberg A., Norlander L., Macellaro A.,
RA Backman A., Boelin I., Wolf-Watz H.;
RT "Analysis of the V antigen lcrGVH-yopBD operon of Yersinia
RT pseudotuberculosis: evidence for a regulatory role of LcrH and LcrV.";
RL J. Bacteriol. 173:1607-1616(1991).
CC -!- FUNCTION: Involved in the down-regulation of lcrGVH transcription
CC in the presence or absence of calcium and is necessary for lcrG
CC protein expression in the absence of calcium. Plays an important
CC role in the regulation of the low-calcium response.
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DR EMBL; M96850; AAA27648.1; -; Genomic DNA.
DR EMBL; BX936399; CAF25402.1; -; Genomic DNA.
DR EMBL; M57893; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; D37314; D37314.
DR GenomeReviews; BX936399 GR; pyV0059.
KW Calcium; Complete proteome; Plasmid.
FT CHAIN 1 146 Low calcium response locus protein R.
FT /FTID=PRO_0000084375.
FT SEQUENCE 146 AA; 16454 MW; 611A80CB2A2FF2F9 CRC64;
Query Match 58.4%; Score 282; DB 1; Length 146;
Best Local Similarity 58.1%; Pred. No. 7e-24;
Matches 54; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
QY 1 MLVRRGERAGLANPFAALYLIAEATLAVLPGHFLYGNVDVFRSSLSSEIRLGRFYLRW 60
Db 54 VLTQRVEQRGLKNPFAALYMLANAARAVLGPDYLYLGNVDVLAGSSLSLSTQRLAHFYRRW 113
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Db 114 TGAKELSTGWFLSKVQSQVITLSNMKKRQNGFA 146
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AC Q84GY7;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE LssR.
GN Name=LssR;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
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DR EMBL; AY144116; AAO18051.1; -; Genomic DNA.
SQ SEQUENCE 144 AA; 16873 MW; A60908CC50676B8A CRC64;
Query Match 57.1%; Score 276; DB 2; Length 144;
Best Local Similarity 62.9%; Pred. No. 3.3e-23;
Matches 56; Conservative 8; Mismatches 25; Indels 0; Gaps 0;
QY 1 MLVRRGERAGLANPFAALYLIAEATLAVLPGHFLYGNVDVFRSSLSSEIRLGRFYLRW 60
Db 52 IMLRRTRQRRGLANPFAPLYLLATATMAVLGPGSLYQVNTLVDSPLNRLARFYHRW 111
QY 61 TGASEPEPGWFMLATEQVCSLRDMRKQK 89
Db 112 TGASEIEPGWFELEASCVISLHQMRKQK 140
RESULT 9
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ID Q6TLM4_AERHY
AC Q6TLM4;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE AcrR.
GN Name=acrR;
OS Aeromonas hydrophila
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH-1;
RX PubMed=14977925; DOI=10.1128/IAI.72.3.1248-1256.2004;
RA Yu H.B., Rao P.S., Lee H.C., Vilches S., Merino S., Tomas J.M.,
RA Leung K.Y.;
RT "A type III secretion system is required for Aeromonas hydrophila AH-1
RT pathogenesis.";
RL Infect. Immun. 72:1248-1256(2004).
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DR EMBL; AY394563; AAR26337.1; -; Genomic DNA.
SQ SEQUENCE 146 AA; 16205 MW; FBD8A6D417A70279 CRC64;
Query Match 56.9%; Score 275; DB 2; Length 146;
Best Local Similarity 60.9%; Pred. No. 4.4e-23;
Matches 56; Conservative 9; Mismatches 27; Indels 0; Gaps 0;
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QY 1 MLVRRERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
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Db 54 VFIERVHERAGLSNPFALYLLAGSAGSVLGSVYLVGNVCLGSLSSDRLSFRFYRCW 113
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QY 61 TGASEPEPGWFLATEQVCSLRDMRKQK 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 114 AGASEPQPGWFLSDVAKVISLTSMRKQNSDL 145

RESULT 10
Q7N0W9_PHOLL
ID Q7N0W9_PHOLL PRELIMINARY; PRT; 144 AA.
AC Q7N0W9;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Similar to transcription regulator proteins LcrR and PcrR.
GN OrderedLocusNames=plu3760;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusniok K., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Bouraux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boenare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313 (2003).
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CC -----
CC EMBL; BX571871; CAE16132.1; -; Genomic_DNA.
DR Photolista; plu3760; -.
DR BioCyc; PLUM243265:PLU3760-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 144 AA; 16934 MW; 3C81F7EA0B53B083 CRC64;

Query Match 54.7%; Score 264; DB 2; Length 144;
Best Local Similarity 59.6%; Pred. No. 7.9e-22;
Matches 53; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 1 MLVRRERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
: : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 52 VMLRRTRQRGLANPFAPLYLATATWMLGPGSRLYGQVNTLVDSPLNDRLARFYHRW 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 TGASEPEPGWFLATEQVCSLRDMRKQK 89
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Db 112 TGANEVPGWFELEASCVISLHQMRRKQK 140

RESULT 11
Q30537_PSEAE
ID Q30537_PSEAE PRELIMINARY; PRT; 144 AA.
AC Q30537; Q7DFC0;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Transcriptional regulator protein PcrR.
GN Name=PcrR; OrderedLocusNames=PA1704;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RC STRAIN=388;
RX MEDLINE=98037517; PubMed=93711466;
RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7163-7168 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Wesbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
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CC -----
CC EMBL; AF010150; AAC45945.1; -; Genomic_DNA.
DR EMBL; AE004597; AAG05093.1; -; Genomic_DNA.
DR PIR; B83432; E83432.
DR BioCyc; PAER287:PA1704-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 144 AA; 16266 MW; 305F197EB33DE171 CRC64;

Query Match 53.4%; Score 258; DB 2; Length 144;
Best Local Similarity 58.4%; Pred. No. 3.8e-21;
Matches 52; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 1 MLVRRERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
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Db 52 VMLRRQARSGLANPFAALYLLAEATLDTLGPQRLYGKVLALAGSLPGRMARFYRRW 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 TGASEPEPGWFLATEQVCSLRDMRKQK 89
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 112 TGAEPADGWFELEAGRVVTVQSLRKRQK 140

RESULT 12
Q6QVS0_VIBHA
ID Q6QVS0_VIBHA PRELIMINARY; PRT; 137 AA.
AC Q6QVS0;
DT 03-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE VcrR.
GN Name=vcrR;
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AY524044; AAS13311.1; -; Genomic_DNA.
DR EMBL; AY524044; AAS13311.1; -; Genomic_DNA.
SQ SEQUENCE 137 AA; 15912 MW; AEBD4CBF8657AF08 CRC64;

Query Match 37.1%; Score 179; DB 2; Length 137;
Best Local Similarity 43.3%; Pred. No. 4e-12;
Matches 39; Conservative 19; Mismatches 28; Indels 4; Gaps 2;

QY 1 MLVRRERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSERLGRFYLRW 60
: : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 51 VLLRRISPNOGLNPFSAFLMLAEHAIRLYPPDWAIRGNVDVLRGNSMSQRLAQFYLR 110
QY 61 TGASEPE-PCWFMLATEQVCSLRDMRKQK 89
Db 111 CGASHDEQEDWYFL---RLSDYRPLKRRKK 137

RESULT 13
Q66PT6_PASPI
ID Q66PT6_PASPI PRELIMINARY; PRT; 137 AA.
AC Q66PT6_PASPI
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Putative TTSS protein R.
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Thune R.L., Benoit J.L., Fernandez D.H., Kelly-Smith M.;
RT "Photobacterium damsela subsp. piscicida encodes a functional type
RL III secretion system (TTSS) that is involved in pathogenesis.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY647224; AAU11480.1; -; Genomic DNA.
SQ SEQUENCE 137 AA; 15905 MW; 368BDA9FEFEB14B5 CRC64;

Query Match 36.2%; Score 175; DB 2; Length 137;
Best Local Similarity 44.4%; Pred. No. 1.1e-11;
Matches 40; Conservative 18; Mismatches 28; Indels 4; Gaps 2;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVPRSSLSERLGRFYLRW 60
Db 51 VLLRRVSPNOGLNPFSAFLMLAEHAIRLYPLDWSIRGNVDVLRSSNMNSQRLAQFYLR 110
QY 61 TGASEPE-PCWFMLATEQVCSLRDMRKQK 89
Db 111 CGASHDEQEDWYFL---RLSDYRPLKRRKK 137

RESULT 14
Q87P57_VIBPA
ID Q87P57_VIBPA PRELIMINARY; PRT; 137 AA.
AC Q87P57;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Putative LcrR.
GN OrderedLocusNames=VP1661;
OC Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RiMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
RA "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
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CC -----
DR EMBL; BA000031; BAC59924.1; -; Genomic DNA.
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KW Complete proteome.
SQ SEQUENCE 137 AA; 15758 MW; 9ASE1454AE98DF3E CRC64;

Query Match 34.0%; Score 164; DB 2; Length 137;
Best Local Similarity 39.3%; Pred. No. 2.1e-10;
Matches 35; Conservative 21; Mismatches 29; Indels 4; Gaps 2;

QY 1 MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVPRSSLSERLGRFYLRW 60
Db 51 VLLKRVSPNLGUSNPFSCFLFLAEHAIRPLPSPDWTIRGNVDVLRGNSMSQRLAQFYLR 110
QY 61 TGAS-EPEPGWEFLATEQVCSLRDMRKQ 88
Db 111 CGASHDQQADWYFL---RLADYRPLKRRK 136

RESULT 15
Q4Q2V5_LEIMA
ID Q4Q2V5_LEIMA PRELIMINARY; PRT; 1872 AA.
AC Q4Q2V5;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=LmjF34.2450;
OS Leishmania major.
OC Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5684;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RX PubMed=16020728; DOI=10.1126/science.1112680;
RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA Berriman M., Sisk E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
RA Apostolou Z., Attipoe P., Bason N., Bauser C., Beck A., Beverley S.M.,
RA Bianchetti G., Borzym K., Bothe G., Bruschi C.V., Collins M.,
RA Cadag E., Ciarlioni L., Clayton C., Coulson R.M.R., Cronin A.,
RA Cruz A.K., Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA Fazalina G., Foster N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA Gobie A., Goffeau A., Harris D., Hertz-fowler C., Hilbert H., Horn D.,
RA Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,
RA Lord A., Louie T., Marra M., Masuy D., Matthews K., Michaeli S.,
RA Mottram J.C., Mueller-Auer S., Munden H., Nelson S., Norbertczak H.,
RA Oliver K., O'neil S., Pentony M., Pohl T.M., Price C., Purnelle B.,
RA Quail M.A., Rabinowitsch E., Reinhardt R., Rieger M., Rinta J.,
RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
RA Volckaert G., Wambutt R., Warren T., Wedler H., Woodward J., Zhou S.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.G.,
RA Myler P.J.;
RT "The genome of the kinetoplastid parasite, Leishmania major.";
RL Science 309:436-442 (2005).
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CC -----
DR EMBL; CT005271; CAJ07958.1; -; Genomic DNA.
DR InterPro; IPR000904; Sec7.
DR Pfam; PF01369; Sec7; 1.
DR SMART; SM00222; Sec7; 1.
DR PROSITE; PS0190; SEC7; 1.
KW Hypothetical protein.
SQ SEQUENCE 1872 AA; 20099 MW; 9883239D88682779 CRC64;

Query Match 15.8%; Score 76.5; DB 2; Length 1872;
Best Local Similarity 31.5%; Pred. No. 42;
Matches 35; Conservative 8; Mismatches 31; Indels 37; Gaps 6;

QY 4 RREGERAGL--ANPEAALYLLA-----EATLAVLPGHF-----LYGNVDVFR 44
Db 1286 KENHPGSLDEASAYAASTELAFICAVVGGAATTAVLPAPHPASTTRVRLLEVDV-- 1343
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Qy 45 SSSLSEELGRFYLRWTCASE-PEPGWFLATEQVCS---LRDMRKQKHG 91
Db 1344 -----YLRDTRASDGVRAVWCTLGNRVVCASLQLMAYVHRGQH 1382

Search completed: June 16, 2006, 19:23:03
Job time : 76.039 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 17.1634 Seconds
(without alignments)
474.285 Million cell updates/sec

Title: US-10-813-908A-6
Perfect score: 483
Sequence: 1 MLVRRGERAGLANPFAALY.....ATQVCSLRDMRKRQKHGLA 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA:*
- 1: /EMC_Celerra_SID3S/ptodata/2/iaa/5_COMB.pep.*
 - 2: /EMC_Celerra_SID3S/ptodata/2/iaa/6_COMB.pep.*
 - 3: /EMC_Celerra_SID3S/ptodata/2/iaa/7_COMB.pep.*
 - 4: /EMC_Celerra_SID3S/ptodata/2/iaa/H_COMB.pep.*
 - 5: /EMC_Celerra_SID3S/ptodata/2/iaa/PTUS_COMB.pep.*
 - 6: /EMC_Celerra_SID3S/ptodata/2/iaa/RE_COMB.pep.*
 - 7: /EMC_Celerra_SID3S/ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	53.4	875	2	US-09-252-991A-30056
2	70.5	14.6	240	2	US-09-138-452A-769
3	70.5	14.6	242	2	US-09-438-185A-725
4	70	14.5	211	2	US-09-252-991A-22971
5	67	13.9	378	2	US-09-252-991A-26944
6	65.5	13.6	375	2	US-09-328-352-6262
7	65.5	13.6	1590	2	US-09-617-0998-1
8	65.5	13.6	1590	2	US-10-180-326A-1
9	64	13.3	440	2	US-09-902-540-15770
10	62.5	12.9	220	2	US-09-252-991A-30182
11	62.5	12.9	1520	2	US-09-252-991A-21336
12	62.5	12.9	1809	2	US-10-324-967-32
13	62	12.8	970	1	US-08-673-789-7
14	61.5	12.7	386	2	US-09-252-991A-25773
15	61	12.6	289	2	US-09-107-532A-4866
16	61	12.6	502	2	US-09-252-991A-29174
17	61	12.6	1184	1	US-08-446-038B-20
18	61	12.6	1184	1	US-08-446-010B-20
19	61	12.6	1184	1	US-08-805-445-20
20	61	12.6	1184	1	US-08-064-667D-20
21	61	12.6	1184	1	US-09-066-208-20
22	60.5	12.5	266	2	US-09-489-039A-7484
23	60.5	12.5	441	2	US-09-949-016-9659
24	60.5	12.5	1059	2	US-09-902-540-10430
25	60	12.4	376	2	US-09-902-540-15516
26	60	12.4	696	2	US-10-104-047-3647

27	60	12.4	1187	1	US-08-357-598-8	Sequence 8, Appli
28	60	12.4	1187	1	US-08-097-997A-13	Sequence 13, Appli
29	60	12.4	1187	1	US-09-003-289-8	Sequence 8, Appli
30	60	12.4	1187	2	US-08-665-574C-13	Sequence 13, Appli
31	60	12.4	1187	2	US-08-946-394-13	Sequence 13, Appli
32	60	12.4	1187	2	US-09-972-800A-18	Sequence 18, Appli
33	60	12.4	1187	2	US-09-397-367A-13	Sequence 13, Appli
34	60	12.4	1187	5	PCT-US95-16435-8	Sequence 8, Appli
35	59.5	12.3	657	2	US-09-489-039A-10221	Sequence 10221, A
36	59	12.2	1572	2	US-09-902-540-12652	Sequence 12652, A
37	58.5	12.1	602	2	US-09-252-991A-30458	Sequence 30458, A
38	58.5	12.1	927	2	US-10-309-059-30	Sequence 30, Appli
39	58	12.0	118	2	US-09-902-540-10791	Sequence 10791, A
40	58	12.0	249	2	US-09-154-083-2	Sequence 2, Appli
41	58	12.0	427	2	US-09-902-540-14252	Sequence 14252, A
42	58	12.0	499	2	US-09-489-039A-12199	Sequence 12199, A
43	58	12.0	628	2	US-09-252-991A-24741	Sequence 24741, A
44	58	12.0	647	2	US-09-252-991A-32816	Sequence 32816, A
45	57.5	11.9	104	2	US-09-270-767-33177	Sequence 33177, A

ALIGNMENTS

RESULT 1
US-09-252-991A-30056
; Sequence 30056, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30056
; LENGTH: 875
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-30056

Query Match	53.4%;	Score 258;	DB 2;	Length 875;
Best Local Similarity	58.4%;	Pred No. 1.9e-26;		
Matches	52;	Conservative	9;	Mismatches 28; Indels 0; Gaps 0;
Qy	1	MLVRRGERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSSESLRGRFYLRW	60	
Db	783	VMLRRQARSGLANPFAALYLLAEATLDTLGPQRQLYKVLALAGSLPGRMARFYRRW	842	
Qy	61	TGASEPFGWFMATQVCSLRDMRKRQK	89	
Db	843	TGAEPADGWFLEAGRVVTQSLRKRQK	871	

RESULT 2
US-09-198-452A-769
; Sequence 769, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griflais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 769

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; LENGTH: 240
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-769

Query Match      14.6%; Score 70.5; DB 2; Length 240;
Best Local Similarity 32.0%; Pred. No. 0.31;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

QY 7 GERAGLANP-----FAALYLLAEATLAVLGP--GHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 29 GEIVGLLGPNGAGKTTAFYL-----TVGLRPDSGKIIFKNVDVTKTMDHRLGLGIGYL- 83
QY 60 WTGASEPEPGWFMLATEQ---VCSLR---DMRKRQKH 90
Db 84 -----AQEPTIFKELTVQDNLICILIIYKARKQQSH 115

RESULT 3
US-09-438-185A-725
; Sequence 725, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 725
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0723
US-09-438-185A-725

Query Match      14.6%; Score 70.5; DB 2; Length 242;
Best Local Similarity 32.0%; Pred. No. 0.31;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

QY 7 GERAGLANP-----FAALYLLAEATLAVLGP--GHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 31 GEIVGLLGPNGAGKTTAFYL-----TVGLRPDSGKIIFKNVDVTKTMDHRLGLGIGYL- 85
QY 60 WTGASEPEPGWFMLATEQ---VCSLR---DMRKRQKH 90
Db 86 -----AQEPTIFKELTVQDNLICILIIYKARKQQSH 117

RESULT 4
US-09-252-991A-22971
; Sequence 22971, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22971
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22971

Query Match      14.5%; Score 70; DB 2; Length 211;
Best Local Similarity 31.2%; Pred. No. 0.3;
Matches 24; Conservative 5; Mismatches 24; Indels 24; Gaps 3;

QY 5 REGERA-----GLANPFAALYLLAEATLAVLGPGHFLYGNVDVFRSSLSLSSERLGRFYLR 59
Db 67 ROGERAGDPTGRTGPGA-----LPGQRRWG-----AFAEHLGRHSCR 107
QY 60 WTGASEPEPGWFMLATE 76
Db 108 QPGRGVYPFGWPPARTE 124

RESULT 5
US-09-252-991A-26944
; Sequence 26944, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26944
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26944

Query Match      13.9%; Score 67; DB 2; Length 378;
Best Local Similarity 26.3%; Pred. No. 1.8;
Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;

QY 4 RREGERAGLANPFAALYLLAE-----TLAVLGPGHFLYGNVDVFRSSLSLSSERLGR 55
Db 191 RYRDAHSGMSGPYAAPRRILQAMTHPAWADVGLLGKPHDL-GNISAYRGNPTGLE--- 246
QY 56 FYLRWTGAS-EPEPGW 70
Db 247 -YIGWLGANFDPESISW 261

RESULT 6
US-09-328-352-6262
; Sequence 6262, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6262
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6262
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Query Match 13.6%; Score 65.5; DB 2; Length 375;
Best Local Similarity 42.9%; Pred. No. 2.9;
Matches 15; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

Qy 57 YLRWTGASEPFGWFMFLATEQVCSLRDMRKQKHG 91
Db 307 YLHWGSGEQED---LSAEQIQALQDQFKKQKTG 338

RESULT 7
US-09-617-099B-1
; Sequence 1, Application US/09617099B
; Patent No. 6790949
; GENERAL INFORMATION:
; APPLICANT: Seino, Susumu
; APPLICANT: Shibasaki, Tadao
; APPLICANT: Ozaki, No. 6790949uaki
; TITLE OF INVENTION: Protein Rim2
; FILE REFERENCE: P19771
; CURRENT APPLICATION NUMBER: US/09/617,099B
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: JP 288372/99
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1590
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-617-099B-1

Query Match 13.6%; Score 65.5; DB 2; Length 1590;
Best Local Similarity 25.7%; Pred. No. 21;
Matches 29; Conservative 8; Mismatches 41; Indels 35; Gaps 4;

Qy 14 NPFAALVLL-----AEATLAVLPGHFLYGNV-----DVFRS 45
Db 851 NPVYKVIYFLPDRSDKNKRTTKVKTLEPKNQTFIYSPVHRRFRERMLEITLWDQARV 910
Qy 46 SSLSSERLGRFYLRW-TGASEPEPGWFMFLATEQVCSLRDMR-----KROKHG 91
Db 911 REESEFLGILILETALLDDDEPHWYKLTQHDVSSLPPLRPPSYLPRRQLHG 963

RESULT 8
US-10-180-326A-1
; Sequence 1, Application US/10180326A
; Patent No. 6956104
; GENERAL INFORMATION:
; APPLICANT: Seino, Susumu
; APPLICANT: Shibasaki, Tadao
; APPLICANT: Ozaki, No. 6956104uaki
; TITLE OF INVENTION: Protein Rim2
; FILE REFERENCE: P21573
; CURRENT APPLICATION NUMBER: US/10/180,326A
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: JP 288372/99
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1590
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-326A-1

Query Match 13.6%; Score 65.5; DB 2; Length 1590;
Best Local Similarity 25.7%; Pred. No. 21;
Matches 29; Conservative 8; Mismatches 41; Indels 35; Gaps 4;

Qy 14 NPFAALVLL-----AEATLAVLPGHFLYGNV-----DVFRS 45

Db 851 NPVYKVIYFLPDRSDKNKRTTKVKTLEPKNQTFIYSPVHRRFRERMLEITLWDQARV 910
Qy 46 SSLSSERLGRFYLRW-TGASEPEPGWFMFLATEQVCSLRDMR-----KROKHG 91
Db 911 REESEFLGILILETALLDDDEPHWYKLTQHDVSSLPPLRPPSYLPRRQLHG 963

RESULT 9
US-09-902-540-15770
; Sequence 15770, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15770
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15770

Query Match 13.3%; Score 64; DB 2; Length 440;
Best Local Similarity 29.7%; Pred. No. 5.8;
Matches 35; Conservative 11; Mismatches 40; Indels 32; Gaps 7;

Qy 4 RREGER-AGLANP-FAALYLLAEATLAVLPGH-FLYGNV--DVFRSSLSSERLGRFYL 58
Db 32 RREIRYAGFPMPRWWSLLFFIPVLAVLSVGHVLYRRLVRDVTKKKWLRTAQGLFAV 91
Qy 59 RWTGASE-----PEPG-----W-----FMLATEQVCSLRDMRKROK 89
Db 92 GFVGALSARAIGSVLPSEGRRLGIVFLLWIGLVLLMFTLAVDMVRAAAWRERK 149

RESULT 10
US-09-252-991A-30182
; Sequence 30182, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30182
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30182

Query Match 12.9%; Score 62.5; DB 2; Length 220;
Best Local Similarity 31.3%; Pred. No. 3.5;
Matches 21; Conservative 8; Mismatches 25; Indels 13; Gaps 3;

Qy 24 EATLAVLPGHFLYGNVDVFRSSLSSERLGRFYLRWTGASEPEPGWFMFLATEQVCSLRD 83
Db 119 EGTLLRGLGPGGWRVRHVHTRADGLRRRLG-----TSGSN-QP-----AHQLRPARD 165
Qy 84 MRKQKH 90

Db 166 RRRPDRH 172

RESULT 11

US-09-252-991A-21336

; Sequence 21336, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 21336

; LENGTH: 1520

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21336

Query Match 12.9%; Score 62.5; DB 2; Length 1520;

Best Local Similarity 26.3%; Pred. No. 53; Mismatches 38; Indels 37; Gaps 5;

Matches 31; Conservative 12; Mismatches 38; Indels 37; Gaps 5;

QY 3 VRRE-GERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSSL-----SSERL 53

Db 1022 LRQDWSGEGIAAAVAALDRACLASLAAMLAGSGLFASATPLDPLATLQRLGTAERQRL 1081

QY 54 GREYLR-----WTGASE-----PEPGWFMLA-----TEQVCSLRD 83

Db 1082 LRHLWRLQEBGGYLRAGEGWLGCARRPAQSPEDAWTAFAGCAPAALWPAELVAVLYRD 1139

RESULT 12

US-10-324-967-32

; Sequence 32, Application US/10324967

; Patent No. 6974680

; GENERAL INFORMATION:

; APPLICANT: Cossou, Pierre

; APPLICANT: Kohler, Thilo

; APPLICANT: Benghezal, Mohammed

; APPLICANT: Marchetti, Anna

; APPLICANT: van Delden, Christian

; TITLE OF INVENTION: VIRULENCE GENES, PROTEINS, AND THEIR USE

; FILE REFERENCE: 25421-502

; CURRENT APPLICATION NUMBER: US/10/324,967

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 32

; LENGTH: 1809

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-10-324-967-32

Query Match 12.9%; Score 62.5; DB 2; Length 1809;

Best Local Similarity 26.3%; Pred. No. 67; Mismatches 38; Indels 37; Gaps 5;

Matches 31; Conservative 12; Mismatches 38; Indels 37; Gaps 5;

QY 3 VRRE-GERAGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSSL-----SSERL 53

Db 981 LRQDWSGEGIAAAVAALDRACLASLAAMLAGSGLFASATPLDPLATLQRLGTAERQRL 1040

QY 54 GREYLR-----WTGASE-----PEPGWFMLA-----TEQVCSLRD 83

Db 1041 LRHLWRLQEBGGYLRAGEGWLGCARRPAQSPEDAWTAFAGCAPAALWPAELVAVLYRD 1098

RESULT 13

US-08-673-789-7

; Sequence 7, Application US/08673789

; Patent No. 5814479

; GENERAL INFORMATION:

; APPLICANT: ZHOU, REMPING; SCHULZ, NICHOLAS,

; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,

; APPLICANT: GEORGE, F.

; TITLE OF INVENTION: BSK RECEPTOR LIKE

; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR

; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA: US/08/673,789

; APPLICATION NUMBER: US/08/673,789

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/177,812

; FILING DATE: 04-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: CAROL M. GRUPPI

; REGISTRATION NUMBER: 37,341

; REFERENCE/DOCKET NUMBER: 2026-4105

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 751-4800

; TELEFAX: (212) 751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 970

; TYPE: AMINO ACID

; STRANDEDNESS: UNKNOWN

; TOPOLOGY: UNKNOWN

US-08-673-789-7

Query Match 12.8%; Score 62; DB 1; Length 970;

Best Local Similarity 34.0%; Pred. No. 33; Mismatches 15; Indels 12; Gaps 2;

Matches 18; Conservative 8; Mismatches 15; Indels 12; Gaps 2;

QY 46 SSLSSERLGRFYLRWTGASEPEPGWFMLA-----TEQVCSLRDMRKQ 89

Db 12 SSRSSRRGVTSELAWT--THPETGWEVSGYDEAMQPIRTYQVCVREAQQQ 62

RESULT 14

US-09-252-991A-25773

; Sequence 25773, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 52.0195 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-6
Perfect score: 483
Sequence: 1 MLVRRGERAGLANPFAALY.....ATEQVSLRDMRKQKHGLA 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA Main.*
- 1: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
 - 2: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
 - 3: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
 - 4: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pap.*
 - 5: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
 - 6: /EMC Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	93	US-10-813-908-6	Sequence 6, Appli
2	72	14.9	929	US-10-450-763-36125	Sequence 36125, A
3	72	14.9	2301	US-10-094-886-138	Sequence 138, App
4	71	14.7	298	US-10-506-454-1151	Sequence 1151, Ap
5	70.5	14.6	240	US-10-289-762-769	Sequence 769, App
6	69	14.3	980	US-10-437-963-128383	Sequence 128383,
7	68.5	14.2	917	US-10-732-923-12941	Sequence 12941, A
8	68.5	14.2	917	US-10-732-923-12942	Sequence 12942, A
9	68	14.1	76	US-09-796-692-1826	Sequence 1826, Ap
10	68	14.1	76	US-10-040-862-1826	Sequence 1826, Ap
11	68	14.1	76	US-10-057-475B-1826	Sequence 1826, Ap
12	68	14.1	76	US-10-154-884B-1826	Sequence 1826, Ap
13	68	14.1	76	US-10-764-324-1826	Sequence 1826, Ap
14	67	13.9	381	US-09-815-242-5199	Sequence 5199, Ap
15	67	13.9	381	US-10-282-122A-43561	Sequence 43561, A
16	66.5	13.8	369	US-10-501-035-281	Sequence 281, App
17	66.5	13.8	427	US-10-938-249-467	Sequence 467, App
18	66.5	13.8	427	US-10-485-788A-503	Sequence 503, App
19	66.5	13.8	1200	US-10-756-149-5235	Sequence 5235, Ap
20	66.5	13.8	1201	US-10-369-493-3949	Sequence 3949, Ap
21	66.5	13.8	1333	US-10-161-927-24	Sequence 24, Appl
22	66	13.7	268	US-10-425-115-187933	Sequence 187933,
23	66	13.7	374	US-10-425-114-55834	Sequence 55834, A
24	66	13.7	661	US-10-425-115-187929	Sequence 187929,
25	65.5	13.6	433	US-11-087-099-3764	Sequence 3764, Ap
26	65.5	13.6	597	US-10-437-963-168169	Sequence 168169,
27	65.5	13.6	804	US-10-156-761-8615	Sequence 8615, Ap

28	65.5	13.6	839	6	US-11-087-099-2713	Sequence 2713, Ap
29	65.5	13.6	841	6	US-11-087-099-10714	Sequence 10714, A
30	65.5	13.6	1590	4	US-10-180-326-1	Sequence 1, Appli
31	65	13.5	378	4	US-10-282-122A-77679	Sequence 77679, A
32	65	13.5	502	4	US-10-437-963-168918	Sequence 168918, A
33	64.5	13.4	163	4	US-10-767-701-31909	Sequence 31909, A
34	64.5	13.4	197	4	US-10-425-114-36734	Sequence 36734, A
35	64.5	13.4	357	6	US-11-188-298-814	Sequence 814, App
36	64.5	13.4	377	4	US-10-425-115-333648	Sequence 333648,
37	64.5	13.4	468	4	US-10-369-493-4868	Sequence 4868, Ap
38	64.5	13.4	468	4	US-10-369-493-7628	Sequence 7628, Ap
39	64.5	13.4	468	4	US-10-282-122A-49776	Sequence 49776, A
40	64.5	13.4	579	4	US-10-437-963-140815	Sequence 140815,
41	64	13.3	220	5	US-10-732-923-16837	Sequence 16837, A
42	64	13.3	220	6	US-11-188-298-9826	Sequence 9826, Ap
43	64	13.3	243	4	US-10-425-115-292119	Sequence 292119,
44	64	13.3	555	4	US-10-413-943-65	Sequence 65, Appl
45	64	13.3	712	4	US-10-413-943-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-10-813-908-6
; Sequence 6, Application US/10813908
; Publication No. US20050058662A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and U
; FILE REFERENCE: MIC01/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813,908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
US-10-813-908-6

Query Match 100.0%; Score 483; DB 5; Length 93;
Best Local Similarity 100.0%; Pred. No. 5,9e-52;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLVRRGERAGLANPFAALYLLAEATLVLGPGHFLYGNVDVFRSSLSRGLGRFYLRW 60
Db 1 MLVRRGERAGLANPFAALYLLAEATLVLGPGHFLYGNVDVFRSSLSRGLGRFYLRW 60
Qy 61 TGASEPEPGWFLATEQVCSLRDMRKQKHGLA 93
Db 61 TGASEPEPGWFLATEQVCSLRDMRKQKHGLA 93

RESULT 2

US-10-450-763-36125
; Sequence 36125, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167


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; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; FILE REFERENCE: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 769
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-769

Query Match      14.6%; Score 70.5; DB 4; Length 240;
Best Local Similarity 32.0%; Pred. No. 4.6;
Matches 31; Conservative 9; Mismatches 34; Indels 23; Gaps 6;

QY 7 GERAGLANP-----FAALYLLAEATLAVLGP--GHFLYGNVDVFRSSLSLSSERLGRFYLR 59
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29 GEIVGLGPGAGKTTAFYL-----TVGLIRPDSGKIIFKNVDVTKTMDHRLRIGIYL- 83
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 60 WTGASEPEPGWFMLATEQ---VCSLR---DMRKQKH 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 84 -----AQEPTIFKELTVQDNLICILEIYYKARKQOSH 115
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US-10-437-963-128383
; Sequence 128383, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128383
; LENGTH: 980
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30741C.1.pep
US-10-437-963-128383

Query Match      14.3%; Score 69; DB 4; Length 980;
Best Local Similarity 28.6%; Pred. No. 39;
Matches 34; Conservative 13; Mismatches 26; Indels 46; Gaps 8;

QY 4 RREGER--AGLANPFAALYLLAEATLAVLGPCHP-----LYGNVDVFRSSSL----- 48
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 148 KREGKRVKAGLT-----ADLSVGPAPHLAGLTGAGRSDRMSKSLTGIORRFD 196
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

QY 49 -----SSERLGR--FYLRWTCASEPEPGWF---MLATE--QVCSLRDMRKQKH 89
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 RRFASSSVRASSSSNRLNRGHYL---PPRTEPKRWPMPKDLMATQRRRLQRLRAQIREK 253
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-10-732-923-12941
; Sequence 12941, Application US/10732923
; Publication No. US20050108791A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 12941
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-732-923-12941

Query Match      14.2%; Score 68.5; DB 5; Length 917;
Best Local Similarity 30.0%; Pred. No. 41;
Matches 27; Conservative 12; Mismatches 32; Indels 19; Gaps 4;

QY 6 EGERAGLANPFAAL--YLLAEATLAVLGPCHFLYGNVDVFRSSLSLSSERLGRFYLRWTG- 62
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 736 ESERHGTPLPIVALTAHANANEKRALQSG-----MDDYLTKPISEERQLAQVVLKWTGL 789
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 -----ASE-PEPGWFMLATEQVCSLR 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 790 ALRNOGPERASERPELGLEQLQVLDQDEGLR 819
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-10-732-923-12942
; Sequence 12942, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 12942
; LENGTH: 917
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-732-923-12942

Query Match      14.2%; Score 68.5; DB 5; Length 917;
Best Local Similarity 30.0%; Pred. No. 41;
Matches 27; Conservative 12; Mismatches 32; Indels 19; Gaps 4;

QY 6 EGERAGLANPFAAL--YLLAEATLAVLGPCHFLYGNVDVFRSSLSLSSERLGRFYLRWTG- 62
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 736 ESERHGTPLPIVALTAHANANEKRALQSG-----MDDYLTKPISEERQLAQVVLKWTGL 789
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 -----ASE-PEPGWFMLATEQVCSLR 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 790 ALRNOGPERASERPELGLEQLQVLDQDEGLR 819
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-09-796-692-1826
; Sequence 1826, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAP
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
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; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1826
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-1826
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```
Query Match 14.1%; Score 68; DB 3; Length 76;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 27; Conservative 5; Mismatches 12; Indels 12; Gaps 3;

QY 16 FAALYLLAEATLAVLPGHF-----LYGNVDVFRSSSLSSERLGRFYLRTWTGASEPE 67
Db 13 FVSLPTMQEASLAVLFYHYHISPCNKVLYRQVRSMSSLSLSPRL--RLRYRGNs-PV 68

QY 68 PGWFML 73
Db 69 QSLFML 74
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```
RESULT 10
US-10-040-862-1826
; Sequence 1826, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
```

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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1826
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-1826
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Query Match 14.1%; Score 68; DB 4; Length 76;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

QY 16 FAALYLLAEATLAVLPGHF-----LYGNVDVFRSSSLSSERLGRFYLRTWTGASEPE 67
Db 13 FVSLPTMQEASLAVLFYHYHISPCNKVLYRQVRSMSSLSLSPRL--RLRYRGNs-PV 68

QY 68 PGWFML 73
Db 69 QSLFML 74
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RESULT 11
US-10-057-475B-1826
; Sequence 1826, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10979

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1826

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-057-475B-1826

Query Match 14.1%; Score 68; DB 4; Length 76;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

Qy 16 FAALYLLAEATLAVLPGPHF-----LYGNVDVFRSSLSSESLGRFYLRWTGASEPE 67

Db 13 FVSLPTMQEASLAVLFYHYHISPCKNKLVRQVRSMSSLSLSPRRL---RLRYRGNs-pv 68

Qy 68 PGWFML 73

Db 69 QSLFML 74

RESULT 12

US-10-154-884B-1826

; Sequence 1826, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc W.

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013521US

; CURRENT APPLICATION NUMBER: US/10/154,884B

; CURRENT FILING DATE: 2002-05-23

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1826

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-154-884B-1826

Query Match 14.1%; Score 68; DB 4; Length 76;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

Qy 16 FAALYLLAEATLAVLPGPHF-----LYGNVDVFRSSLSSESLGRFYLRWTGASEPE 67

Db 13 FVSLPTMQEASLAVLFYHYHISPCKNKLVRQVRSMSSLSLSPRRL---RLRYRGNs-pv 68

Qy 68 PGWFML 73

Db 69 QSLFML 74

RESULT 13

US-10-764-324-1826

; Sequence 1826, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/764,324

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US 60/040,862

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10467

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1826

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-764-324-1826

Query Match 14.1%; Score 68; DB 4; Length 76;
Best Local Similarity 40.9%; Pred. No. 2.4;
Matches 27; Conservative 5; Mismatches 22; Indels 12; Gaps 3;

Qy 16 FAALYLLAEATLAVLPGPHF-----LYGNVDVFRSSLSSESLGRFYLRWTGASEPE 67

Db 13 FVSLPTMQEASLAVLFYHYHISPCKNKLVRQVRSMSSLSLSPRRL---RLRYRGNs-pv 68

Qy 68 PGWFML 73

Db 69 QSLFML 74

RESULT 14

US-09-815-242-5199

; Sequence 5199, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5199
LENGTH: 381
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5199

Query Match 13.9%; Score 67; DB 3; Length 381;
Best Local Similarity 26.3%; Pred. No. 22;
Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;
QY 4 RREGERAGLANPFAALYLIAEA-----TLAVLPGHFLYGNVDVFRSSLSRRLGR 55
Db 164 RYRDAHSGMSGPYAAPRRILQANTHPAWAWDVGLLGKPHDL-GNISAYRGNPTGLED--- 219
QY 56 FYLRWTGAS-EPEPGW 70
Db 220 -YIGWLGANFDPISW 234

RESULT 15
US-10-282-122A-43561
Sequence 43561, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 43561
LENGTH: 381
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-43561
Query Match 13.9%; Score 67; DB 4; Length 381;
Best Local Similarity 26.3%; Pred. No. 22;
Matches 20; Conservative 14; Mismatches 28; Indels 14; Gaps 4;
QY 4 RREGERAGLANPFAALYLIAEA-----TLAVLPGHFLYGNVDVFRSSLSRRLGR 55
Db 164 RYRDAHSGMSGPYAAPRRILQANTHPAWAWDVGLLGKPHDL-GNISAYRGNPTGLED--- 219
QY 56 FYLRWTGAS-EPEPGW 70
Db 220 -YIGWLGANFDPISW 234
Search completed: June 16, 2006, 20:24:58
Job time : 53.0195 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: June 16, 2006, 20:13:41 ; Search time 4.00732 Seconds
(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 96747 seqs, 22556637 residues
Total number of hits satisfying chosen parameters: 96747
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications AA New:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pap:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pap:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pap:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pap:*
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7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pap:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pap:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	13.0	550	6	US-10-449-902-48072 Sequence 48072, A
2	62	12.8	110	6	US-10-953-349-28302 Sequence 28302, A
3	62	12.8	446	6	US-10-449-902-42048 Sequence 42048, A
4	62	12.8	446	6	US-10-449-902-56774 Sequence 56774, A
5	61.5	12.7	810	6	US-10-953-349-33953 Sequence 33953, A
6	61.5	12.7	1871	6	US-10-501-834-26 Sequence 26, Appl
7	61	12.6	466	6	US-10-449-902-48431 Sequence 48431, A
8	60.5	12.5	185	6	US-10-953-349-25312 Sequence 25312, A
9	60.5	12.5	313	6	US-10-953-349-25311 Sequence 25311, A
10	60	12.4	450	7	US-11-165-586-67 Sequence 67, Appl
11	60	12.4	1730	7	US-11-270-040-6 Sequence 6, Appl
12	59.5	12.3	503	6	US-10-449-902-34748 Sequence 34748, A
13	59.5	12.3	1207	6	US-10-449-902-51740 Sequence 51740, A
14	59	12.2	422	6	US-10-474-853-2 Sequence 2, Appl
15	58.5	12.1	507	6	US-10-449-902-48555 Sequence 48555, A
16	58.5	12.1	519	6	US-10-449-902-45544 Sequence 45544, A
17	58.5	12.1	623	6	US-10-449-902-54759 Sequence 54759, A
18	58	12.0	261	6	US-10-449-902-39053 Sequence 39053, A
19	57.5	11.9	456	6	US-10-449-902-51837 Sequence 51837, A
20	57	11.8	103	6	US-10-953-349-28303 Sequence 28303, A
21	57	11.8	335	6	US-10-449-902-34705 Sequence 34705, A
22	57	11.8	391	6	US-10-449-902-53912 Sequence 53912, A
23	57	11.8	826	6	US-10-449-902-52861 Sequence 52861, A
24	56	11.6	305	6	US-10-953-349-28270 Sequence 28270, A
25	56	11.6	311	6	US-10-953-349-28269 Sequence 28269, A

26	56	11.6	353	6	US-10-953-349-28268	Sequence 28268, A
27	56	11.6	446	6	US-10-449-902-35807	Sequence 35807, A
28	56	11.6	627	6	US-10-449-902-54730	Sequence 54730, A
29	56	11.6	627	6	US-10-449-902-56559	Sequence 56559, A
30	56	11.6	723	6	US-10-449-902-41317	Sequence 41317, A
31	55.5	11.5	349	6	US-10-449-902-53510	Sequence 53510, A
32	55.5	11.5	375	6	US-10-449-902-52896	Sequence 52896, A
33	55.5	11.5	624	6	US-10-449-902-45350	Sequence 45350, A
34	55.5	11.5	637	6	US-10-449-902-45350	Sequence 45350, A
35	55	11.4	160	6	US-10-449-902-49421	Sequence 49421, A
36	55	11.4	333	6	US-10-449-902-33310	Sequence 33310, A
37	55	11.4	333	6	US-10-449-902-44132	Sequence 44132, A
38	55	11.4	448	6	US-10-449-902-50772	Sequence 50772, A
39	55	11.4	455	6	US-10-953-349-35537	Sequence 35537, A
40	55	11.4	478	6	US-10-953-349-29864	Sequence 29864, A
41	55	11.4	494	6	US-10-953-349-35596	Sequence 35596, A
42	55	11.4	527	6	US-10-953-349-35595	Sequence 35595, A
43	55	11.4	578	6	US-10-449-902-43095	Sequence 43095, A
44	55	11.4	831	6	US-10-449-902-51780	Sequence 51780, A
45	54.5	11.3	115	7	US-11-293-697-3980	Sequence 3980, Ap

ALIGNMENTS

RESULT 1
US-10-449-902-48072
; Sequence 48072, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48072
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48072
Query Match 13.0%; Score 63; DB 6; Length 550;
Best Local Similarity 32.5%; Pred. No. 6.5;
Matches 25; Conservative 6; Mismatches 24; Indels 22; Gaps 4;
Qy 19 LYLAAATATL-----GPGHLYGNVDVFRSSLSERLGRFVLRWTGAS-----EP 66
; 177 IYAKKEITTAPLVSNPDLPAP---LFRNVSVFRSSVELMERLLKVFVYHDGAKPIFHPSP 233
; 67 E-----PGWFMLATE 76
; 234 ELKGIYASEGWFMKLME 250
Db
RESULT 2
US-10-953-349-28302
; Sequence 28302, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28302
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-28302

Query Match 12.8%; Score 62; DB 6; Length 110;
Best Local Similarity 30.4%; Pred. No. 1.3;
Matches 28; Conservative 10; Mismatches 36; Indels 18; Gaps 5;

QY 7 GERAGLANPAALYLLAEATLAVLG--PGHFLYGNVDVFRSSLSERLGRFYLRWTGAS 64

Db 3 GTKVTWASAVALLLMAAVSAGAAPGLMNCNVDVYRMIGACRSYCAR-----GSR 56

QY 65 EPEPGFWMLATEQVC-SLRDMRKR---QKHGL 92

Db 57 EATP-----SGQCCAALRGANLRCVCQKGL 82

RESULT 3

US-10-449-902-42048
; Sequence 42048, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 42048

; LENGTH: 446

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-42048

Query Match 12.8%; Score 62; DB 6; Length 446;

Best Local Similarity 28.9%; Pred. No. 6.7;

Matches 22; Conservative 11; Mismatches 29; Indels 14; Gaps 3;

QY 13 ANPFAALYLLAEATLAVLGPH--FLYGNVDVFRSSLSERLGRFYLRWTGA----- 63

Db 136 ATTSAAARLLDSGNLVVQSGGTALWQSFDPYPTNTLLPGMKIGK--NRWTGAEWYLLSW 193

QY 64 ---SEPEPGWFMLATE 76

Db 194 RSPADSPGSRXYVTD 209

RESULT 4

US-10-449-902-56774
; Sequence 56774, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56774
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-56774

Query Match 12.8%; Score 62; DB 6; Length 446;

Best Local Similarity 28.9%; Pred. No. 6.7;

Matches 22; Conservative 11; Mismatches 29; Indels 14; Gaps 3;

QY 13 ANPFAALYLLAEATLAVLGPH--FLYGNVDVFRSSLSERLGRFYLRWTGA----- 63

Db 136 ATTSAAARLLDSGNLVVQSGGTALWQSFDPYPTNTLLPGMKIGK--NRWTGAEWYLLSW 193

QY 64 ---SEPEPGWFMLATE 76

Db 194 RSPADSPGSRXYVTD 209

RESULT 5

US-10-953-349-33953

; Sequence 33953, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 33953

; LENGTH: 810

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

US-10-953-349-33953

Query Match 12.7%; Score 61.5; DB 6; Length 810;

Best Local Similarity 29.9%; Pred. No. 16;

Matches 23; Conservative 11; Mismatches 22; Indels 21; Gaps 4;

QY 21 LLAEATLAVLGPHGLYGN---VDVFRSS--LSERLGRFYLRWTGASEPEPGWFMLA 74

Db 5 LPGAAPLSAAGPGHALSASAPSEVDLAQLSAAIAAGEDLGPVRRACGRPEP---LLA 61

QY 75 T-----EQVC 79

Db 62 SLRGAARDREABIEELC 78

RESULT 6

US-10-501-834-26

; Sequence 26, Application US/10501834

; Publication No. US20060088828A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,

; APPLICANT: Vicente E.

; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids

; FILE REFERENCE: 07039/386US1

; CURRENT APPLICATION NUMBER: US/10/501,834

; CURRENT FILING DATE: 2004-07-19

; PRIOR APPLICATION NUMBER: PCT/US03/02038

; PRIOR FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: 60/351,110

; PRIOR FILING DATE: 2002-01-23

```
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 1871
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-501-834-26

Query Match      12.7%; Score 61.5; DB 6; Length 1871;
Best Local Similarity 27.5%; Pred. No. 42;
Matches 25; Conservative 5; Mismatches 24; Indels 37; Gaps 4;

QY 11 GLANPEAA-----LYLLA-----EATLAVLGGHLYGNVDVFRSSLSLSSRLGRFYLRWT 61
Db 1493 GVINVFAEARHPLLYLVFGNIEATYVPAGPAHL-----QLASTAAG----- 1534

QY 62 GASEPEPGFWMLATEQVCSLRDMRKQKHGL 92
Db 1535 -----CLATEPLCGLNDTRVKHSNKL 1555

RESULT 7
US-10-449-902-48431
; Sequence 48431, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48431
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-48431

Query Match      12.6%; Score 61; DB 6; Length 466;
Best Local Similarity 32.9%; Pred. No. 9.3;
Matches 24; Conservative 7; Mismatches 24; Indels 18; Gaps 4;

QY 22 LABATLAVLGP-----GHFLYGNVDVFRSSLSLSSRLGRFYLRWTGASEPEPGW-----FM 72
Db 358 LAHAATAIMGFWETLGNPCVGGNDIFRSTTFFSQ-----PIPLGLSGSIFM 408

QY 73 LATEQVCSLRDMR 85
Db 409 ADRWSPSELDRSR 421

RESULT 8
US-10-953-349-25312
; Sequence 25312, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25312
```

```
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81)..(81)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25312

Query Match      12.5%; Score 60.5; DB 6; Length 185;
Best Local Similarity 34.3%; Pred. No. 3.5;
Matches 23; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 45 SSSLSE-----RLGRFYLRWTGASEPEPGWF-----MLATEQVCSLRDMRX 86
Db 63 SESESEEEQDQQRVETVXRAGVARLGVGAARP-PRWRSRRPAAAAATLQVVVLRDQR 121

QY 87 RQKHGLA 93
Db 122 AREGVA 128

RESULT 9
US-10-953-349-25311
; Sequence 25311, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25311
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (209)..(209)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25311

Query Match      12.5%; Score 60.5; DB 6; Length 313;
Best Local Similarity 34.3%; Pred. No. 6.6;
Matches 23; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 45 SSSLSE-----RLGRFYLRWTGASEPEPGWF-----MLATEQVCSLRDMRX 86
Db 191 SESESEEEQDQQRVETVXRAGVARLGVGAARP-PRWRSRRPAAAAATLQVVVLRDQR 249

QY 87 RQKHGLA 93
Db 250 AREGVA 256

RESULT 10
US-11-165-586-67
; Sequence 67, Application US/11165586
; Publication No. US20060121060A1
; GENERAL INFORMATION:
; APPLICANT: Seattle Biomedical Research Institute
; APPLICANT: Kappe, Stefan H.I.
; APPLICANT: Matuschewski, Kai
; TITLE OF INVENTION: LIVE GENETICALLY ENGINEERED PROTOZOAN VACCINE
; FILE REFERENCE: SBHUI24889
; CURRENT APPLICATION NUMBER: US/11/165,586
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: PCT/US2004/043023
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: US 60/633,242
```

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; PRIOR FILING DATE: 2004-12-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
US-11-165-586-67

Query Match          12.4%; Score 60; DB 7; Length 450;
Best Local Similarity 31.5%; Pred. No. 12;
Matches 23; Conservative 7; Mismatches 19; Indels 24; Gaps 3;

QY 18 ALYLAEAT-----LAVLPGHFLYGNVDVF--RSSLSRSLG-----54
|||:::
86 ALTLLAQSPPPGRKPTAVFLNGVVIQNSDIYWTLSHLSKARLGTENCCLPDQCAALIE 145
|||:::

QY 55 -RFLRWGTASEP 66
|||:::
146 KRFRQMGGASTP 158

RESULT 11
US-11-270-040-6
; Sequence 6, Application US/11270040
; Publication No. US20060110762A1
; GENERAL INFORMATION:
; APPLICANT: Kapil, Sanjay
; APPLICANT: Kim, Jeong-Ki
; TITLE OF INVENTION: PORCINE REPRODUCTIVE AND RESPIRATORY
; TITLE OF INVENTION: SYNDROME VIRUS RECEPTOR COMPONENTS AND USES THEREOF
; FILE REFERENCE: 14337/004001
; CURRENT APPLICATION NUMBER: US/11/270,040
; CURRENT FILING DATE: 2005-11-09
; PRIOR APPLICATION NUMBER: 60/680,297
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/626,788
; PRIOR FILING DATE: 2004-11-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1730
; TYPE: PRT
; ORGANISM: Sus scrofa
US-11-270-040-6

Query Match          12.4%; Score 60; DB 7; Length 1730;
Best Local Similarity 29.4%; Pred. No. 59;
Matches 15; Conservative 10; Mismatches 26; Indels 0; Gaps 0;

QY 10 AGLANPFAALYLLAEATLAVLPGHFLYGNVDVFRSSLSRSLGRFYLRLW 60
:|:::
693 SALGNASASATLDAQTLVLITPSTLQEGIEANLTCNVSRASGPANFSW 743

RESULT 12
US-10-449-902-34748
; Sequence 34748, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34748
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-34748

Query Match          12.3%; Score 59.5; DB 6; Length 503;
Best Local Similarity 23.1%; Pred. No. 15;
Matches 21; Conservative 14; Mismatches 27; Indels 29; Gaps 3;

QY 8 ERAGLANPFAALYLLAE-----ATLAVLPGHFLYGNVD-----41
|||:::
210 ERSVVNVGGANYWLTEDBESVYKHAVVTFDLSEELFQWLQLPADVDPANYVLGDPDQWLI 269
|||:::

QY 42 --VFRSSLSRSLGRFYLRLWTGASEPEPGW 70
|:|:::
270 TEVDSNVSVSYETGKLHI-WTIDSKIEQSW 299

RESULT 13
US-10-449-902-51740
; Sequence 51740, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51740
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51740

Query Match          12.3%; Score 59.5; DB 6; Length 1207;
Best Local Similarity 33.9%; Pred. No. 44;
Matches 21; Conservative 5; Mismatches 17; Indels 19; Gaps 3;

QY 5 REGERAGLANPFAALY-----LLAEATLAVLG-----PGHFLYGNVDVFRSS 46
:|:::
643 QEGEAGGTTQIGATYFTTENIRRTKELKADATLKVGLLVITDPGHESFSNLR-SRGS 701
|||:::

QY 47 SL 48
||
702 SL 703

RESULT 14
US-10-474-853-2
; Sequence 2, Application US/10474853
; Publication No. US20060088546A1
; GENERAL INFORMATION:
; APPLICANT: RIDING, GEORGE ALFRED
; APPLICANT: HOPE, MICHELLE ANNE
; APPLICANT: WILLADSEN, PETER
; TITLE OF INVENTION: Antigens for raising an immune response against Rickettsiae and Ehrlichiae pathogens
; FILE REFERENCE: RICE-025
; CURRENT APPLICATION NUMBER: US/10/474,853
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: AU PR4400
; PRIOR FILING DATE: 2001-04-12
```


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[illegible]

CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism
XX
SQ Sequence 1289 AA;

Query Match 17.3%; Score 81; DB 4; Length 1289;
Best Local Similarity 30.1%; Pred. No. 1.8;
Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3

QY 5 RFADHSETISQAEHGIADSHRNALLOEMLAGL-ALS---DQTCLL----- 47
Db 345 RLAVASEELAAHSVAEELSTRAESIQTWFGLSALAEVDATVRIASERAHLDIEPVA 404
QY 48 -----FEAPTQVAEAEQELLAEIQRROALLPAQPGCE 79
Db 405 VSDTDKPKPELEAEACQVAEQQLLAEALDAARLARLDAARAE 447

RESULT 5
ABU36881
ID ABU36881 standard; protein; 1289 AA.
XX
AC ABU36881;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #22408.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Mycobacterium tuberculosis.
XX
PN W0200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JF, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI
XX
WPI: 2003-029926/02.
DR N-PSDB; ACA40751.
XX
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 64805; 1766pp; English.
XX
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC

CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism
XX
SQ Sequence 1289 AA;

Query Match 17.3%; Score 81; DB 4; Length 1289;
Best Local Similarity 30.1%; Pred. No. 1.8;
Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3

QY 5 RFADHSETISQAEHGIADSHRNALLOEMLAGL-ALS---DQTCLL----- 47
Db 345 RLAVASEELAAHSVAEELSTRAESIQTWFGLSALAEVDATVRIASERAHLDIEPVA 404
QY 48 -----FEAPTQVAEAEQELLAEIQRROALLPAQPGCE 79
Db 405 VSDTDKPKPELEAEACQVAEQQLLAEALDAARLARLDAARAE 447

RESULT 5
ABU36881
ID ABU36881 standard; protein; 1289 AA.
XX
AC ABU36881;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #22408.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Mycobacterium tuberculosis.
XX
PN W0200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JF, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI
XX
WPI: 2003-029926/02.
DR N-PSDB; ACA40751.
XX
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 64805; 1766pp; English.
XX
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC

CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1289 AA;

Query Match 17.3%; Score 81; DB 6; Length 1289;
Best Local Similarity 20.1%; Pred. No. 1.8;
Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3;

QY 5 RFADHSETISQAEHGIAADSDHNRALQEMLAGL-ALS---DOTCOLL----- 47
Db 345 RLAVASEELAHHESAVALSTRAESIQHTWFGLSALAERVDATVRIASERAHLDIEPVA 404
QY 48 -----FRAPTEQVAVAEQELLAEIQRQALLPAQGE 79
Db 405 VSDTPRKPPELEAAEQQVAVAEQQLLAELDAARLDAAAE 447

RESULT 6
AAB54325
ID AAB54325 standard; protein; 211 AA.
XX
AC AAB54325;
XX
DT 09-MAR-2001 (first entry)
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:777.
XX
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW diagnosis; identification; cytostatic; neuroprotective; neurotropic;
KW immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic; neural;
KW immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW cardiovascular; renal; proliferative.
XX
OS Homo sapiens.
XX
FN WO200055320-A1.
PD 21-SRP-2000.
XX
PF 08-MAR-2000; 2000WO-US005989.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
XX WPI; 2000-579444/54.
DR N-PSDB; AAC99090.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition.
XX
PS Claim 11; Page 1215-1216; 1379pp; English.

XX AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 211 AA;

Query Match 17.0%; Score 79.5; DB 3; Length 211;
Best Local Similarity 31.0%; Pred. No. 0.26;
Matches 35; Conservative 12; Mismatches 39; Indels 27; Gaps 4;

QY 2 KQPRFADHSETISQAEHGIAADSDHNRAL---LQEML-----AGLAL 39
Db 27 KSKQFLDLMETIDKQREEMAKSRASARVKGLOEALNHRHSIINALKAKLQWTEAALAL 86
QY 40 SDQTCQLLFEAPTEQVAVAEQELLAEIQRQALLPAQGEGRKSRRTIMRGL 92
Db 87 SEQKAQDL---GELLATAEQQLSQRQAKELKLEQQEAAE-RESKLRDL 134

RESULT 7
ADC31377
ID ADC31377 standard; protein; 483 AA.
XX
AC ADC31377;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel polypeptide sequence, SEQ ID NO:1459.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; neurotropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulneryary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy.
XX
OS Homo sapiens.
XX
FN WO2003029271-A2.
PD 10-APR-2003.
XX
XX 24-SEP-2002; 2002WO-US030474.
PF 24-SEP-2001; 2001US-0324631P.
PR (HYSE-) HYSEQ INC.
XX
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asaundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;

XX WPI: 2003-371981/35.
DR N-PSDB; ADC30406.
XX
PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX
PS Claim 20; SEQ ID NO 1459; 1185pp; English.
XX
CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human polypeptide sequence of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 483 AA;
Query Match 17.0%; Score 79.5; DB 7; Length 483;
Best Local Similarity 31.0%; Pred. No. 0.78;
Matches 35; Conservative 12; Mismatches 39; Indels 27; Gaps 4;
Qy 2 KQPRFADHSETISQAEHGIADSDHRNAL----LQEML-----AGLAL 39
Db 255 KSKQFLDLMETIDKOREEMAKSSRSAAARVQQLCEALNERHSIINALKAKLQMTFAALAL 314
Qy 40 SDOTCOLLFEAPTEQVAEQLLAETQRQALLPAQGEGRKSRRTMRGL 92
Db 315 SEQKAQDL----GSLTAEQEQLSLQRAKELKLEQEEAAE-RESKLRDL 362
RESULT 8
AAB50381
ID AAB50381 standard; protein; 323 AA.
AC AAB50381;
XX
DT 12-MAR-2001 (first entry)
DE Human uncoupling protein #4.
XX
KW Human; uncoupling protein; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cardiant; vasotropic;
KW cerebroprotective; neuroprotective; antibacterial; ophthalmological;
KW gastrointestinal; nephrotropic; gynaecological; vulnery; thrombolytic;

KW gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
KW infertility.
XX
OS Homo sapiens.
XX
PN WO2000061614-A2.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009534.
XX
PR 09-APR-1999; 99US-0128701P.
PR 08-JUL-1999; 99US-0142821P.
PR 18-AUG-1999; 99US-0149448P.
PR 12-NOV-1999; 99US-0164751P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Komatsoulis G, Rosen CA, Soppet DR;
XX
DR WPI; 2000-656322/63.
DR N-PSDB; AAC90455.
XX
PT Uncoupling proteins and nucleic acid sequences encoding them, useful for
PT detecting, preventing and treating proliferative, neurological, immune
PT system, cardiovascular and gastrointestinal disorders.
XX
PS Claim 11; Page 320-321; 343pp; English.
XX
CC The present sequence is a human uncoupling protein. The nucleotide
CC sequences encoding the uncoupling proteins may be used for the detection
CC of various disorders such as cancer, for chromosome identification, as
CC chromosome markers and for numerous other diagnostic or research
CC purposes. The uncoupling protein encoded by the nucleotide sequences may
CC be used to treat disorders such as neural, immune, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal and
CC proliferative disorders, wounds, infectious diseases, thrombosis,
CC arthritis, and infertility
XX
SQ Sequence 323 AA;
Query Match 16.2%; Score 76; DB 3; Length 323;
Best Local Similarity 30.0%; Pred. No. 1.3;
Matches 24; Conservative 14; Mismatches 30; Indels 12; Gaps 3;
Qy 18 HGIADSDHRNALQEMLAGLALSDOTCOLLFEAPTEQVAV-----AEQELLAEIQR 68
Db 92 HQLSKDGCKLTLKXEMLAGGAG--TCQVITVTTPMELKIQLDQAGRIAAQRKILAAQGG 149
Qy 69 RQALLPAQPG-EGRKSRRT 87
Db 150 LSAQGGQAQPSVEAPAPRPT 169
RESULT 9
AAB94434
ID AAB94434 standard; protein; 323 AA.
XX
AC AAB94434;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human protein sequence SEQ ID NO:15054.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.

CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.

XX Sequence 1179 AA;

Query Match 15.9%; Score 74.5; DB 7; Length 1179;
Best Local Similarity 39.2%; Pred. No. 11;
Matches 20; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

Qy 19 GIADSDHRNALLQEMLAGLSDOTCQLLFEAPTEQVAVARQELIAEIQR 69
Db 12 GNGKKDHQVLIDEASAWLD-QDASNQVFFLVPNYSKFEQEILLAEWRR 61

RESULT 15

ADJ50279
ID ADJ50279 standard; protein; 364 AA.

XX AC ADJ50279;

XX DT 06-MAY-2004 (first entry)

XX DE Oil-associated gene related protein #1779.

XX KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.

XX OS Unidentified.

XX PN US2004025202-A1.

XX PD 05-FEB-2004.

XX PF 14-MAR-2003; 2003US-00389566.

XX PR 15-MAR-2002; 2002US-0365301P.

XX PR 26-JUN-2002; 2002US-0391786P.

XX PR 26-JUN-2002; 2002US-0392018P.

XX PA (LAUR/) LAURIE C C.

XX PA (SAVA/) RAVANELLO M.

XX PA (LEDE/) LEDEAUX J R.

XX PA (ROGE/) ROGERS J A.

XX PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;

XX WPI; 2004-142683/14.

XX PT Novel recombinant DNA construct comprising a promoter functional in

XX PT plants operably linked to an oil-associated gene for producing transgenic

XX PS Example 3; SEQ ID NO 2283; 22pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a

XX CC promoter functional in plants operably linked to an oil-associated gene.

XX CC The construct is useful for transgenic plant seed which has in its genome

XX CC the construct, that is functional in the plant to transcribe the oil-

XX CC associated gene. The transgenic plant seed grows into a plant having

XX CC enhanced seed oil as compared to wild type. The construct is useful for

XX CC producing hybrid maize seed. The transgenic plant seed is useful for

XX CC producing vegetable oil. The present sequence represents the amino acid

XX CC sequence of an oil-associated gene related protein.

XX SQ Sequence 364 AA;

Query Match 15.7%; Score 73.5; DB 8; Length 364;

Best Local Similarity 29.5%; Pred. No. 3.1;

Matches 26; Conservative 16; Mismatches 37; Indels 9; Gaps 4;

Qy 1 MKQPRFADHSBTISQABHGIAADSDHRNALLQEMLAGL-----ALSDQTCQLLFEAPTEQV 55

Db 1 MLEPN-ADHRAVAQAA-GVNASRITLTVMLDEWAGADARRRAVDITVCALATCCSLAA 58

Qy 56 AVARQELIAEIQRQALLPAQPGEGRKS 83
Db 59 AIAEGPLAGDLAR--TLSSGEAGEGQKA 84

Search completed: June 16, 2006, 19:06:47
Job time : 64.2846 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 9.55285 Seconds
(without alignments)
946.773 Million cell updates/sec

Title: US-10-813-908A-7
Perfect score: 459
Sequence: 1 MKQPRFADHSETISQAEHGI.....AQPEGKRKRPTIMRGLMI 94

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195.5	41.7	95	2 A33601	low calcium respon
2	195.5	41.7	95	2 A37314	regulatory protein
3	179.5	38.3	98	2 P83432	regulator in type
4	81	17.3	1289	2 B70748	probable smc prote
5	75.5	16.1	177	2 B87146	50S ribosomal prot
6	74	15.8	222	2 T16731	hypothetical prote
7	73.5	15.7	364	1 PAXXF	fructose-bisphosph
8	73.5	15.7	678	2 B70913	probable penicilli
9	72.5	15.5	496	2 B83160	hypothetical prote
10	71.5	15.2	1829	2 T26135	hypothetical prote
11	71	15.1	477	2 F87329	hypothetical prote
12	68.5	14.6	939	2 C70876	hypothetical prote
13	68.5	14.6	1148	2 T13347	Cnn protein - frui
14	68	14.5	439	1 TVHUM	transforming prote
15	68	14.5	440	4 TVHUT	transforming prote
16	68	14.5	2670	2 A46719	inositol 1,4,5-tri
17	67.5	14.4	492	2 S76612	ATP-dependent RNA
18	67	14.3	675	2 F85071	hypothetical prote
19	67	14.3	728	2 S59964	procollagen-lysine
20	67	14.3	1426	2 T00337	hypothetical prote
21	66.5	14.2	873	2 B87049	conserved hypothet
22	66	14.1	2434	2 S44861	DNA topoisomerase
23	66	14.1	2671	2 A49873	inositol 1,4,5-tri
24	65.5	14.0	115	2 P70027	tandem repeat prot
25	65.5	14.0	608	2 T37864	hypothetical prote
26	65	13.9	379	2 E69824	two-component sens
27	65	13.9	449	2 A57562	mannosyltransferas
28	64.5	13.8	1075	1 OYRTHX	heat-stable entero
29	64.5	13.8	1115	2 A70990	carbamoyl-phosphat

30	64.5	13.8	1203	2 G87112	probable cell divi
31	64	13.6	219	2 AF1683	probable endonucle
32	64	13.6	284	2 H83119	probable transcrip
33	64	13.6	358	2 T31624	hypothetical prote
34	64	13.6	535	1 A69771	two-component sens
35	64	13.6	614	2 S43427	intermediate filam
36	64	13.6	710	2 AD3479	ATP-dependent heil
37	64	13.6	960	2 T50383	homolog to yeast c
38	64	13.6	1560	2 T30282	calcium-binding pr
39	63.5	13.5	228	2 E75469	conserved hypothet
40	63.5	13.5	230	2 B95353	protein (imported
41	63.5	13.5	328	2 A84291	ornithine cyclodea
42	63.5	13.5	488	2 F84001	glycine chydrogen
43	63	13.4	376	2 S47986	actin-related prot
44	63	13.4	642	2 B81917	probable chaperone
45	63	13.4	799	2 S53349	phosphoribosyl-AMP

ALIGNMENTS

RESULT 1

A33601
low calcium response protein G - Yersinia peestis plasmid pCD1
N/Alternate names: V-antigen
C/Species: Yersinia pestis
C/Date: 17-Jan-1990 #sequence revision 17-Jan-1990 #text_change 09-Jul-2004
C/Accession: A33601; T43593; T42888
R/Price: S.B.; Leung, K.Y.; Barve, S.S.; Straley, S.C.
J. Bacteriol. 171, 5646-5653, 1989
A/Title: Molecular analysis of lcrGVH, the V antigen operon of Yersinia pestis.
A/Reference number: A33601; MUID:90008806; PMID:2477361
A/Accession: A33601
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-95 <P>
A/Cross-references: UNIPROT:P19394; UNIPARC:UPI000012E2B4; GB:M26405; NID:9155448; PIDN:R/Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker, J. Bacteriol. 180, 5192-5202, 1998
A/Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A/Reference number: 222578; MUID:98422474; PMID:9748454
A/Accession: T43593
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-95 <HUP>
A/Cross-references: UNIPARC:UPI000012E2B4; EMBL:AF053946; NID:g2996222; PIDN:AAC62573.1
A/Experimental source: strain KIM
R/Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Infect. Immun. 66, 4611-4623, 1998
A/Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia pestis.
A/Reference number: 222273; MUID:98427122; PMID:9746557
A/Accession: T42888
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-95 <PER>
A/Cross-references: UNIPARC:UPI000012E2B4; EMBL:AF074612; NID:g3822037; PIDN:AAC69798.1
A/Experimental source: strain KIMS
C/Genetics:
A/Gene: lcrG
A/Genome: plasmid
A/Note: plasmid pCD1

Query Match 41.7%; Score 195.5; DB 2; Length 95;
Best Local Similarity 43.2%; Pred. No. 2.6e-13;
Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;

Qy	1	MKQPRFADHSETISQAEHGIADSDHRNALQEMAGLALSDQTCLLFEA-PTQVAVAE	59
Db	1	MKSSHFDYDKTLKQAEALAIADSDHRNAKLQEMCADIGLTPEAVMKIFAGRSABEIKPAE	60
Qy	60	QELLAETQRQALLPAQPEGKRKRPTIMRGLMI	94
Db	61	RELLDEIKRQERQPHPYDGKRPKPTMMRGQII	95

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: B70748
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1289 <COL>
 A:Cross-references: UNIPARC:UPI0000165322; GB:Z74697; GB:AL123456; NID:g3261602; PID:N.C
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: smc
 C:Superfamily: chromosome segregation protein SMC1

Query Match 17.3%; Score 81; DB 2; Length 1289;
 Best Local Similarity 30.1%; Pred. No. 3.9;
 Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3;

QY 5 RFADHSETISQAEHGATSDHRNALLOEMLAGL-ALS---DOTCOLL----- 47
 Db 345 RLAVASEELAAHSAVAELSTRAESIQHTWFGSALAAERVDATVRIASERAHHLIDIEPVA 404
 QY 48 -----FEAPTQVAVAEQELAEIQRQALLPAQPG 79
 Db 405 VSDTPRKPPELEAQAQVAVAEQQLLAELDAARLDAARAE 447

RESULT 5
 B87146
 50S ribosomal protein L10 [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: B87146
 R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sulston
 A:Title: Massive gene decay in the leprosy bacillus
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: B87146
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-177 <STO>
 A:Cross-references: UNIPROT:Q9CBK7; UNIPARC:UPI0000133B3A; GB:AL450380; NID:g13093566;
 C:Genetics:
 A:Gene: rplJ
 C:Superfamily: Escherichia coli ribosomal protein L10

Query Match 16.1%; Score 75.5; DB 2; Length 177;
 Best Local Similarity 32.8%; Pred. No. 1.4;
 Matches 22; Conservative 12; Mismatches 28; Indels 5; Gaps 2;

QY 9 HSETISQAEHGATSDHRNALLOEMLAGLSDOTCOLLFEAPTQVAVAEQELAEIQR 68
 Db 113 HPMTVAEVR-IADLESREVLAKLAGAMKGTFAKIGLFNAPTSQMA----RLTAALQE 167
 QY 69 RQALLPA 75
 Db 168 KKAFEP 174

RESULT 6
 T16731
 hypothetical protein R12C12.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T16731
 R:Favell, T.
 submitted to the EMBL Data Library, July 1995
 A:Description: The sequence of C. elegans cosmid R12C12.
 A:Reference number: Z18568

A;Accession: T16731
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-222 <FAV>
A;Cross-references: UNIPROT:Q21959; UNIPARC:UPI000017A00C; EMBL:U23510; NID:g746453; PID
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:RI2C12.5
A;Introns: 98/3; 185/3

Query Match 15.8%; Score 74; DB 2; Length 222;
Best Local Similarity 29.9%; Pred. No. 2.6;
Matches 29; Conservative 12; Mismatches 28; Indels 28; Gaps 5;

Qy 9 HSETIS-----QAEHGTAADSHRNALQEMLAGLSDQTCQLLFEAPTEQVAE 59
Db 116 HNEIVIDVLGKTTETLKKEHAKMDIDKVHDLMDIADGLAMSEELNEAI-SAPIGDVA-DE 173
Qy 60 QELLAETORRQ-----ALLPAQP-GE 79
Db 174 DELMOELQELQDNVADLSTTTKLPDVPATLPEAPESG 210

RESULT 7
PAQXF
fructose-bisphosphatase (EC 3.1.3.11) - Xanthobacter flavus
N;Contains: sedoheptulose-bisphosphatase (EC 3.1.3.37)
C;Species: Xanthobacter flavus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A45867; S13576
R;Meijer, W.G.; Enequist, H.G.; Terpstra, P.; Dijkhuizen, L.
J. Gen. Microbiol. 136, 2225-2230, 1990
A;Title: Nucleotide sequences of the genes encoding fructosebisphosphatase and phosphori
A;Reference number: A45867; MUID:91178501; PMID:1964170
A;Accession: A45867
A;Molecule type: DNA
A;Residues: 1-364 <ME2>
A;Cross-references: UNIPROT:P23014; UNIPARC:UPI000012A3E0; EMBL:X17252; NID:g48543; PIDN
R;Meijer, W.G.; Arnborg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuizen,
Mol. Gen. Genet. 225, 320-330, 1991
A;Title: Identification and organization of carbon dioxide fixation genes in Xanthobacte
A;Reference number: S13573; MUID:91172133; PMID:1900916
A;Accession: S13576
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-364 <ME1>
A;Cross-references: UNIPARC:UPI000012A3E0; EMBL:X17252; NID:g48543; PIDN:CAA35118.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
C;Genetics:
A;Gene: cfxP
C;Superfamily: fructose-1,6-bisphosphatase
C;Keywords: Calvin cycle; phosphoric monoester hydrolase

Query Match 15.7%; Score 73.5; DB 1; Length 364;
Best Local Similarity 23.5%; Pred. No. 5.3;
Matches 26; Conservative 16; Mismatches 37; Indels 9; Gaps 4;

Qy 1 MKQPRFADHSFTISQAEHGTAADSHRNALQEMLAGL-----ALSDQTCQLLFEAPTEQV 55
Db 1 MLEFN-ADHRAVAQA-A-GVAASRITLTVMLDEWAGARRAVADTVCALATGCASIAA 58

Qy 56 AVAEQELLAEIQRQALLPAQPGGRKS 83
Db 59 AIAEGLAGDLAR--TLSSGEAGEGQKA 84

RESULT 8
B70913
probable penicillin-binding protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70913
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70913
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-678 <COL>
A;Cross-references: UNIPROT:P71707; UNIPARC:UPI00000D4705; GB:Z80775; GB:AL123456; NID
A;Experimental source: strain H37rv
C;Genetics:
A;Gene: ponA
C;Superfamily: penicillin-binding protein 1B

Query Match 15.7%; Score 73.5; DB 2; Length 678;
Best Local Similarity 40.4%; Pred. No. 11;
Matches 19; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

Qy 48 FEAPTEQVAEAEQELLAEIQRQALL-PAQPGEGKRKRRTIMRGLM 93
Db 172 FDKPVEQLTVAEGALLAALIRRPSTLDPVDPGAGAHARNWVLDGMV 218

RESULT 9
B83160
hypothetical protein PA3894 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83160
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Li
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83160
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-496 <SPO>
A;Cross-references: UNIPROT:Q9HXB9; UNIPARC:UPI00000C5B62; GB:AE004806; GB:AE004091; NI
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3894

Query Match 15.5%; Score 72.5; DB 2; Length 496;
Best Local Similarity 33.3%; Pred. No. 9.6;
Matches 27; Conservative 12; Mismatches 29; Indels 13; Gaps 3;

Qy 21 ADSDHRNALQEMLAGLALSDQTCQ-----LLFEAPTEQVAEAEQ-----LLAEIQRQA 71
Db 191 AEMDIKAMLQQQORDILALAQRRLGGIGTHFEVSAQAEVPLPETERIEVIDEIIQLTRN 250

Qy 72 LLPA----QPGEGRKSRRTI 88
Db 251 LLAALAGKPGEGRTTIRPSL 271

RESULT 10
T26135
hypothetical protein Y6B3B.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26135; T27328
R;Dobson, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20158
A;Accession: T26135
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1829 <WIL>
A;Cross-references: UNIPROT:O18164; UNIPARC:UPI0000007C881; EMBL:Z82068; PIDN:CAB04901.1

A;Experimental source: clone W04A4
R;White, S.
Submitted to the EMBL Data Library, October 1998
A;Reference number: Z20345
A;Accession: T27328
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1829 <W12>
A;Cross-references: UNIPARC:UPI000007C881; EMBL:AL032655; PIDN:CAA21727.1; GSPDB:GN00019
A;Experimental source: clone Y6B3B
C;Genetics:
A;Gene: CESP:Y6B3B.1
A;Map position: 1
A;Introns: 20/2; 53/3; 82/3; 329/3; 332/3; 355/3; 396/3; 462/3; 1799/3

Query Match 15.2%; Score 71.5; DB 2; Length 1829;
Best Local Similarity 27.2%; Pred. No. 56;
Matches 31; Conservative 14; Mismatches 36; Indels 33; Gaps 6;

QY 1 MKQPRFAD-----HS-----ETISQAEH-----GIADSDHRNALQEMLAGLSD 41
DB 1421 VKDPRMQEVQLRQNSHLEDLRPQDQAEHLEPNQGVERRDRRGGIATLUSA---SH 1477

QY 42 QTQQLFEAPTEQVAVAEQELAEIQRRQALLPAQGE-----GRKSRP 86
DB 1478 QDCQTGSEEP--QVSQVPESPAATERQEPPLSPQSGDPVGPPIAKKGLSRQP 1529

RESULT 11
F87329
hypothetical protein CC0649 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87329
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Shapiro, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87329
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <STO>
A;Cross-references: UNIPROT:Q9AAF2; UNIPARC:UPI00000C7105; GB:AE005673; NID:g13421864; E
C;Genetics:
A;Gene: CC0649

Query Match 15.1%; Score 71; DB 2; Length 477;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 26; Conservative 12; Mismatches 36; Indels 4; Gaps 2;

QY 12 TTSQAEHGADSDHRNALQEMLAGLSDQTCQLLFEAPTEQVAVAEQELAEIQRRQA 71
DB 158 TVARADGG-NDGKRRLMSVQGLDGVESFDVYPLLFGARHTAVWEG---ADGRRRTL 213

QY 72 LLPAQPGEGKSRRTIM 89
DB 214 VAPAVSLEQRRAPPRM 231

RESULT 12
C70876
hypothetical protein Rv1179c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: C70876
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70876
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-939 <COL>
A;Cross-references: UNIPROT:O50435; UNIPARC:UPI00000C152C; GB:AL010186; GB:AL123456; N
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv1179c
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1179c

Query Match 14.6%; Score 68.5; DB 2; Length 939;
Best Local Similarity 34.7%; Pred. No. 52;
Matches 25; Conservative 10; Mismatches 24; Indels 13; Gaps 4;

QY 20 IADSDHRNALQEMLAGLSDQTCQLLFEAPTEQVAVAEQELAEIQRRQALLPAQGE 79
DB 455 LAASDHR---RTPLHALLVTGQT----FACP----AAIEDDLIAFCAERGALVTAEPLD 503

QY 80 GRKSRRTIMRG 91
DB 504 AHPSLR--VMRG 513

RESULT 13
T13347
Cnn protein - fruit fly (Drosophila melanogaster)
N;Alternate names: centrosomin
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13347
R;Heuer, J.G.; Li, K.; Kaufman, T.C.
Development 121, 3861-3876, 1995
A;Title: The Drosophila homeotic target gene centrosomin (cnn) encodes a novel centrosom
A;Reference number: Z17655; MUID:96102828; PMID:8582295
A;Accession: T13347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1148 <HEU>
A;Cross-references: UNIPROT:P54623; UNIPARC:UPI0000127C2A; EMBL:U35621; NID:g2570233; P
A;Experimental source: strain Oregon R
C;Genetics:
A;Gene: Cnn
A;Cross-references: FlyBase:FBgn0013765
A;Map position: 2
C;Function:
A;Description: may participate in mitotic spindle assembly and the mechanics of morphog
C;Keywords: leucine zipper

Query Match 14.6%; Score 68.5; DB 2; Length 1148;
Best Local Similarity 29.6%; Pred. No. 66;
Matches 24; Conservative 10; Mismatches 30; Indels 17; Gaps 2;

QY 9 HSETISQAEHGADSDHR-----NALQEMLAGLSDQTCQL-----LFEP 51
DB 720 NSERIAQLEEQIAQKDERMLNVQCMVELDNRVKEQLRCLDITQQLRQALNEALTAD 779

QY 52 TEQVAVAEQELAEIQRRQA 72
DB 780 LQAIGSHEERVMVELQRL 800

RESULT 14
TVHUM
transforming protein C-myc - human
N;Alternate names: p64 myc oncogene
C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A01349; A26245; A26246; A21061; I67315; I53224; I61947; I38052; I57605; I
R;Watson, D.K.; Psallidopoulos, M.C.; Samuel, K.P.; Dalla-Favera, R.; Papas, T.S.
Proc. Natl. Acad. Sci. U.S.A. 80, 3642-3645, 1983
A;Title: Nucleotide sequence analysis of human c-myc locus, chicken homologue, and myel
A;Reference number: A01349; MUID:83221652; PMID:6304729

Qy 4 PRFADHSETISQAEHGIADSDHRNALIQEMLAGLALSDQ-----TC 44
Db 346 PRSSDTEENVKRRTHNVLERQRRNELKRSP---FALRDQIPELENNEKAPKVILKKATA 402
Qy 45 QLLFEAPTEQVAVAEQELLAEIORRQAL 72
Db 403 YILSVQAEQKLISEEDLLR--KRREQ 428

Search completed: June 16, 2006, 19:25:07
Job time : 11.5528 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 73.8244 Seconds
(without alignments)
1177.815 Million cell updates/sec

Title: US-10-813-908A-7
Perfect score: 459
Sequence: 1 MKQPRFADHSETISQAEHGI.....AQPGEGRKRRPTIMRGLMI 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469	100.0	94	Q8GA89_AERSA	Q8ga89 aeromonas s
2	422	90.0	94	Q5CC98_AERSO	Q5cc98 aeromonas s
3	421	89.8	94	Q699R1_AERHY	Q699r1 aeromonas h
4	400	85.3	94	Q5XL05_AERHY	Q5xl05 aeromonas h
5	198.5	42.3	95	Q93KU3_YEREN	Q93ku3 yersinia en
6	196.5	41.9	95	Q52157_YEREN	Q52157 yersinia en
7	195.5	41.7	95	LCRG_YERPE	P69957 yersinia pe
8	179.5	38.3	98	Q91326_PSEAE	P69958 yersinia ps
9	175.5	37.4	98	Q30526_PSEAE	Q91326 pseudomonas
10	168	35.8	99	Q6TLM3_AERHY	Q30526 pseudomonas
11	168	35.8	99	Q6TLM3_AERHY	Q6tlm3 aeromonas h
12	140	29.9	94	Q87P58_VIBPA	Q87p58 vibrio para
13	137.5	29.3	92	Q84G16_PHOLU	Q84g16 photorhabdu
14	137.5	29.3	92	Q7N0X0_PHOLU	Q7n0x0 photorhabdu
15	128	27.9	96	Q6QV51_VIBHA	Q6qvs1 vibrio harv
16	126	26.3	96	Q66PT5_PASPI	Q66pt5 pasteurella
17	81	17.3	842	Q54MH2_DICDI	Q54mh2 dictyosteli
18	81	17.3	1205	SMC_MYCTU	Q10970 mycobacteri
19	81	17.3	1205	Q7TXM2_MYCBO	Q7txm2 mycobacteri
20	79.5	17.0	670	LRC45_HUMAN	Q96cn5 homo sapien
21	79	16.8	325	Q4J2M9_AZOVI	Q4j2m9 azotobacter
22	77	16.4	236	Q21959_CAEEL	Q21959 caenorhabdi
23	77	16.4	323	Q5RDB1_PONPY	Q5rdb1 pongo pygma
24	76.5	16.3	1104	Q9W6R6_FUGRU	Q9w6r6 fugu rubrip
25	76	16.2	323	GHC1_HUMAN	Q9n936 homo sapien
26	75.5	16.1	177	RL10_MYCLE	Q9cbk7 mycobacteri
27	74.5	15.9	699	Q4UUA6_XANC8	Q4uuu6 xanthomonas
28	74.5	15.9	699	Q8P918_XANCP	Q8p918 xanthomonas
29	74.5	15.9	829	Q40PN4_DESAC	Q40pn4 desulfuroco
30	74.5	15.9	1175	Q3XZV8_ENTFC	Q3xzv8 enterococcu
31	74	15.8	692	Q2UEG2_ASPOR	Q2ueg2 aspergillus

32	74	15.8	1168	2	Q873C1_NEUCR	Q873c1 neurospora
33	73.5	15.7	326	2	Q35QL0_9BRAD	Q35ql0 bradyrhizob
34	73.5	15.7	364	1	F16P_XANFL	P23014 xanthobacte
35	73.5	15.7	678	2	P71707_MYCTU	P71707 m probable
36	73.5	15.7	680	2	Q7U2Y6_MYCBO	Q7u2y6 m probable
37	73.5	15.7	820	2	Q8VKS5_MYCTU	Q8vks5 mycobacteri
38	73	15.6	233	2	Q621B2_CAEER	Q621b2 caenorhabdi
39	73	15.6	456	2	Q44D99_CHRSL	Q44d99 chromohalob
40	72.5	15.5	496	2	Q9HXB9_PSEAE	Q9hxb9 pseudomonas
41	72.5	15.5	697	2	Q7UHM1_RHOBA	Q7uhm1 rhodopirell
42	72.5	15.5	1162	2	Q3KFB4_PSEPF	Q3kfb4 pseudomonas
43	72	15.4	100	2	Q5KVL9_GEOKA	Q5kvl9 geobacillus
44	72	15.4	603	2	Q89N77_BRAJA	Q89n77 bradyrhizob
45	72	15.4	681	2	Q356X6_9BRAD	Q356x6 bradyrhizob

ALIGNMENTS

RESULT 1
Q8GA89_AERSA
ID Q8GA89_AERSA PRELIMINARY; PRT; 94 AA.
AC Q8GA89;
DT 01-MAR-2003, integrated into UniProtKB/TREMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Acrg protein.
GN Name=acrg;
OS Aeromonas salmonicida subsp. salmonicida.
OG Plasmid pASvira.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RX MEDLINE=2262111; PubMed=12374830;
RX DOI=10.1128/JB.184.21.5966-5970.2002;
RA Burr S.E., Stuber K., Wahli T., Frey J.;
RT "Evidence for a type III secretion system in Aeromonas salmonicida subsp. salmonicida";
RL J. Bacteriol. 184:5966-5970(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267; PLASMID=pASvira;
RX MEDLINE=22957181; PubMed=14594831;
RX DOI=10.1128/JB.185.22.6583-6591.2003;
RA Burr S.E., Stuber K., Frey J.;
RT "The ADP-ribosylating toxin, AexT, from Aeromonas salmonicida subsp. salmonicida is translocated via a type III secretion pathway.";
RL J. Bacteriol. 185:6583-6591(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model";
RL Microbiol. 151:2111-2118(2005).
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CC -----
CC EMBL; AJ458292; CAD30220.1; -; Genomic DNA.
CC EMBL; AJ516009; CAD56768.1; -; Genomic DNA.
CC EMBL; AJ516218; CAB83107.1; -; Genomic DNA.
CC InterPro; IPR009863; LcrG.
CC Pfam; PF07216; LcrG; 1.
KW Plasmid.
SQ SEQUENCE 94 AA; 10461 MW; F17EFD8A18205EC CRC64;

Query Match 100.0%; Score 469; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 3e-38;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MKQPRFADHSETISOAEGHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
|
Db 1 MKQPRFADHSETISOAEGHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
|
QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
|
Db 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
|
RESULT 2
Q5CC98_AERSO
ID Q5CC98_AERSO PRELIMINARY; PRT; 94 AA.
AC Q5CC98;
DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Acg protein.
GN Name=acrg;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, Perca fluviatilis.";
RT J. Fish Dis. 28:141-150(2005).
|
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|
EMBL: A749609; CAG44557.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 94 AA; 10482 MW; 1B962F431578F69B CRC64;

Query Match 90.0%; Score 422; DB 2; Length 94;
Best Local Similarity 89.4%; Pred. No. 1.2e-33;
Matches 84; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKQPRFADHSETISOAEGHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
|
Db 1 MKQPRFADHSETISOAEGHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
|
QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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Db 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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RESULT 3
Q699R1_AERHY
ID Q699R1_AERHY PRELIMINARY; PRT; 94 AA.
AC Q699R1;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Acg.
GN Name=acrg;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpull G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
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RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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EMBL: AV528667; AAS91818.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 94 AA; 10622 MW; 99BA1C5E7B3815F5 CRC64;

Query Match 89.8%; Score 421; DB 2; Length 94;
Best Local Similarity 90.4%; Pred. No. 1.6e-33;
Matches 85; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MKQPRFADHSETISOAEGHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
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QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
|
Db 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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RESULT 4
Q5XL05_AERHY
ID Q5XL05_AERHY PRELIMINARY; PRT; 94 AA.
AC Q5XL05;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Acg.
GN Name=acrg;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
|
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EMBL: AV763611; AAV30232.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 94 AA; 10624 MW; B7C944CD55ED6C7B CRC64;

Query Match 85.3%; Score 400; DB 2; Length 94;
Best Local Similarity 83.0%; Pred. No. 1.8e-31;
Matches 78; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

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Db 1 MKQPRFADHSETISOAEGHGIADSDHRNALLQEMLAGLALSDQTCOLLFEAPTEQVAVAEQ 60
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QY 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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Db 61 ELLAEIQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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RESULT 5
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ID Q93KU3_YEREN PRELIMINARY; PRT; 95 AA.
AC Q93KU3;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
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07-FEB-2006, entry version 12.
LcrG.
Name=lcrG;
Yersinia enterocolitica.
Plasmid pYve8081, and Plasmid pYval27/90.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
NCBI_TaxID=630;
[1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=8081; PLASMID=pYve8081;
RX MEDLINE=21295118; PubMed=11402007;
RA DOI=10.1128/IAI.69.7.4627-4638.2001;
RA Snellings N.J., Popok M., Lindler L.E.;
RT "Complete DNA sequence of Yersinia enterocolitica serotype 0:8 low-
RT calcium-response plasmid reveals a new virulence plasmid-associated
RT replicon";
RL Infect. Immun. 69:4627-4638(2001).
[2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=A127/90; PLASMID=pYval27/90;
RA Foulter B.G.F., Bernard A., Purnelle B., Cornelis G.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
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EMBL; AF336309; AAK69214.1; -; Genomic_DNA.
DR EMBL; AY150843; AAN37512.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
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Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;
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Qy 60 QELLAETQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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RESULT 6
O52157_YEREN PRELIMINARY; PRT; 95 AA.
AC O52157;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE LcrG.
GN Name=lcrG;
OS Yersinia enterocolitica.
OG Plasmid pYve227.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
[1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=W22703;
RX MEDLINE=98143428; PubMed=9484897;
RA Boyd A.P., Sory M.P., Iriarte M., Cornelis G.R.;
RT "Heparin interferes with translocation of Yop proteins into Hela cells
RT and binds to LcrG, a regulatory component of the Yersinia Yop
RT apparatus";
RL Mol. Microbiol. 27:425-436(1998).
[2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=W22703;

RA Iriarte M., Lambermont I., Kerbouch C., Cornelis G.R.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
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EMBL; AF102990; AAD16816.1; -; Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
KW Plasmid.
SQ SEQUENCE 95 AA; 10961 MW; 474CB07840EABD6E CRC64;
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Best Local Similarity 42.1%; Pred. No. 1.8e-11;
Matches 40; Conservative 21; Mismatches 33; Indels 1; Gaps 1;
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Qy 60 QELLAETQRQALLPAQPGEGKRSRRPTIMRGLMI 94
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RESULT 7
LCRG_YERPE STANDARD; PRT; 95 AA.
AC P69957; P19394; Q663K8;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 04-JAN-2005, sequence version 1.
DT 07-MAR-2006, entry version 8.
DE Low calcium response locus protein G.
GN Name=lcrG; OrderedLocusNames=YPCD1.32c, Y5046, Y0049, pCD51;
OS Yersinia pestis.
OG Plasmid pCD1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
[1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=90008806; PubMed=2477361;
RA Price S.B., Leung K.Y., Barve S.S., Straley S.C.;
RT "Molecular analysis of lcrGVH, the V antigen operon of Yersinia
RT pestis";
RL J. Bacteriol. 171:5646-5653(1989).
[2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98427122; PubMed=9746557;
RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA Blattner F.R.;
RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RT Yersinia pestis KIM5";
RL Infect. Immun. 66:4611-4623(1998).
[3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
RT pestis";
RL J. Bacteriol. 180:5192-5202(1998).
[4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whithead S., Barrell B.G.,
RT "Genome sequence of *Yersinia pestis*, the causative agent of plague,"
RL Nature 413:523-527(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.,
RT "Complete genome sequence of *Yersinia pestis* strain 91001, an isolate
RT avirulent to humans,"
RL DNA Res. 11:179-197(2004).
RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-6.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=90330579; PubMed=1695896;
RA Barve S.S., Straley S.C.;
RT "lcrR, a low-Ca2(+)-response locus with dual Ca2(+)-dependent
RT functions in *Yersinia pestis*,"
RL J. Bacteriol. 172:4661-4671(1990).
CC -!- FUNCTION: Not known.
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CC -----
DR EMBL; M26405; AAA27640.1; -; Genomic DNA.
DR EMBL; AF074612; AAC69798.1; -; Genomic DNA.
DR EMBL; AF053946; AAC62573.1; -; Genomic DNA.
DR EMBL; AL117189; CAB54309.1; -; Genomic DNA.
DR EMBL; AE017043; AAS58570.1; -; Genomic DNA.
DR EMBL; M35740; AAA98220.1; -; Genomic DNA.
DR PIR; A33601; A33601.
DR GenomeReviews; AE017043 GR; pCDS1.
DR GenomeReviews; AL117189 GR; YPCD1.32c.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
KW Complete proteome; Plasmid.
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FT Low calcium response locus protein G.
FT /FTId=PRO_0000084371.
SQ SEQUENCE 95 AA; 11020 MW; 5E21543540EBF92B CRC64;
Query Match 41.7%; Score 195.5; DB 1; Length 95;
Best Local Similarity 43.2%; Pred. No. 2.3e-11;
Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;
QY 1 MKQPRFADHSETISQAEHGIAADSHRNALLQEMKLAGLSDDTCQLLFEA-PTEQVAVAE 59
Db 1 MKSSHDFEYDKTLQAEALAIADSHRAKLLQEMCADIGLTPEAVMKIFAGRSAAEIKPAE 60
QY 60 QELLAIQRQALLPAQGEGRKSRPTIMRGLMI 94
Db 61 RELLEIKRQRERQHPYDGKRPKPTMWRGQII 95
RESULT 8
LCRG_YERPS STANDARD; PRT; 95 AA.
AC P69958; P19394; Q663K8;
DT 04-JAN-2005, integrated into UniProtKB/Swiss-Prot.
DT 04-JAN-2005, sequence version 1.
DT 07-MAR-2006, entry version 7.
DE Low calcium response locus protein G.
GN Names=LCrG; OrderedLocusNames=pYV0058;
OS *Yersinia pseudotuberculosis*.
OC Plasmid pIB1, and Plasmid pYV.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Yersinia*.
OX NCBI_TaxId=633;
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RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=VEPIII / Serotype O:3; PLASMIID=pIB1;
RX MEDLINE=91154114; PubMed=1705541;
RA Bergman T., Haakansson S., Forsberg A., Norlander L., Macellaro A.,
RA Baeckman A., Boelin I., Wolf-Watz H.;
RT "Analysis of the V antigen lcrGVH-yopBD operon of *Yersinia*
RT pseudotuberculosis: evidence for a regulatory role of LcrH and LcrV,"
RL J. Bacteriol. 173:1607-1616(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP3953 / Serotype I; PLASMIID=pYV;
RX PubMed=15368858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of *Yersinia pestis* through whole-genome
RT comparison with *Yersinia pseudotuberculosis*,"
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Not known.
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DR EMBL; M57893; AAA27644.1; -; Genomic DNA.
DR EMBL; BX936399; CAF25401.1; -; Genomic DNA.
DR PIR; A37314; A37314.
DR GenomeReviews; BX936399 GR; pYV0058.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
KW Complete proteome; Plasmid.
FT CHAIN 1 95
FT Low calcium response locus protein G.
FT /FTId=PRO_0000084372.
SQ SEQUENCE 95 AA; 11020 MW; 5E21543540EBF92B CRC64;
Query Match 41.7%; Score 195.5; DB 1; Length 95;
Best Local Similarity 43.2%; Pred. No. 2.3e-11;
Matches 41; Conservative 20; Mismatches 33; Indels 1; Gaps 1;
QY 1 MKQPRFADHSETISQAEHGIAADSHRNALLQEMKLAGLSDDTCQLLFEA-PTEQVAVAE 59
Db 1 MKSSHDFEYDKTLQAEALAIADSHRAKLLQEMCADIGLTPEAVMKIFAGRSAAEIKPAE 60
QY 60 QELLAIQRQALLPAQGEGRKSRPTIMRGLMI 94
Db 61 RELLEIKRQRERQHPYDGKRPKPTMWRGQII 95
RESULT 9
Q91326_PSEAE PRELIMINARY; PRT; 98 AA.
AC Q91326;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Regulator in type III secretion.
GN Name=prg; OrderedLocusNames=PA1705;
OS *Pseudomonas aeruginosa*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; *Pseudomonas*.
OX NCBI_TaxId=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of *Pseudomonas aeruginosa* PA01, an

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RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
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DR EMBL; AE0045597; AAC05094.1; -; Genomic_DNA.
DR PIR; F83432; F83432.
DR DR BioCyc; PAER287; PAI705-MONOMER; -.
DR DR InterPro; IPR009863; LcrG.
DR DR Pfam; PF07216; LcrG; 1.
KW Complete proteome.
SQ SEQUENCE 98 AA; 10995 MW; 6B972DAE22C710FC CRC64;
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Matches 40; Conservative 15; Mismatches 28; Indels 1; Gaps 1;
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QY 71 ALLPAQPGEGKSRRTIMRGLMI 94
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RESULT 10
O30526_PSEAE
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AC O30526;
DT 01-JAN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JAN-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE PcrG.
GN Name=pcrG;
GS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=388;
RX MEDLINE=38037517; PubMed=9371466;
RA Yahr T.L., Mende-Mueller L.M., Friese M.B., Frank D.W.;
RT "Identification of type III secreted products of the Pseudomonas
RT aeruginosa exoenzyme S regulon.";
RL J. Bacteriol. 179:7165-7168(1997).
RN RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PAK;
RX MEDLINE=22830436; PubMed=12949185; DOI=10.1099/mic.0.26322-0;
RA Broms J.E., Forslund A.L., Forsberg A., Francis M.S.;
RT "Dissection of homologous translocon operons reveals a distinct role
RT for YopD in type III secretion by Yersinia pseudotuberculosis.";
RL Microbiology 149:2615-2626(2003).
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DR EMBL; AF010149; AAC45934.1; -; Genomic_DNA.
DR EMBL; AY232997; AAC01770.1; -; Genomic_DNA.
DR DR InterPro; IPR009863; LcrG.
DR DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 98 AA; 11029 MW; 619D2DA428C710FC CRC64;
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Best Local Similarity 46.4%; Pred. No. 2.2e-09;
Matches 39; Conservative 15; Mismatches 29; Indels 1; Gaps 1;
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Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
15 TVQAAELAIRDSERGLLAEMWQGLAADAGELLFQAPERELARAAEBELLAEIQRMR 74

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DR EMBL; BA000031; BAC59923.1; -, Genomic_DNA.
DR InterPro; IPR009863; LcrG.
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KW Complete proteome.
SQ SEQUENCE 94 AA; 10616 MW; 6B92B932BBD0ACA0 CRC64;

Query Match      29.3%; Score 140; DB 2; Length 94;
Best Local Similarity 36.7%; Pred. No. 6.4e-06;
Matches 36; Conservative 20; Mismatches 34; Indels 8; Gaps 3;

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Db 57 AEQELIEEVRRAQQHQHQLQGVGKRRKRPMTMRGMVI 94

RESULT 13
Q84GY6 PHOLU PRELIMINARY; PRT; 92 AA.
AC Q84GY6
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE LcrG.
GN Names=lsag;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M14;
RX MEDLINE=22454990; PubMed=12564993; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., French-Constant R.H.;
RT "Genomic islands in Photorhabdus.";
RL Trends Microbiol. 10:541-545(2002).
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CC -----
DR EMBL; AY144116; AAO18052.1; -, Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 92 AA; 10366 MW; D5204E9DD69C31F5 CRC64;

Query Match      29.3%; Score 137.5; DB 2; Length 92;
Best Local Similarity 39.1%; Pred. No. 1.1e-05;
Matches 34; Conservative 14; Mismatches 38; Indels 1; Gaps 1;

QY 9 HSETISOAEHGIADSDHRNALLQEMLAGLSDQCQLL-FAPTEQVAVAEQELLAETQ 67
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 6 NAKVLQAAEAAIKDSHRLQLQEMWQSLGINPNVGTGLFSGHADVTLAQNASEQLLTVN 65

RESULT 14
Q7NOX0 PHOLL PRELIMINARY; PRT; 92 AA.
AC Q7NOX0;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Similar to the regulator in type III secretion LcrG and PcrG.
```

```
GN OrderedLocusNames=plu3759;
OS Photorhabdus luminescens subsp. laumondii;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=225957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaut E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanols A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BX571871; CAE16131.1; -, Genomic_DNA.
DR PhotoList; plu3759; -.
DR BioCyc; PLUM243265:PLU3759-MONOMER; -.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
KW Complete proteome.
SQ SEQUENCE 92 AA; 10452 MW; 14597B7D29865921 CRC64;

Query Match      29.3%; Score 137.5; DB 2; Length 92;
Best Local Similarity 39.1%; Pred. No. 1.1e-05;
Matches 34; Conservative 14; Mismatches 38; Indels 1; Gaps 1;

QY 9 HSETISOAEHGIADSDHRNALLQEMLAGLSDQCQLL-FAPTEQVAVAEQELLAETQ 67
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 6 NAKVLQAAEAAIKDSHRLQLQEMWQSLGINPNVGTGLFSGHADVTLAQNASEQLLTVN 65

QY 68 RQALLPAQPGEGKRSRRPTIMRGLMI 94
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 66 RLRSNQPSPLEEGKRLRRPPMRGIIV 92

RESULT 15
Q6QVS1 VIBHA PRELIMINARY; PRT; 96 AA.
AC Q6QVS1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE VcrG.
GN Name=vcrG;
OS Vibrio harveyi;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Bassler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY524044; AAS13310.1; -, Genomic_DNA.
DR InterPro; IPR009863; LcrG.
DR Pfam; PF07216; LcrG; 1.
SQ SEQUENCE 96 AA; 10851 MW; 43C2BBB0CB34323A CRC64;

Query Match      27.3%; Score 128; DB 2; Length 96;
Best Local Similarity 35.0%; Pred. No. 9.9e-05;
Matches 35; Conservative 19; Mismatches 36; Indels 10; Gaps 3;

QY 1 MKQPRADHSETISOAEHGIADSDHRNALLQEMLAGLSDQCQLLFE---APTEQVAV 57
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Db 1 MKQP----FTETIENSELAIRNAEDRTDVFNELLEGLGVGPVAGNILLDGLNASPQLMKQ 56
Qy 58 AEQELLAEIQR---QALLPAQPGEGGRKSRPTIMRGLMI 94
Db 57 AEHELLEEVQRRROQHQPOAASTKGTFRKPTMMRGWVI 96

Search completed: June 16, 2006, 19:22:59
Job time : 76.8244 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 17.348 Seconds
(without alignments) 474.285 Million cell updates

Sequence: 1 MKQPRFADHSETISQAEHGI.....AQPGEGRKSRPTIMRGLMI 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	179.5	38.3	107	2	US-09-252-991A-30057	Sequence 30057, A	
2	81	17.3	1289	2	US-09-712-363-259	Sequence 259, App	
3	74.5	15.9	1179	2	US-09-107-532A-6126	Sequence 6126, Ap	
4	73.5	15.7	678	2	US-09-712-363-158	Sequence 158, App	
5	73.5	15.7	957	2	US-09-252-991A-21104	Sequence 21104, A	
6	72.5	15.5	274	2	US-09-252-991A-1989	Sequence 21989, A	
7	72.5	15.5	548	2	US-09-252-991A-20379	Sequence 20379, A	
8	71.5	15.2	402	2	US-09-252-991A-35289	Sequence 25289, A	
9	70.5	15.0	453	2	US-09-252-991A-24830	Sequence 24830, A	
10	69	14.7	452	2	US-09-252-991A-25395	Sequence 25395, A	
11	69	14.7	607	2	US-09-252-991A-26137	Sequence 26137, A	
12	68.5	14.6	875	2	US-09-252-991A-29161	Sequence 29161, A	
13	68.5	14.6	859	2	US-09-252-991A-14220	Sequence 14220, A	
14	68	14.5	186	1	US-07-960-981-5	Sequence 5, Appli	
15	68	14.5	186	5	PCT-US93-09634-5	Sequence 5, Appli	
16	68	14.5	285	2	US-09-252-991A-23737	Sequence 23737, A	
17	68	14.5	455	2	US-09-949-016-11307	Sequence 11307, A	
18	67.5	14.4	693	2	US-09-540-236-3793	Sequence 3793, Ap	
19	67	14.3	462	2	US-09-252-991A-29947	Sequence 29947, A	
20	66.5	14.2	142	2	US-09-902-540-14271	Sequence 14271, A	
21	66.5	14.2	330	2	US-09-252-991A-18311	Sequence 18311, A	
22	66.5	14.2	355	2	US-09-902-540-15046	Sequence 15046, A	
23	66	14.1	845	2	US-09-252-991A-17856	Sequence 17856, A	
24	65.5	14.0	183	2	US-09-248-796A-18172	Sequence 18172, A	
25	65.5	14.0	214	2	US-09-248-796A-18171	Sequence 18171, A	
26	65.5	14.0	258	2	US-09-252-991A-25067	Sequence 25067, A	

ALIGNMENTS

RESULT 1

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US-09-252-991A-30057
; Sequence 30057; Application US/09252991A
; Patent No. 6551795
;
; GENERAL INFORMATION:
;
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIORITY FILING DATE: 1999-02-18
; PRIORITY APPLICATION NUMBER: US 60/074,788
; PRIORITY FILING DATE: 1998-02-18
; PRIORITY APPLICATION NUMBER: US 60/094,190
; PRIORITY FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
;
; SEQ ID NO 30057
; LENGTH: 107
; TYPE: PRT
;
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30057

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	Query Match	38.3%	Score 179.5;	DB 2;	Length 107;
	Best Local Similarity	47.6%;	Pred. No. 1.3e-15;		
	Matches	40;	Conservative 15;	Mismatches 28;	Indels 1; Gaps 1;
Qy	12	TISCAHGIIADSHRNALLOEMLAGIALSDOTCOLFEAPTEQVA-VAECELLAEIQRQ	70		
Db	24	TVQAELAIRDSERGLFLAEMQGILAADAGELLFQAPERELARAAEEELAELRMR	83		
Qy	71	ALLPAQFGEGKRRRPTIMRGLMI	94		
Db	84	SSOPTGEOGTTPRRPPTPMREGLLI	107		

RESULT 2

```

RES0011-2
US-09-712-363-259
; Sequence 259, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712.363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246

```

```

; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 1289
; TYPE: PRI
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-259

Query Match 17.3%; Score 81; DB 2; Length 1289;
Best Local Similarity 30.1%; Pred. No. 0.27; Indels 28; Gaps 3;
Matches 31; Conservative 12; Mismatches 32;

QY 5 RFADHSETISQAEHGADSDHRNALQEMLAGL-ALS---DQTCQLL----- 47
Db 345 RLAVASEELAAHSAVAELSTRAESIHTWFGLSALAEVRDATVRIASERAHLDIEPVA 404

QY 48 -----FPAPTEQVAVAEQELLAEIQRQALLPQPG 79
Db 405 VSDTPRKPPELEAEQAQVAVAEQELLAEIQRQALLPQPG 79

RESULT 3
US-09-107-532A-6126
; Sequence 6126, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007

```

```

; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1179
; SEQUENCE DESCRIPTION: SEQ ID NO: 6126:
US-09-107-532A-6126

Query Match 15.9%; Score 74.5; DB 2; Length 1179;
Best Local Similarity 39.2%; Pred. No. 1.7;
Matches 20; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

QY 19 GIADSDHRNALQEMLAGLSDDTCQLLFPAPTEQVAVAEQELLAEIQR 69
Db 12 GNGKKDHRQVLIDEASAWLD-QDASNQVFLVPNYSKFEEQEI LAEMRR 61

RESULT 4
US-09-712-363-158
; Sequence 158, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 678
; TYPE: PRI
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-158

Query Match 15.7%; Score 73.5; DB 2; Length 678;
Best Local Similarity 40.4%; Pred. No. 1.1;
Matches 19; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

QY 48 FPAPTEQVAVAEQELLAEIQRQALL-PAQPGEGKRSRPTIMRG 93
Db 172 FDKPVEQLTVAECALLAIRRPSTLDPVDFEGAHARNWVLDGMV 218

```

[illegible]

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; Sequence 24830, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24830
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24830

Query Match 15.0%; Score 70.5; DB 2; Length 453;
Best Local Similarity 30.0%; Pred. No. 1.5;
Matches 27; Conservative 10; Mismatches 32; Indels 21; Gaps 3;

QY 5 RFAD--HSETISOAEHGIA-----DSDHRNALLQEMLAGLALSDQTCQLLFEAPTEQV 55
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 211 RVADVVAAEQVEAAEHRIAGRGQQPEQGRGAILVEGVADF-----LPVEIL 258
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 56 AVAQELLAEIQRQALLPAQPGEGRKSR 85
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 259 HQEOQHQRDQHEERQGPQAPAPVRAARR 288
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 10
US-09-252-991A-25395
; Sequence 25395, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25395
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25395

Query Match 14.7%; Score 69; DB 2; Length 452;
Best Local Similarity 29.0%; Pred. No. 2.4;
Matches 29; Conservative 10; Mismatches 31; Indels 30; Gaps 4;

QY 1 MKQPRFADHSETISOAEHGIA-----SDH--RNALLQEMLAGLALSDQTCQLL---- 47
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 98 LRDSRVAQHGETQAEAGTGTGRFQAGYLVAHLLRQARRQRRRAALAKDFQKAQHVAGA 157
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 48 -----FEAPTEQVAEQELLAEIQRQALLP 74
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 158 ADHPRPAGRIGRRFEGPTREANAD-----AVLERRHGLPP 193
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 11
US-09-252-991A-26137
; Sequence 26137, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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```
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26137
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26137

Query Match 14.7%; Score 69; DB 2; Length 607;
Best Local Similarity 23.5%; Pred. No. 3.5;
Matches 23; Conservative 18; Mismatches 39; Indels 18; Gaps 3;

QY 7 ADHSETISOAEHGIAADSDHRNALLQEMLAGLALSDQTCQLLFEAPTEQVAQVAEQL---- 62
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 355 AEYLRLLVDQFEQGLGVAERNRHQAQARMGLQGQFQRRGMLPG---QLQVADQHLHRRFG 411
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 63 -----LAEIQRQALLPAQPGEGRKSRRTIMRGLMI 94
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 412 VOPHRLQGVARAQQAMPAGMAEG-----PDAVQGRV 444
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 12
US-09-252-991A-29161
; Sequence 29161, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29161
; LENGTH: 675
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29161

Query Match 14.6%; Score 68.5; DB 2; Length 675;
Best Local Similarity 29.5%; Pred. No. 4.7;
Matches 26; Conservative 12; Mismatches 29; Indels 21; Gaps 4;

QY 2 KOPR--FADHSETISOAEHGIAADSDHRNALLQEMLAGLALSDQTCQLLFEAPTEQVAQVAE 59
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 415 RHPRHRHFAPHASAAGDAQGDA-----TVVHQRFAGLAVADQ-----QLAQVR 457
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 60 QELLAEIQR--RQALLPAQPGEGRKSR 85
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 458 RRIAAEGPRGTLEQCLAGQCGEGGLLR 485
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 13
US-09-902-540-14220
; Sequence 14220, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```


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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 52.5789 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-7
Perfect score: 469
Sequence: 1 MKQPRFADHSETISQAEHGI.....AQPGEGRKRRPTIMRGLMI 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US07_PUBCOMB.pbp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pbp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pbp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10A_PUBCOMB.pbp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pbp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469	100.0	94	5	US-10-813-908-7
2	88.5	18.9	232	4	US-10-425-114-37773
3	81	17.3	1289	3	US-09-712-363-259
4	81	17.3	1289	4	US-10-282-122A-64805
5	79.5	17.0	211	3	US-09-925-297-777
6	76.5	16.3	1104	5	US-10-732-923-1294
7	76	16.2	323	4	US-10-116-255-23
8	75.5	16.1	177	4	US-10-282-122A-63970
9	74.5	15.9	204	4	US-10-425-114-41502
10	74.5	15.9	1175	4	US-10-282-122A-57712
11	73.5	15.7	364	4	US-10-389-566-2283
12	73.5	15.7	364	5	US-10-732-923-17917
13	73.5	15.7	364	6	US-11-188-298-3185
14	73.5	15.7	384	4	US-10-282-122A-64971
15	73.5	15.7	678	3	US-09-712-363-158
16	73.5	15.7	678	4	US-10-282-122A-64334
17	73.5	15.7	822	4	US-10-282-122A-62677
18	72.5	15.5	102	4	US-10-425-115-228565
19	72.5	15.5	1162	4	US-10-369-493-13727
20	72	15.4	754	4	US-10-437-963-103758
21	72	15.4	897	4	US-10-425-115-236512
22	72	15.4	1220	5	US-10-732-923-1294
23	71	15.1	149	4	US-10-424-599-176461
24	71	15.1	344	4	US-10-767-701-41882
25	71	15.1	369	4	US-10-425-115-340472
26	70.5	15.0	91	4	US-10-424-599-158968
27	70.5	15.0	943	6	US-11-097-143-13047

28	70	14.9	274	4	US-10-425-115-224142	Sequence 224142,
29	70	14.9	310	6	US-11-087-099-11274	Sequence 11274, A
30	70	14.9	360	6	US-11-087-099-11236	Sequence 11236, A
31	70	14.9	564	4	US-10-425-114-67912	Sequence 67912, A
32	69.5	14.8	180	4	US-10-437-963-172642	Sequence 172642,
33	69.5	14.8	314	4	US-10-425-115-207227	Sequence 207227,
34	69.5	14.8	360	4	US-10-282-122A-68181	Sequence 68181, A
35	69.5	14.8	417	4	US-10-437-963-144004	Sequence 144004,
36	69.5	14.8	1699	4	US-10-437-963-177020	Sequence 177020,
37	69	14.7	352	4	US-10-437-963-172825	Sequence 172825,
38	69	14.7	739	4	US-10-425-115-224132	Sequence 224132,
39	68.5	14.6	164	4	US-10-195-730-328	Sequence 328, App
40	68.5	14.6	164	4	US-10-799-747-328	Sequence 328, App
41	68.5	14.6	164	5	US-10-979-183-328	Sequence 328, App
42	68.5	14.6	182	5	US-10-820-474A-97	Sequence 97, Appl
43	68.5	14.6	220	4	US-10-425-114-68161	Sequence 68161, A
44	68.5	14.6	373	4	US-10-424-599-158968	Sequence 158968,
45	68.5	14.6	440	5	US-10-450-763-33072	Sequence 33072, A

ALIGNMENTS

RESULT 1

US-10-813-908-7
; Sequence 7, Application US/10813908
; Publication No. US2005005862A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and
; FILE REFERENCE: MIC01/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813,908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
US-10-813-908-7

Query Match	100.0%;	Score 469;	DB 5;	Length 94;
Best Local Similarity	100.0%;	Pred. No. 4.3e-47;		
Matches	94;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	MKQPRFADHSETISQAEHGIADSDHRNALLQELMAGLALSDQTCQLLFEAPTEQVAVAEQ	60	
Db	1	MKQPRFADHSETISQAEHGIADSDHRNALLQELMAGLALSDQTCQLLFEAPTEQVAVAEQ	60	
Qy	61	ELLAETORRQALLPAQPGEGKRSRRPTIMRGLMI	94	
Db	61	ELLAETORRQALLPAQPGEGKRSRRPTIMRGLMI	94	

RESULT 2

US-10-425-114-37773
; Sequence 37773, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37773
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700421759_FLI.pep
US-10-425-114-37773

Query Match      18.9%; Score 88.5; DB 4; Length 232;
Best Local Similarity 31.1%; Pred. No. 0.074;
Matches 28; Conservative 14; Mismatches 35; Indels 13; Gaps 2;

QY 4 PFADHSG-----ETISQAEHGIADSDHNRNLLQEMLAGLSDOTCOLLFEAPTEQV 55
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 28 PRFAPGDDRRCPCLQVSGGCHLQSPFHEHNVLPEDA-----DGAAGVFGDLSAV 82
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 56 AVAEQELLAIEIQRQALLPAQPGEGKRSR 85
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 RFSEERGEAEARRGRVPVVRGRRRR 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
US-09-712-363-259
; Sequence 259, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 259
; LENGTH: 1289
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-259

Query Match      17.3%; Score 81; DB 3; Length 1289;
Best Local Similarity 30.1%; Pred. No. 5;
Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3;

QY 5 RFADHSETISQAEHGIADSDHNRNLLQEMLAGL-ALS-----DOTCQLL----- 47
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 RLVAASEELAAHSAVAELSTRAESIQTHTWFGLSALAEVDTVRIASERAHHLDTPEVA 404
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 48 -----PEAPTEQVAVAEQELLAEIQRQALLPAQPG 79
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 VSDTPRKPPELEAEAAQVVAEQELLAEALDAARLDAARAE 447
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-925-297-777
; Sequence 777, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
```

```
RESULT 4
US-10-282-122A-64805
; Sequence 64805, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64805
; LENGTH: 1289
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64805

Query Match      17.3%; Score 81; DB 4; Length 1289;
Best Local Similarity 30.1%; Pred. No. 5;
Matches 31; Conservative 12; Mismatches 32; Indels 28; Gaps 3;

QY 5 READHSETISQAEHGIADSDHNRNLLQEMLAGL-ALS-----DOTCQLL----- 47
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 345 RLVAASEELAAHSAVAELSTRAESIQTHTWFGLSALAEVDTVRIASERAHHLDTPEVA 404
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 48 -----PEAPTEQVAVAEQELLAEIQRQALLPAQPG 79
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 VSDTPRKPPELEAEAAQVVAEQELLAEALDAARLDAARAE 447
      ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
US-09-925-297-777
; Sequence 777, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
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; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 777
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (137)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-777

Query Match      17.0%; Score 79.5; DB 3; Length 211;
Best Local Similarity 31.0%; Pred. No. 0.75;
Matches 35; Conservative 12; Mismatches 39; Indels 27; Gaps 4;

QY  2 KQRFADHSETISQAEHGIADSDHRNAL-----LQEML-----AGLAL 39
Db  27 KSKQFLDMETIDQREEMAKSRASAARVGKLOEALNERHSIINALKAKIQMTFAALAL 86
QY  40 SDQTCQLLFEAPTRQVAVAEOLLAETORQALLPAQPGEGKRSRRPTIMRGL 92
Db  87 SEKAQADL-----GELLATAEQEQLSLSORAKELKLEQEEAAE-RESKLLRDL 134

RESULT 6
US-10-732-923-1294
; Sequence 1294, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1294
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-732-923-1294

Query Match      16.3%; Score 76.5; DB 5; Length 1104;
Best Local Similarity 29.4%; Pred. No. 14;
Matches 30; Conservative 11; Mismatches 32; Indels 29; Gaps 5;

QY  4 PRF-----ADHSETISQAEHGIADSDHRNALQEMLAGLALSDQTCQLLFEAPTRQVA 56
Db  228 PRFHGIRFPSTVHTQTLRRYQGI-----LSGLML-DLMKNLLLNPTERY- 272
QY  57 VAEOL-----LAEITORQALLPAQPGEGKRSRRPTIMRG 91
Db  273 LTEQSLNHPAFQPLQRVERERPAPPASPNNPPRSKRKTHHG 314

RESULT 7
US-10-116-255-23
; Sequence 23, Application US/10116255
; Publication No. US20030036646A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Uncoupling Protein Polynucleotides, Polypeptides, and
```

```
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT009P1
; CURRENT APPLICATION NUMBER: US/10/116,255
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/685,897
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09534
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,701
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 60/142,821
; PRIOR APPLICATION NUMBER: 60/149,448
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 60/164,751
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-255-23

Query Match      16.2%; Score 76; DB 4; Length 323;
Best Local Similarity 30.0%; Pred. No. 3.3;
Matches 24; Conservative 14; Mismatches 30; Indels 12; Gaps 3;

QY  18 HGTADSDHRNALQEMLAGLALSDQTCQLLFEAPTRQVAV-----AEQELLAEIQR 68
Db  92 HQSKGQCKUTLUKEMLAGGCAG--TCQVITTPMEMLKITQLQDAGRIAAQRKILAAQGG 149
QY  69 RQALLPAQPG-EGRKSRPT 87
Db  150 LSAQGGAGQPSVEAPAPRPT 169

RESULT 8
US-10-282-122A-63970
; Sequence 63970, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63970
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-282-122A-63970

Query Match          16.1%; Score 75.5; DB 4; Length 177;
Best Local Similarity 32.8%; Pred. No. 1.8;
Matches 22; Conservative 12; Mismatches 28; Indels 5; Gaps 2;

Qy 9 HSETISQAEHGTDSDHRNALQEMLAGLSDQTCOLLFEAPTEQVAVAEQELAEIQR 68
Db 113 HPMTVAEVER-IADLESREVLLAKLAGAMKGTFAKAIGLFNAPTQMA---RLTAALQE 167

Qy 69 QOALLPA 75
Db 168 KKAPEPA 174

RESULT 9
US-10-425-114-41502
; Sequence 41502, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53)1313B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41502
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3078-002-H8_FLI.pep
US-10-425-114-41502

Query Match          15.9%; Score 74.5; DB 4; Length 204;
Best Local Similarity 30.8%; Pred. No. 2.8;
Matches 16; Conservative 12; Mismatches 15; Indels 9; Gaps 1;

Qy 37 LALSQTCOLLFEAPTEQVAVAEQELAEIQRQALLPAQCGCKSRPTI 88
Db 14 MAIAGQSSCVYTSFTLQ-----QLQRHSHLPQQAARRRRPRL 56

RESULT 10
US-10-282-122A-57712
; Sequence 57712, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeelbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

```

D6

59 AIAEGPLAGDLAR--TLSSGAGEGQKA 84

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RESULT 14
US-10-282-122A-64971
; Sequence 64971, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64971
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64971

Query Match      15.7%   Score 73.5; DB 4; Length 384;
Best Local Similarity 40.4%; Pred.No. 8.2;
Matches    19; Conservative     9; Mismatches    18; Indels    1; Gaps    1;

Qy      48 FEAPTOVAEAEELLAEATRRQALL-PAQPEGKRSRPTINRGLM 93
       |:|::|||::|||::|||::|||::|||::|||::|||::|:
Db      204 FDKPEVQLTVAEGALLAALIRPSTLDPADVDEGAHARNWVDGMV 250

RESULT 15
US-09-712-363-158
; Sequence 158, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
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; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-158

Query Match      15.7%  Score 73.5; DB 3; Length 678;
Best Local Similarity 40.4%  Pred. No. 17;
Matches 19; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

Qy      48 FEAPTEQVAVAGQELLAEIQRRQALL-PAQPGEGKSRRTIMRGILM 93
      | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      172 FDKPVSQLTVAEGALLAALIRRPSTLDPAVDPEGAHARNWNWLDGMV 218

Search completed: June 16, 2006, 20:24:56
Job time : 54.5789 secs

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; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48872
; LENGTH: 417
; TYPE: prt
; ORGANISM: Oryza sativa
US-10-449-902-48872

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Query Match      14.7%; Score 69; DB 6; Length 277;
Best Local Similarity 26.7%; Pred.No. 2.6;
Matches 28; Conservative 15; Mismatches 36; Indels 26; Gaps 5;
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Qy	7	ADHSETI-SQAEGHIASDRNALQEWLAGLALSDOTC-----LLFPAETQVAVA	58
		: : : : : : : : :	
Db	147	ADAEEITMQSGTQEPVAEGDHSRDAMQGNAGQA--STCSMSBQGAITYSSMTEQIATA	203

Qy	59	EQELLARIQR-QALLPAQP-----GGRKSRRPPI	88
		: : : : : : : : : : :	
Db	204	SSSMTGWRSREAAFLCSRPMISTALPEPFWKAGEYSVAOPTI	248

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; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 439
; TYPE: PRN
; ORGANISM: HUMAN
US-11-242-111-25
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Query Match	14.4%	Score	67.5;	DB	6;	Length	226;
Best Local Similarity	27.7%;	Pred.	No. 3;				
Matches	18;	Conservative	18;	Mismatches	26;	Indels	3; Gaps
							1;
Qy	9	HSETISQAEGHGIADSDHRNALLQEMLAGLALSQSOTCOLLFAPTEQVAVAEQLLAELQR	68				
		::::: :::	:	:	:	:	:
Dd	137	HNKMLEAKHGSRSEETKK--YQEEIGALNEDMKKLQVQEKTEEVEHVVAEDKALAIRKQ	193				
		::::: :::	:	:	:	:	:
Qy	69	RQALL	73				
		::					
Dd	194	SESLL	198				

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RESULT 6
US-10-505-928-784
; Sequence 784, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2

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```
; SEQ ID NO 784
; LENGTH: 2671
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-784

Query Match      14.1%; Score 66; DB 6; Length 2671;
Best Local Similarity 27.5%; Pred. No. 76;
Matches 22; Conservative 16; Mismatches 40; Indels 2; Gaps 1;

Qy 10 SETISOAEHGIADSDHNRNALLQEMLAGLALSDQTCQLLFEAPTEQVAVAEQELLAEIQ 67
Db 1746 NEKIFQESIGLAHLLDGGNTEIQSFHNLMMSDKKSERFFKVLHDKMKRAQQETKTVA 1805

Qy 68 RQALLPAQPGEGKRRRPT 87
Db 1806 VNMNDLGSQPHEDREPVDPT 1825

RESULT 7
US-10-449-902-52171
; Sequence 52171, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52171
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-52171

Query Match      14.0%; Score 65.5; DB 6; Length 618;
Best Local Similarity 27.8%; Pred. No. 16;
Matches 25; Conservative 14; Mismatches 36; Indels 15; Gaps 5;

Qy 10 SETISOAEHGIADSDHNRNALLQEMLAGLALSDQTCQLLFEAPTEQVAVAEQEL----- 62
Db 253 SRNVSPLUHGGNSEH-----QETVGDVADQNPFIHTL-ETPPEDTTPNQSEIHRGSIK 306

Qy 63 LAETQRQALLPAQPGEGR-KSRPTTMRG 91
Db 307 LA-VDKSNALSPSQGKHGRGKNKQPSKRG 335

RESULT 8
US-10-449-902-35865
; Sequence 35865, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
```

```
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35865
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35865

Query Match      13.8%; Score 64.5; DB 6; Length 234;
Best Local Similarity 27.5%; Pred. No. 6.5;
Matches 19; Conservative 16; Mismatches 29; Indels 5; Gaps 2;

Qy 9 HSTISOAEHGIADSDHNRNALLQ-----EMLAGLALSDQTCQLLFEAPTEQVAVAEQELLA 64
Db 5 HSAEILDG-HNVADFLDPDILQRCBELREGLRLEEEAAQEAQFIDGHTELTEQREILG 63

Qy 65 EIQRQALL 73
Db 64 QIRKKALL 72

RESULT 9
US-10-449-902-35269
; Sequence 35269, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35269
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-35269

Query Match      13.5%; Score 63.5; DB 6; Length 394;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 31; Conservative 7; Mismatches 44; Indels 11; Gaps 4;

Qy 3 QPRFADHSETISOAEHGIADSDH--RNALLQEMLAGLALSDQTCQLLFEAPTEQ-----VA 56
Db 185 QRPFDHQLSYNGNETKILSLERPLRFADFAARLAGLAGSPGDFCVKYQLPGEDLALVS 244

Qy 57 VABQE-----LLAFIQRQALLPAQPGEGKRRR 85
Db 245 VTNDEDLHLVLEYDRLHLRPA-PGSGGSSR 276

RESULT 10
US-11-293-697-4145
; Sequence 4145, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
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Db 105 SRTIPACNAVVDNSTNSRLIERLSAFQGLDNLRL-----PATPQALLEALGSNGA 160
Qy 60 --QELLAEIQRQALLPAQPGEGRKSRPTIMR 90
Db 161 TGSEAVAAAEKHAALLTARAGARDPSAVPSICR 193

RESULT 15
US-10-449-902-40851
; Sequence 40851, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40851
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-40851

Query Match 13.4%; Score 63; DB 6; Length 431;
Best Local Similarity 27.5%; Pred. No. 19;
Matches 19; Conservative 15; Mismatches 27; Indels 8; Gaps 2;
Qy 18 HGIADSHRNALLQEMLAGLSQTCQLLFEAPTEQVAV-AEQELLAEIQRQALLPAQ 76
Db 271 HPSSDSYRDSILSRVHPGISMVD-----ERAVDRVGYRRELDLRDEERRDLLERE 323
Qy 77 PGEGRKSRR 85
Db 324 KERDRER 332

Search completed: June 16, 2006, 20:25:53
Job time : 4.05041 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 239.199 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-8
Perfect score: 1816
Sequence: 1 MSTIPDNTNPGAFVGLDV.....ALNRFQKYDSIMRDILGAI 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*1: Geneseqp1980s:.*
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3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*
10: Geneseqp2006s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	361	5	ABB80776
2	625	34.4	307	6	ABM69448
3	560	30.8	349	9	ADY73654
4	557	30.7	326	9	ADY73655
5	557	30.7	326	9	ADZ97834
6	557	30.7	326	9	AE09748
7	557	30.7	326	10	AEF93450
8	557	30.7	329	2	AAR79961
9	557	30.7	329	2	AAW01041
10	557	30.7	329	2	AAW01040
11	557	30.7	478	9	AE09750
12	557	30.7	501	2	AAW01044
13	554	30.5	329	2	AAR79962
14	554	30.5	480	2	AAW01045
15	474	26.1	297	7	ABO81312
16	253	13.9	142	2	AAZ29686
17	253	13.9	142	5	AAU93812
18	253	13.9	142	7	ADE10800
19	253	13.9	142	7	ADM33705
20	253	13.9	142	8	ADG63900
21	253	13.9	142	8	ADP73435
22	253	13.9	142	8	ADR12727
23	129	7.1	459	8	ADO15316

24	129	7.1	2013	4	ABB62322	Abb62322 Drosophil
25	127	7.0	367	3	AAB05956	Aab05956 Protein d
26	127	7.0	646	7	ADF06555	Adf06555 Bacterial
27	127	7.0	2539	8	ADU25430	Adu25430 L. acidop
28	125	6.9	643	6	ABU40893	Abu40893 Protein e
29	124	6.8	1254	2	AAR07503	Aar07503 Merozoite
30	124	6.8	1254	2	AAW24575	Aaw24575 Merozoite
31	121.5	6.7	1196	6	ABU24813	Abu24813 Protein e
32	121	6.7	366	5	ABB84782	Abb84782 DNA polym
33	121	6.7	366	8	ADJ67914	Adj67914 T. mariti
34	121	6.7	366	8	ADJ68126	Adj68126 T. mariti
35	121	6.7	366	8	ADK01204	Adk01204 DNA polym
36	121	6.7	366	8	ADJ79423	Adj79423 T. mariti
37	121	6.7	366	8	ADJ84863	Adj84863 T. mariti
38	121	6.7	366	8	ADM77651	Adm77651 DNA polym
39	121	6.7	366	8	ADM66318	Adm66318 T. mariti
40	121	6.7	366	8	ADO04371	Ado04371 T. mariti
41	121	6.7	366	8	ADP82448	Adp82448 Thermotog
42	121	6.7	366	8	ADS15655	Adsi15655 T. mariti
43	121	6.7	366	9	ADY55146	Ady55146 T. mariti
44	121	6.7	366	9	ADZ76722	Adz76722 T. mariti
45	121	6.7	366	9	AEA24730	Aea24730 Thermotog

ALIGNMENTS

RESULT 1
ABB80776
ID ABB80776 standard; protein; 361 AA.
XX
AC ABB80776;
XX
DT 23-SEP-2002 (first entry)
XX
DE A. salmonicida type III secretion protein acrV sequence.
XX
KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;
KW acrV; acrH; antibiotic; vaccine; fish.
XX
OS Aeromonas salmonicida.
XX
PN WO2002040514-A2.
XX
PD 23-MAY-2002.
XX
PF 15-NOV-2001; 2001WO-CA001589.
XX
PR 15-NOV-2000; 2000US-0248864P.
XX
(FREY/) FREY J.
(STUB/) STUBER K.
PA (THOR/) THORNTON J C.
PA (KUZU/) KUZYSK M A.
PA (BUR/) BURIAN J.
XX
PI Frey J, Stuber K, Thornton JC, Kuzyk WA, Burian J;
XX WPI: 2002-537338/57.
DR N-PSDB; ABN86172.
XX
PT Novel protein from Aeromonas salmonicida and nucleic acid encoding the
PT protein, useful for reducing susceptibility of fish to infection by a
PT virulent strain of Aeromonas salmonicida.
XX
PS Claim 13; Page 28-29; 39pp; English.
XX
CC The invention relates to A. salmonicida type III secretion genes and
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.
CC A. salmonicida type III secretion apparatus is useful for producing
CC selected products, especially Aext. AcrV in vaccine, epitope or epitopic
CC region of AcrV or any other protein of A. salmonicida type III secretion
CC apparatus is useful for reducing the susceptibility of fish to infection

CC by a virulent strain of A. salmonicida. The proteins and encoding DNA are
CC useful for manufacturing a diagnostic agent. Detecting the presence of
CC the genes of AcrD, AcrV or any other components of the A. salmonicida type
CC III secretion apparatus is useful for the production or quality control
CC or efficacy of vaccines made from A. salmonicida or its genes. The present
CC sequence represents the A. salmonicida type III secretion protein acrv
XX
XX

SQ Sequence 361 AA;
Query Match 100.0%; Score 1816; DB 5; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.1e-135;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTIPDYNTPGAFVGVLDVQALNTLPGNKNPKLTVELLKGKTIISADSTALSKEQL 60
DB 1 MSTIPDYNTPGAFVGVLDVQALNTLPGNKNPKLTVELLKGKTIISADSTALSKEQL 60
QY 61 EKLLAAYLTPASINGWANGQFKGGQDAIAAIAKGVIERGAKOTPPVTHWTIPEFMLLS 120
DB 61 EKLLAAYLTPASINGWANGQFKGGQDAIAAIAKGVIERGAKOTPPVTHWTIPEFMLLS 120
QY 121 LSALTWERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
DB 121 LSALTWERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NQTFKTNFNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQQDFTNAKNELENTV 240
DB 181 NQTFKTNFNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQQDFTNAKNELENTV 240
QY 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFLSDLLKSGAMSGIEAEYKYDKD 300
DB 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFLSDLLKSGAMSGIEAEYKYDKD 300
QY 301 NNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDSIMRDILGA 360
DB 301 NNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDSIMRDILGA 360
QY 361 I 361
DB 361 I 361

RESULT 2
ABM69448
ID ABM69448 standard; protein; 307 AA.
AC ABM69448;
XX
XX 20-NOV-2003 (first entry)
DE Photorhabdus luminescens protein sequence #2545.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.
XX
OS Photorhabdus luminescens.
XX
PN WO200294867-A2.
XX
XX 28-NOV-2002.
XX
XX 07-FEB-2002; 2002WO-IB003040.
XX
XX 07-FEB-2001; 2001FR-00001659.
XX
XX (INSP) INST PASTEUR.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX

DR WPI; 2003-148459/14.
XX
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
XX Claim 2; SEQ ID NO 2545; 1205pp; French.
XX
XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins
XX
XX Sequence 307 AA;
Query Match 34.4%; Score 625; DB 6; Length 307;
Best Local Similarity 41.8%; Pred. No. 3.7e-41;
Matches 151; Conservative 47; Mismatches 101; Indels 62; Gaps 6;
QY 4 IPDYNTPGAFVGVLDVQALNTLPGNKNPKLTVELLKGK-ITISADSTAL-SKEQLE 61
DB 5 IRPYQNDPOLFLADLEKVSQAQLOGSGSELDRNLIPDKIGIKITSDSVVTENKELLK 64
QY 62 KLLAAYLTPASINGWANGQFKGGQDAIAAIAKGVIERGAKOTPPVTHWTIPEFMLLSL 121
DB 65 KLIAYFLPADAVVEGGHLDQIKNG-----INNLESFLNSSTLTK-----WTUKDFLAAVH 115
QY 122 SALTWERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAASN 181
DB 116 FNLTPDLDDDDVIDIFVSVMSGHDKKRLRLDELATLTAEIKIYGVIOSEINAKLAANGE 175
QY 182 QTFKTN-FNLMDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQQDFTNAKNELENTV 240
DB 176 LKIDDNSFNLLDHHKKYGFSDQPTFEKSAEYKLLRKISSGSE----- 216
QY 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFLSDLLKSGAMSGIEAEYKYDKD 300
DB 217 -----ISITKFLSSNKGSGAMGLNSYEYDK 245
QY 301 NNKLGNFSTVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIOKYDSIMRDILGA 360
DB 246 NNRLANFSTVSDRVSPLNNTVQKTRLNNEASSRYNAIAEALNRFIOKYDSIIRNILGA 305
QY 361 I 361
DB 306 I 306
RESULT 3
ADY73654
ID ADY73654 standard; protein; 349 AA.
XX
XX AC ADY73654;
XX
XX 02-JUN-2005 (first entry)
XX
XX Yersinia pestis tPA/V antigen construct.

XX V antigen; immune stimulation; tissue plasminogen activator; tPA;
KW Yersinia pestis infection; antibacterial; vaccine; gene therapy.
XX
OS Yersinia pestis.
OS Synthetic.
XX WO2005023205-A2.
PN
XX
PD 17-MAR-2005.
XX
XX 08-MAR-2004; 2004WO-US007190.
XX PF
XX 07-MAR-2003; 2003US-0452657P.
XX PR
XX (UYMA-) UNIV MASSACHUSETTS.
XX PA
XX Lu S, Goguen JD, Wang S;
XX PI
XX WPI; 2005-223254/23.
DR N-PSDB; ADY73643.
XX
XX New polynucleotide comprising a nucleic acid encoding a signal sequence
PT and a second nucleic acid encoding a Yersinia pestis antigen polypeptide,
PT useful in preparing a composition for treating Yersinia pestis infection.
XX
XX Disclosure; SEQ ID NO 12; 79pp; English.
XX
XX This invention describes a novel fusion construct comprising a tissue
CC plasminogen activator (tPA) fused to a nucleic acid that encodes a
CC Yersinia pestis antigen polypeptide, selected from V, Fl, Pla, YopB,
CC YopD, YopE or YscF antigen polypeptide. The invention also describes 1)
CC an expression vector containing the construct; 2) a cell comprising the
CC construct; 3) a process for producing a Yersinia pestis antigen
CC polypeptide; 4) a composition comprising the construct, preferably a
CC multimeric V antigen; 5) a kit comprising the construct; 6) a modified
CC Yersinia pestis antigen polypeptide sequence linked to a signal sequence
CC sufficient for secretion from a cell; 7) a method of inducing a
CC protective immune response in a mammal and 8) an isolated immunoglobulin
CC that specifically binds to a modified Yersinia pestis antigen polypeptide
CC or its fragment. The signal sequence is sufficient for secretion, however
CC when expressed in a cell, the polynucleotide produces a Yersinia pestis
CC antigen polypeptide that is free of the signal sequence. The isolated
CC polynucleotide is useful in preparing a composition for treating Yersinia
CC pestis infection. This sequence represents the tPA/V antigen construct.
XX
XX Sequence 349 AA;
Query Match 30.8%; Score 560; DB 9; Length 349;
Best Local Similarity 37.5%; Pred. No. 6.5e-36;
Matches 139; Conservative 61; Mismatches 107; Indels 64; Gaps 9;
QY 2 STIPDYNTPGAFVGLDVOALNTLPGNKPKLTVELLKGK-ITIS-----ADSTTA 54
DB 23 SMIRAYEQNFHIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKSEVF 82
QY 55 LSK-----EQLEKLLAAYLTDPASINGWAMQFGKGDAAIAAIGKVIERGAKQTTPPV 108
DB 83 ANRVITDDIELLKKILAYFLPEDAILKGHYDNLQNG----IKRVKEFLE-----SSPN 133
QY 109 THWTIPFLLLSALTNWERTDDDLITFTFGVMFQDNQRKGRDELAEATKELKYGVI 168
DB 134 TQWELRAFMAVMHFSLTADRIDDDILKVIIVDSNMHHGDARSKLRELAELTAEIKYSVI 193
QY 169 QSEINOVLSAASN-QTFKTFNFMIDYKLYGVESLAKFMEGGEFKLLSKMFSDDQVTKAQ 227
DB 194 QAEINKHLSGGTINIHDKSINLMKMLYGTDEEIPKAAEYKILEKM---PQTT----- 246
QY 228 DFTNAKNELENVTSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLTKLESDLKSGA 287
DB 247 -----IQVDGS-----EKKIVSIKDFLGSNKETGA 272
QY 288 MSGIEABYKYDKNNKLCNFTSVSDRSRPRNLNVSEKTLARLNDVSRNNAEALNRFI 347

DB 273 LGNLKNSYSYNKONNELSHFATTCSDKSRPLNDLVSKTTQLSDITSRFRNSAIEALNRFI 332
QY 348 QKYDSIMRDIL 358
DB 333 QKYDSVMQRL 343
RESULT 4
ADY73655
ID ADY73655 standard; protein; 326 AA.
XX
AC ADY73655;
XX
XX 02-JUN-2005 (first entry)
XX
DE Yersinia pestis V antigen.
XX
XX V antigen; immune stimulation; Yersinia pestis infection; antibacterial;
KW vaccine; gene therapy.
XX
OS Yersinia pestis KIM.
XX
XX WO2005023205-A2.
PN
XX 17-MAR-2005.
XX
XX 08-MAR-2004; 2004WO-US007190.
XX
XX 07-MAR-2003; 2003US-0452657P.
XX
XX (UYMA-) UNIV MASSACHUSETTS.
XX
XX Lu S, Goguen JD, Wang S;
XX WPI; 2005-223254/23.
DR N-PSDB; ADY73644.
XX
XX New polynucleotide comprising a nucleic acid encoding a signal sequence
PT and a second nucleic acid encoding a Yersinia pestis antigen polypeptide,
PT useful in preparing a composition for treating Yersinia pestis infection.
XX
XX Claim 3; SEQ ID NO 13; 79pp; English.
XX
XX This invention describes a novel fusion construct comprising a tissue
CC plasminogen activator (tPA) fused to a nucleic acid that encodes a
CC Yersinia pestis antigen polypeptide, selected from V, Fl, Pla, YopB,
CC YopD, YopE or YscF antigen polypeptide. The invention also describes 1)
CC an expression vector containing the construct; 2) a cell comprising the
CC construct; 3) a process for producing a Yersinia pestis antigen
CC polypeptide; 4) a composition comprising the construct, preferably a
CC multimeric V antigen; 5) a kit comprising the construct; 6) a modified
CC Yersinia pestis antigen polypeptide sequence linked to a signal sequence
CC sufficient for secretion from a cell; 7) a method of inducing a
CC protective immune response in a mammal and 8) an isolated immunoglobulin
CC that specifically binds to a modified Yersinia pestis antigen polypeptide
CC or its fragment. The signal sequence is sufficient for secretion, however
CC when expressed in a cell, the polynucleotide produces a Yersinia pestis
CC antigen polypeptide that is free of the signal sequence. The isolated
CC polynucleotide is useful in preparing a composition for treating Yersinia
CC pestis infection. This sequence represents the Yersinia pestis V antigen.
XX
XX Sequence 326 AA;
Query Match 30.7%; Score 557; DB 9; Length 326;
Best Local Similarity 37.4%; Pred. No. 1e-35;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;
QY 7 YNTNPGAFVGLDVOALNTLPGNKPKLTVELLKGK-ITIS-----ADSTLASK-- 57
DB 5 YEQNPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKSEVFANRVI 64
QY 58 -----EQLEKLLAAYLTDPASINGWAMQFGKGDAAIAAIGKVIERGAKQTTPVTHWTI 113

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Db      65  TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSPNTQWEL 115
QY      114  PEFMLLSLALTWERTDDDLITFTTGMVPMQDNORGLRDELAEMLTAELKIYGVIOSEIN 173
Db      116  RAFMAVMHFLSTADRIDDDILKIVVDSMNHGARGSKJRELAELTAELKIYSVIOAEIN 175
QY      174  QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKWFSDEQVTKAQDPTNA 232
Db      176  KHLSSSGTINIHKSNLMDKNLYGYTDEEIFKASAEYKILEKM---PQTT----- 223
QY      233  KNELENVTSLSNPKIQAEAKTDYERKKAIFEBIVETQIITLTFLESDLKKSGAMSGIE 292
Db      224  -----IQVDGS-----EKKIVSIKDFLGSENKRTGALGNLK 254
QY      293  ABEYKDKNNKLNKFNSTSVSDRSRPLNDLVSEKTAELNDVSSRYNAALNRFIQKYS 352
Db      255  NSYSYNKNNELSHFATTCDSKRPLNDLVSKTQLSDITSRFSNAIEALNRFIQKYS 314
QY      353  IMRDIL 358
Db      315  VMQRL 320

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RESULT 5
ADZ97834
ID ADZ97834 standard; protein; 326 AA.
XX
AC ADZ97834;
XX
DT 28-JUL-2005 (first entry)
XX
DE Amino acid sequence for Yersinia pestis V-antigen.
XX
KW monoclonal antibody; antibody production; antibody therapy;
KW virulence antigen; V-antigen; yersinia pestis infection; infection;
KW antibacterial; vaccine; epitope mapping.
XX
OS Yersinia pestis.
XX
FH Key Location/Qualifiers
FT Region 2..135
FT /note= "Mildly protective sequence identified by prior
FT art"
FT Peptide 4..18
FT /note= "tryptic peptide binding tightly to mAb 84-1.
FT Given as SEQ ID No:3 in the specification and
FT specifically claimed in Claim 26"
FT Region 135..245
FT /note= "Mildly protective sequence identified by prior
FT art"
FT Peptide 166..176
FT /note= "tryptic peptide binding tightly to mAb 141-1.
FT Given as SEQ ID No:2 in the specification and
FT specifically claimed in Claim 25"
XX
PN WO2005047309-A2.
XX
PD 26-MAY-2005.
XX
PF 12-NOV-2004; 2004WO-US038480.
XX
PR 12-NOV-2003; 2003US-0519384P.
XX
PA (USSA ) US ARMY MEDICAL RES INST INFECTIOUS DISE.
XX
PI Chanh TC, Andrews GP, Adamovic JJ, Powell BS;
XX WPI; 2005-372342/38.
XX
DR New monoclonal antibody, useful for preventing and treating Yersinia
PT pestis infection, specifically pneumonic plague infection.
XX
XX

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PS Example 6; SEQ ID NO 1; 43pp; English.
XX
CC The invention relates to monoclonal antibodies (mAb) against the
CC virulence antigen (V-antigen) of Yersinia pestis, where the antibody
CC protects against an aerosol challenge with Y. pestis. Also described are:
CC (1) an antibody which competes with the antibody above for binding to Y.
CC pestis V-antigen; (2) a composition comprising one or more antibodies
CC selected from an antibody produced by hybridomas 74-1, 84-1, 125-1, or
CC 141-1, or comprising one or more antigenic peptide epitopes recognized by
CC any monoclonal antibody, e.g. mAb 74-1, mAb 84-1, mAb141-1, or mAb 124-1;
CC (3) a therapeutic composition, for ameliorating symptoms of Y. pestis
CC infection, comprising the composition of (2); a passive vaccine against
CC pneumonic plague infection comprising the composition of (2); (4) a
CC prophylactic composition, for reducing severity of Y. pestis infection,
CC comprising the composition of (2); (5) a hybridoma selected from 74-1, 84
CC -1, 125-1, or 141-1; (6) a method for detecting, in a sample, Y. pestis;
CC and (7) a method of treating Y. pestis infection. The antibody,
CC composition, and methods are useful for preventing and treating Y. pestis
CC infection, specifically pneumonic plague infection. This sequence
CC represents Y. pestis V-antigen to which monoclonal antibodies are
CC generated.
XX
SQ Sequence 326 AA;
Query Match 30.7%; Score 557; DB 9; Length 326;
Best Local Similarity 37.4%; Pred. No. 1e-35;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;
QY 7 YNTNPGAFVGLDVOALNTLPGNKNPKLTVELVLLKGGK-ITIS-----ADSTALSK-- 57
Db 5 YEQNPPQHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDEVFANRVI 64
QY 58 ----EOLEKLLAAYLTDPASINGHAMGQFKGGQDAIAAIKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSPNTQWEL 115
QY 114 PEFMLLSLALTWERTDDDLITFTTGMVPMQDNORGLRDELAEMLTAELKIYGVIOSEIN 173
Db 116 RAFMAVMHFLSTADRIDDDILKIVVDSMNHGARGSKJRELAELTAELKIYSVIOAEIN 175
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKWFSDEQVTKAQDPTNA 232
Db 176 KHLSSSGTINIHKSNLMDKNLYGYTDEEIFKASAEYKILEKM---PQTT----- 223
QY 233 KNELENVTSLSNPKIQAEAKTDYERKKAIFEBIVETQIITLTFLESDLKKSGAMSGIE 292
Db 224 -----IQVDGS-----EKKIVSIKDFLGSENKRTGALGNLK 254
QY 293 ABEYKDKNNKLNKFNSTSVSDRSRPLNDLVSEKTAELNDVSSRYNAALNRFIQKYS 352
Db 255 NSYSYNKNNELSHFATTCDSKRPLNDLVSKTQLSDITSRFSNAIEALNRFIQKYS 314
QY 353 IMRDIL 358
Db 315 VMQRL 320
RESULT 6
AEB09748
ID AEB09748 standard; protein; 326 AA.
XX
AC AEB09748;
XX
DT 25-AUG-2005 (first entry)
XX
DE Yersinia pestis V antigen.
XX
KW vaccine; yersinia pestis infection; V antigen; growth; antibacterial.
XX
OS Yersinia pestis.
XX
WO2005056769-A2.
XX

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23-JUN-2005.

09-DEC-2004; 2004WO-US041282.

09-DEC-2003; 2003US-0528140P.

02-APR-2004; 2004US-059259P.

22-MAY-2004; 2004US-0573517P.

16-SEP-2004; 2004US-061047P.

(AVAN-) AVANT IMMUNOTHERAPEUTICS INC.

Sizemore D, Tinge SA, Killen KP;

WPI; 2005-435585/44.

N-PSDB; AEB09747.

New live vaccine composition comprising live attenuated serovar of Salmonella enterica, useful for protecting against plague.

Example 4; SEQ ID NO 4; 50pp; English.

The invention relates to a live vaccine composition, for protecting against plague, comprising a live attenuated bacterium that is a Typhimurium serovar of Salmonella enterica. The vaccine composition comprises an attenuating mutation in a genetic locus of the chromosome of the bacterium that attenuates virulence of the bacterium and where the attenuating mutation is not a single mutation in a gene that encodes a protein that is essential for the synthesis of an aromatic compound and is not a single mutation in a gene for galactose utilization, a lethal mutation in a genetic locus in the chromosome of the bacterium where the lethal mutation prevents expression from the genetic locus of a protein that has an activity that is essential for cell wall synthesis of the bacterium, and an antigen-expressing, multi-copy plasmid comprising: (1) a nucleotide sequence coding for an immunogenic polypeptide comprising a Yersinia pestis V antigen, an immunogenic portion of the V antigen, a Y. pestis F1 antigen, an immunogenic portion of the F1 antigen, or their combination, where the nucleotide sequence is operably linked to a promoter that permits intracellular expression of the immunogenic polypeptide from the plasmid, (2) a gene encoding a protein that has an activity that is essential for cell wall synthesis, where expression of the protein is essential for cell wall synthesis complements the lethal mutation in the chromosome of the bacterium and thus permits growth of the bacterium, and (3) an origin of replication that permits multiple copies of the plasmid to be maintained in the bacterium, where the live vaccine composition elicits an immune response to one or more Y. pestis antigens when administered orally to an individual. The live vaccine composition is administered to an individual by swallowing from the mouth, by a nasogastric tube, by a gastrostomy tube, or by a suppository. The live vaccine composition is useful for protecting an individual against plague. The strains of S. enterica serovar Typhimurium stated above are useful for manufacturing a live vaccine composition to protect against plague. This sequence represents Yersinia pestis V antigen.

Sequence 326 AA;

Query Match
Best Local Similarity 30.7%; Score 557; DB 9; Length 326;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

7 YNTNPGAFVGLWDVQALNTLPNGKNPKLTVELLKGK-ITIS-----ADSTALS-- 57

5 YEONPHQFIEDLEKRVVEQLTGHGSSVLDELVOLVKDKNDISIKYDPRKDSEVPANRVI 64

58 ----EOLKLLAAYLTDPAISINGWAMGFQGGQDAATAAIKGVIERGAKQTPTTHWTI 113

65 TDDEILKKILAYFLPEDAILKGGHVDNLONG----IKRVKEFLE-----SSPNQWEL 115

114 PEFMLLSALTMTERTDDLIITFTGWMMFNQRKRLDELAEATMALKYGVIOBSIN 173

116 RAFPVAWHFSLTADRIDDILKVIVDSMMHGGAASKULEELAEILTAEKIYSVLQASIN 175

174 QVLSAAASN-QTFKTNFNLMDYKLKYGESIAKMEGGEFKLLSKMFSDSQVTKAQQODFTNA 232

176 KHLSSGTINIHDKSINLMDNLYGYTDEEIFKASAAYKILEKM---POTT----- 222

233 KNLENVTSTSLNPKIQAQEAKTDERKKAIFEIEIVETQIIITLKTFLESDLKKSGAMSGIE 292

224 -----IQVDS-----EKIVSIKDFLGSENKRTGALCNLK 352

293 AEYKYDKNNKLNFGSTVSRSRPLNDLVSEKTAERLNDVSRYNAAIEALNRFIQKYDS 352

255 NSYSYNKDNNELSHFATTSCDKSRPLNDLVSOQTTLSDITSFRNSAIEALNRFIQKYDS 314

353 IMRDIL 358

315 VMORLL 320

RESULT 7

AEF93450

ID AEF93450 standard; protein; 326 AA.

XX AC AEF93450;

XX DT 20-APR-2006 (first entry)

XX DE Y. pestis F1 capsule antigen (Caf1).

XX KW gram-neg. bacterium; outer surface protein; pharmaceutical; vaccine;

XX KM F1 capsule antigen; Caf1.

XX OS Yersinia pestis.

XX FN WO2006014292-A2.

XX PD 09-FEB-2006.

XX PF 30-JUN-2005; 2005WO-US023106.

XX PR 02-JUL-2004; 2004US-0585057P.

XX PA (DATT/) DATTWYLER R J.

XX PA (GOME/) GOMES-SOLECKI M.

XX PI Dattwyler RJ, Gomes-Solecki M;

XX DR WPI; 2006-145890/15.

XX PT New composition comprising a bacterium engineered to express at least one outer surface protein of Borrelia burgdorferi, useful for immunizing a subject against Borrelia burgdorferi infections.

XX PS Disclosure; SEQ ID NO 18; 95pp; English.

XX CC The invention relates to a composition comprising a bacterium engineered to express at least one outer surface protein of Borrelia burgdorferi, selected from OspA or OspC antigens. It is especially useful as an oral vaccine composition also containing a food carrier or an excipient. The oral vaccine composition comprises a bacterium selected from Escherichia coli, and Lactobacillus plantarum. The bacterium is lyophilized. The food carrier comprises a dairy product selected from milk, yogurt, and cheese, or a grain product selected from grain, seed, bread, and cereal. The excipient is selected from a sugar, a starch, a gum, and a protein. The food carrier comprises animal chow. The composition is useful for immunizing a subject against Borrelia burgdorferi infections. The present sequence represents a Y. pestis F1 capsule antigen (Caf1).

XX SQ Sequence 326 AA;

Query Match
Best Local Similarity 30.7%; Score 557; DB 10; Length 326;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

7 YNTNPGAFVGLWDVQALNTLPNGKNPKLTVELLKGK-ITIS-----ADSTALS-- 57

5 YEONPHQFIEDLEKRVVEQLTGHGSSVLDELVOLVKDKNDISIKYDPRKDSEVPANRVI 64

58 ----EOLKLLAAYLTDPAISINGWAMGFQGGQDAATAAIKGVIERGAKQTPTTHWTI 113

65 TDDEILKKILAYFLPEDAILKGGHVDNLONG----IKRVKEFLE-----SSPNQWEL 115

114 PEFMLLSALTMTERTDDLIITFTGWMMFNQRKRLDELAEATMALKYGVIOBSIN 173

116 RAFPVAWHFSLTADRIDDILKVIVDSMMHGGAASKULEELAEILTAEKIYSVLQASIN 175

174 QVLSAAASN-QTFKTNFNLMDYKLKYGESIAKMEGGEFKLLSKMFSDSQVTKAQQODFTNA 232

KW		antibacterial; fusion protein; muten.
XX		
OS		Yersinia pestis.
QS		Synthetic.
XX		
PN		WO2005056769-A2.
XX		
PD		23-JUN-2005.
XX		
PF		09-DEC-2004; 2004WO-US041282.
XX		
PR		09-DEC-2003; 2003US-0528140P.
PR		02-APR-2004; 2004US-0559259P.
PR		22-MAY-2004; 2004US-0573517P.
PR		16-SEP-2004; 2004US-0610474P.
XX		
PA	(AVAN-) AVANT IMMUNOTHERAPEUTICS INC.	
XX		
PI	Sizemore D, Tinge SA, Killeen KP;	
XX		
DR	WPI; 2005-435585/44.	
DR	N-PSDB; AEB09749.	
XX		
PT	New live vaccine composition comprising live attenuated serovar of	
PT	Salmonella enterica, useful for protecting against plague.	
XX		
PS	Example 2; SEQ ID NO 6; 50pp; English.	
XX		
CC	The invention relates to a live vaccine composition, for protecting	
CC	against plague, comprising a live attenuated bacterium that is a	
CC	Typhimurium serovar of Salmonella enterica. The vaccine composition	
CC	comprises an attenuating mutation in a genetic locus of the chromosome of	
CC	the bacterium that attenuates virulence of the bacterium and where the	
CC	attenuating mutation is not a single mutation in a gene that encodes a	
CC	protein that is essential for the synthesis of an aromatic compound and	
CC	is not a single mutation in a gene for galactose utilization, a lethal	
CC	mutation in a genetic locus in the chromosome of the bacterium where the	
CC	lethal mutation prevents expression from the genetic locus of a protein	
CC	that has an activity that is essential for cell wall synthesis of the	
CC	bacterium, and an antigen-expressing, multi-copy plasmid comprising: (1)	
CC	a nucleotide sequence coding for an immunogenic polypeptide comprising:	
CC	Yersinia pestis V antigen, an immunogenic portion of the V antigen, a Y.	
CC	pestis F1 antigen, an immunogenic portion of the F1 antigen, or their	
CC	combination, where the nucleotide sequence is operably linked to a	
CC	promoter that permits intracellular expression of the immunogenic	
CC	polypeptide from the plasmid, (2) a gene encoding a protein that has an	
CC	activity that is essential for cell wall synthesis, where expression of	
CC	the protein essential for cell wall synthesis complements the lethal	
CC	mutation in the chromosome of the bacterium and thus permits growth of	
CC	the bacterium, and (3) an origin of replication that permits multiple	
CC	copies of the plasmid to be maintained in the bacterium, where the live	
CC	vaccine composition elicits an immune response to one or more Y. pestis	
CC	antigen when administered orally to an individual. The live vaccine	
CC	composition is administered to an individual by swallowing from the	
CC	mouth, by a nasogastric tube, by a gastrostomy tube, or by a suppository.	
CC	The live vaccine composition is useful for protecting an individual	
CC	against plague. The strains of S. enterica serovar Typhimurium stated	
CC	above are useful for manufacturing a live vaccine composition to protect	
CC	against plague. This sequence represents Yersinia pestis FI-V antigen	
CC	fusion protein.	
XX		
SQ	Sequence 478 AA;	
	Query Match 30.7%; Score 557; DB 9; Length 478;	
	Best Local Similarity 37.4%; Pred. NO. 1.7e-35;	
	Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9	
QY	7 YNTNPGAFGWLGDVQALNTLPGKNKPKLTVELLVLLKGK-ITIS-----ADSTALS-- 57	
Dd	157 YEQNPOHFTEDLEKVRVQLTGHGSSVLEEVLQVLVKDKNIDISIKYDPKXDSVFANRV 216	
QY	58 ----EQLEKLAAAYLTDPASINGGWAMQGFKGGDAAIAAKGVIERGAQTPTPVTHWT 113	

Example 3; Page 65-69; 98pp; English.

A fusion protein (AAW01044) comprises the F1 antigen (see also AAW01043) and V antigen (see also AAW01041) of Yersinia pestis joined by a linker that allows each protein to attain its conformational state. It is the product of a gene fusion (AAT38249) obtd. by PCR amplification of Y. pestis DNA. Fl/V fusion protein can be expressed by gut-colonising organism transforants, to induce an immune response against Y. pestis, CC the causative organism of plague

XX
PS
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

Sequence 501 AA;
Query Match 30.7%; Score 557; DB 2; Length 501;
Best Local Similarity 37.4%; Pred. No. 1.8e-35;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

QY 7 YNTNPGAFVGLDVOALNTLPGNKPKLTVELLLAGK-ITIS-----ADSTALS-K-- 57
DB 180 YEONPOHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPKDSSEVFANRVI 239
QY 58 ----EOLKLLAAYLTPASINGGWAMGQFKGGODAAIAAIKGVIERGAKOTPPVTHWTI 113
DB 240 TDDIELLKILAYFLPEDAILKGGHYDNQLQNG----IKRVKEFLE-----SSPNTQWEL 290
QY 114 PEFMLLSALTMTERTDDDLITFTGVMMFDNQKGLRDELAEIMTAELKIYGVIOSEIN 173
DB 291 RAFMAVMHFSLTADRIDDILKVIVDSMNHHGDARSLRELAELTAEELKIYSVIOAEIN 350
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGESLAKMEWGGEFKLLSKMFSDSQVTKAQQDFNA 232
DB 351 KHLSSSGTINIHDENINLMNDKNLYGYTDDEIFKASAEYKILEKM---POTT----- 398
QY 233 KNELENVTSTSLNPKIQAERAKTYERKKAIFEIEVETQIITLTKTFLESCLKKSAMSGIE 292
DB 399 -----IQVDGS-----EKIVISKDFLGSENKRTGALGNLK 429
QY 293 AEKYKDNNKLGNFSTSVSDRSRLNDLVSEKTLARNLDVSSRYNAALRNRIQKYDS 352
DB 430 NSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDS 489
QY 353 IMRDIL 358
DB 490 VMQRLL 495

RESULT 13
AAR79962
ID AAR79962 standard; protein; 329 AA.
XX
XX
XX
DT 18-APR-1996 (first entry)
DE Partial LcrV (V antigen) of Y. pestis.
XX
XX
XX
OS LcrV; V antigen; virulence; plaque; vaccine; epitope.
OS Yersinia pestis.
PN WO9524475-A1.
XX
PD 14-SEP-1995.
XX
XX
PF 06-MAR-1995; 95WO-GB000481.
XX
PR 08-MAR-1994; 94GB-00004577.
XX
XX (MINA) UK SEC FOR DEFENCE.
XX
XX Titball RW, Williamson ED, Leary SE;
XX
XX WPI; 1995-328268/42.
DR N-PSDB; AAT04223.

Recombinant DNA expressing Yersinia pestis V antigen - useful in oral or parenteral vaccines for protection against plague.
Claim 6; Page 15-16; 25pp; English.
XX
CC AAR79961-62 are encoded by AAT04222-23 (resp.), DNA sequences (lcrv) encoding all or a protective epitopic part of the mature V protein of Yersinia pestis. The protein was expressed as a fusion protein with maltose binding protein or glutathione-S-transferase in 3 different plasmid vectors. Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. The V antigen (lcrv) is an unstable 37.3 kDa monomeric peptide encoded on the ca. 70 kb lcr plasmid. The V antigen is postulated to act as a virulence antigen, and transformed microorganisms contg. recombinant DNA encoding a V antigen protein/peptide are useful in vaccines to protect against plague

XX
SQ
Sequence 329 AA;
Query Match 30.5%; Score 554; DB 2; Length 329;
Best Local Similarity 37.2%; Pred. No. 1.8e-35;
Matches 136; Conservative 62; Mismatches 104; Indels 64; Gaps 9;

QY 7 YNTNPGAFVGLDVOALNTLPGNKPKLTVELLLAGK-ITIS-----ADSTALS-K-- 57
DB 8 YEONPOHFIEDLEKVRVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPKDSSEVFANRVI 67
QY 58 ----EOLKLLAAYLTPASINGGWAMGQFKGGODAAIAAIKGVIERGAKOTPPVTHWTI 111
DB 68 TDDIELLKILAYFLPEDAILKGGHYDNQLQNG----IKRVKEFLE-----SSPNTQWEL 111
QY 114 PEFMLLSALTMTERTDDDLITFTGVMMFDNQKGLRDELAEIMTAELKIYGVIOSEIN 173
DB 119 RAFMAVMHFSLTADRIDDILKVIVDSMNHHGDARSLRELAELTAEELKIYSVIOAEIN 173
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGESLAKMEWGGEFKLLSKMFSDSQVTKAQQDFNA 233
DB 179 KHLSSSGTINIHDENINLMNDKNLYGYTDDEIFKASAEYKILEKM---POTT----- 222
QY 233 KNELENVTSTSLNPKIQAERAKTYERKKAIFEIEVETQIITLTKTFLESCLKKSAMSGIE 295
DB 227 -----IQVDGS-----EKIVISKDFLGSENKRTGALGNLK 251
QY 293 AEKYKDNNKLGNFSTSVSDRSRLNDLVSEKTLARNLDVSSRYNAALRNRIQKYDS 353
DB 258 NSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIQKYDS 311
QY 353 IMRDIL 358
DB 318 VMQRLL 323

RESULT 14
AAW01045
ID AAW01045 standard; protein; 480 AA.
XX
XX
AC AAW01045;
XX
DT 28-DEC-1996 (first entry)
XX
DE Y. pestis Fl/V antigen fusion.
XX
KW Plaque; vaccine; genetic immunisation; V antigen; lcrv; F1 antigen; cagl
XX
OS Yersinia pestis; strain GB.
OS Synthetic.
OS Chimeric.
FH Key Location/Qualifiers
FT Protein 1..149
FT /label= F1_antigen
FT /note= "mature F1 antigen"
FT Peptide 150..155

```
FT FT /label= Linker
FT FT /note= "6-amino acid peptide linker"
FT FT 156 480
FT FT /label= V_antigen
FT FT /note= "mature V antigen"
XX XX
PN WO9628551-A1.
XX PN
PD 19-SEP-1996.
XX PD
XX 13-MAR-1996; 96WO-GB000571.
XX PF
XX 13-MAR-1995; 95GB-00005059.
XX PR
XX 15-SEP-1995; 95GB-00018946.
XX PR
XX 05-DEC-1995; 95GB-00024825.
XX PR
XX (MINA ) UK SEC FOR DEFENCE.
XX PA
XX
XX Titball RW, Williamson ED, Leary SEC, Oyston PCF, Bennett AM;
XX PN
XX WPI; 1996-433824/43.
XX DR
XX N-PSDB; AAT38256.
XX DR
XX
XX Yersinia pestis V antigen and F1 antigen or their protective epitopic
XX FT parts - useful in vaccine for protection against plague.
XX FT
XX PS Disclosure; Page 51-55; 98pp; English.
XX CC
XX A fusion protein (AAW01045) comprises the F1 antigen (see also AAW01042)
XX CC and V antigen (see also AAW01041) of Yersinia pestis joined by a linker
XX CC that allows each protein to attain its conformational state. It is the
XX CC product of a gene fusion (AAT38256) obtd. by PCR amplification of Y.
XX CC pestis DNA. F1/V fusion protein can be expressed by gut-colonising
XX CC organism transformants, to induce an immune response against Y. pestis,
XX CC the causative organism of plague
XX CC
XX SQ Sequence 480 AA;
Query Match 30.5%; Score 554; DB 2; Length 480;
Best Local Similarity 37.2%; Pred. No. 3e-35;
Matches 136; Conservative 62; Mismatches 104; Indels 64; Gaps 9;
QY 7 YNTNPGAFVGLVDQALNTLPNGNPKLTTELVELLKGK-ITIS-----ADSGTALSK-- 57
Db 159 YEQNPHQFIEDLEKRVQEQTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSVFNARVI 218
QY 58 -----EOLEKLLAAYLTDPASINGGWAMGQFKGGQDAIAAIAKGVIRGAKQTPPVTHWTI 113
Db 219 TDDIELLKKILAYFLPEDAILKGHYDNLQNG-----IKRVKEFL-----SSPNTQWEL 269
QY 114 PEFMLLSLSALTMTERTDDDLITTTFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSETN 173
Db 270 RAPMAVHFSLTADRIDDDLKLVIVDSMMHGDARSKREELAEALTAEUKIYSVIOAEIN 329
QY 174 QVLSAASN-QTEKTNFNLMDYKLYGYESLAKMEGGEFKLLSKMFSDEQVTKAQDFTNA 232
Db 330 KHLSSSGTINIHDKSINLMDKNLYGYTDEEIFKASAEYKILEKM-----PQT----- 377
QY 233 KNELENTVSTSLNPKIQAEAKTDYERKKAIFEIVETQIITKTFLFESLKKSGAMSGIE 292
Db 378 -----IQVDGS-----EKKIVSKNDFLGSNKRTGALGNL 408
QY 293 AEYKDKNNKLNFGSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALARFIQKYDS 352
Db 409 NSYSYNKDNNELSHFATTCSDKSRPLNDLVSQKTTQVSDITSRFSNAIEALARFIQKYDS 468
QY 353 IMRDIL 358
Db 469 VMQRLL 474
RESULT 15
AB081312
```

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ID AB081312 standard; protein; 297 AA.
XX AC
XX AB081312;
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polypeptide #13487.
XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX OS Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX XX (GENO-) GENOME THERAPEUTICS CORP.
XX XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX DR N-PSDB; ABD14883.
XX XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX XX
XX PS Disclosure; SEQ ID NO 30058; 455pp; English.
XX CC
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-P. aeruginosa drugs, as templates for recombinant
XX CC production of P. aeruginosa-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of P. aeruginosa-caused
XX CC infection, and in detection of P. aeruginosa sequences or other sequences
XX CC of Pseudomonas species using biochip technology. Sequences AB067826-
XX CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html
XX SQ Sequence 297 AA;
Query Match 26.1%; Score 474; DB 7; Length 297;
Best Local Similarity 36.0%; Pred. No. 3.5e-29;
Matches 118; Conservative 50; Mismatches 94; Indels 66; Gaps 7;
QY 36 ELVELLKGKITISADSSTALSKEOLEKLLAAYLTDPASINGGWAMGQFKGGQDAIAAIAK 95
Db 34 ELALLRSERIVLAHAGQPLSEAQVLKALAWLLAANPSAPPG-----QGLEVLR 82
QY 96 GVIERGAKQTPPVTHWTIPEFMLLSLSALTMTERTDDDLITTTFTGVMMFQDNQKGLRDEL 155
Db 83 EVLQ---ARRQPGAGMDREFLVSAFSL-HCRLEDVIGVYKDVLTQDGRKALLDEL 138
QY 156 AEMTAELKIYGVIOSEINQVLSAASNQTFKT-NFNLMYKLYGYE-SLAKFMEGGEFKLL 213
Db 139 KALTAELKVYSIQSQINAALSAKQIRIDAGGIDLVDPPTLYGYAVGDPWRKDSPEYALL 198
QY 214 SKMFSDEQVTKAQDFTNAKNELENTVSTSLNPKIQAEAKTDYERKKAIFEIVETQIIT 273
Db 199 SNL-----DTFSGK-----LS 209
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Search completed: June 16, 2006, 19:06:40
Job time : 243.199 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 36.687 Seconds
(without alignments)
946.773 Million cell updates/sec

Title: US-10-813-908A-8
Perfect score: 1916
Sequence: 1 MSTIPDYNTPGAPVGMGLDV.....ALNRFIQKYSIMRDILGAI 361
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	564	31.1	326	B37314	regulatory protein
2	556	30.6	326	B33601	lcrV protein - yer
3	474	26.1	294	G83432	type III secretion
4	133.5	7.4	624	PC6003	surface membrane p
5	129	7.1	841	A86188	hypothetical prote
6	128.5	7.1	1939	T18372	repeat organellar
7	124	6.8	1252	B42771	reticulocyte-bind
8	123.5	6.8	2269	T28677	rhostry protein -
9	121.5	6.7	2166	G70163	hypothetical prote
10	121	6.7	366	E72400	DNA polymerase III
11	121	6.7	616	G82885	hypothetical prote
12	121	6.7	629	A29666	keratin, 65k type
13	121	6.7	1302	JC6009	surface-located me
14	120.5	6.6	995	T27327	hypothetical prote
15	120	6.6	628	A82889	hypothetical prote
16	120	6.6	1736	F86178	hypothetical prote
17	119.5	6.6	1312	EWBYDL	RAD50 protein - ye
18	119	6.6	1025	E86355	hypothetical prote
19	119	6.6	2116	A26655	myosin heavy chain
20	119	6.6	4919	T31105	hypothetical prote
21	118.5	6.5	1098	B70232	hypothetical prote
22	118	6.5	2052	C97038	phage-related prot
23	117.5	6.5	478	E43599	toxin apixid secret
24	117.5	6.5	880	F75103	conserved hypothet
25	117.5	6.5	982	I64232	protein p115 homol
26	117.5	6.5	1268	D33411	botulinum neurotox
27	117	6.4	935	T51930	kinesin (imported)
28	116	6.4	390	H64603	probable aspartate
29	116	6.4	581	S63183	CNM1 protein - yea

30 116 6.4 1170 2 A56157 chromosome segrega
31 115.5 6.4 1751 2 A45604 major blood-stage
32 115 6.3 1271 2 D64237 hypothetical prote
33 114.5 6.3 864 2 B90395 purine NTPase [imp
34 114.5 6.3 1127 2 T28317 ORF MSV156 hypothe
35 114.5 6.3 2017 1 A36014 myosin heavy chain
36 114.5 6.3 2057 2 S61477 myosin II heavy ch
37 114 6.3 1005 2 A64465 hypothetical prote
38 114 6.3 1279 2 G86684 probable pil prote
39 113.5 6.2 461 2 S23420 unknown protein, 7
40 113.5 6.2 555 2 C96667 hypothetical prote
41 113 6.2 781 2 F90547 p115 protein homol
42 113 6.2 982 2 S73741 hypothetical prote
43 113 6.2 1718 2 T31638 giantin - human
44 113 6.2 3225 2 I52300 B. subtilis negati
45 112.5 6.2 571 2 AC1637

ALIGNMENTS

RESULT 1
B37314
regulatory protein lcrV - Yersinia pseudotuberculosis
C;Species: Yersinia pseudotuberculosis
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C;Accession: B37314
R;Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.; Macellaro, A.; Baeckman, A.;
J. Bacteriol. 173, 1607-1616, 1991
A;Title: Analysis of the V antigen lcrGVH-yopBD operon of Yersinia pseudotuberculosis:
A;Reference number: A37314; MUID:91154114; PMID:1705541
A;Accession: B37314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <BER>
A;Cross-references: UNIPROT:P23994; UNIPARC:UPI000012E2BC; GB:M57893; NID:g155456; PIDN

Query Match 31.1%; Score 564; DB 2; Length 326;
Best Local Similarity 37.7%; Pred. No. 9.7e-28;
Matches 138; Conservative 59; Mismatches 105; Indels 64; Gaps 8;
QY 7 YNTNPGAFVGLDVOALNTLPGNKNPKLTVELLKGK-ITIS-----ADSTALSK-- 57
Db 5 YEQNPQHFTEDLEKVRVEQLTGHGSSVLEELVQLVKRKNIDISIKYDPRKDSVFANRVI 64
QY 58 ----EQLKLAAYLTDPASINGWAMGQFKGQDAAIAIKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKILAYFLPEDAILKGHYDNLQNG-----IKRVKEFL-----SSPNTQWEL 115
QY 114 PEFMLLSALTMTERTDDDLITFTTGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEIN 173
Db 116 RAFMAVHFSLTADRIDDDILKVIYVDSMNHGDKSLREELAEALTAELKIYSVIOAEIN 175
QY 174 QVLSAASN-QTFKTNFNLMDYKLYGYESLAKFMWEGEFKLLSKMFSDEQVTKAQQFTNA 232
Db 176 KHLSSGGTINIHKDSINLMDKQLYGTDEEIFKASAEYKILEKM---POTT----- 223
QY 233 KNELENVTSNLNPKIQAEAKTDYERKKAIFEIVETQIITLTFLFESLDLKKSGAMSGIE 292
Db 224 -----IQGETEKKIVSKNFLESEKRTGALGNLK 254
QY 293 AEYKYDKNNKLGNFSTSVSDSRPLNDLVSEKTAFLNDVSSRYNAIAEALNRFIOKYS 352
Db 255 DSVSYNKNDELNSHPATTCDSKSRPLNDLVSQKTTQLSDITSRFNSAIEALNRFIOKYS 314
QY 353 IMRDIL 358
Db 315 VMQRL 320
RESULT 2
B33601
lcrV protein - Yersinia pestis plasmid pCD1

Db 49 TNPVSTLISELTSKSDSKNSITNSSNKSNDIETANTTELKQALAKANTDKQAQADNLARSTK 108
QY 58 BOLEK-----LLAAYLTD-----PASINGGWAMQFGGQDAA 90
Db 109 EQLNKSISANTLLAKLTKDNTIQQAQTELEKEVQKQANQAVASNTTASMQSAKSSLDAA 168
QY 91 IAAIKGVIE-----RGAK-QTPPPVTHWTIPFEMLLS-----LSALTWERTDDDLIT 135
Db 169 VTEITKKLETNKKDAKFKELQOQTRKNIDFINTKPNPNYSBELISQLTSKRDSKNSVT 228
QY 136 TFTGVMMFQ-----DNQRGLRDE-----LAEMT----- 159
Db 229 NSSNKSNDIETANTTELKQALAKANTDKQAQADNLAKSAKEQLNNSVSSANTLLAKLTKDNT 288
QY 160 ---AELKIYGVIOSEINQVLSAANSQTKTNFNLMDYK-----YGVESLAKPME- 206
Db 289 IQQAQTELEKEVQ-KANQAVASNTTASMQSAKSSLDAAVTEITKKLETFFNKDKAKFKEL 347
QY 207 -----GGEFKLSKMFSDSQVTKAQQDFTNAKNELENTVTSU-- 244
Db 348 EOTRKDIDEFIKQIENDPQTKKNYQNVINKLKKAEKNSITFSGNKEIQDANKSLQDE 407
QY 245 --NPKIOAEAKTDYERKKAIFEEIVETQIITLTKTFLESDLKKSGAMSGIEAEYKYDKDN 302
Db 408 LNNAKIYKGGITDFNSKKQLEDIKT-----DDAKVGT-----TEADTILDHYKN 454
QY 303 KLGNFSTSVSRPLNDLVSEKTLARLNDVS-----SRYNAAIBALNRFI 347
Db 455 -----ISDASK-NEEIKQATQKINDIKKIIETKIQEKKNRNEFSQFEQIKNELQSF 504
QY 348 -----QKYDSIMEDI 357
Db 505 NKLDKQKYNISRTKI 520

RESULT 5
A86188
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86188
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Chin, C.W.; Hughes, B.; Huizar, L.
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-841 <STO>
A:Cross-references: UNIPROT:023037; UNIPARC:UPI00000AABE8; GB:AE005172; NID:G2388564; PI
C:Genetics:
A:Map position: 1

Query Match 7.1%; Score 129; DB 2; Length 841;
Best Local Similarity 19.7%; Pred. No. 2.5;
Matches 70; Conservative 75; Mismatches 138; Indels 72; Gaps 13;
QY 33 KTELVELLKGKITISADSSFALSKEQLEKLAAYLTPASINGGWAMQFGGQDAAIA 92
Db 272 KKLDELAIQVNSLEATLSVAMEKER-----DUSENLNVAWEKLSSEER--- 317
QY 93 AIKGVIERGAKQTPPVTHWTIPFEMLLSLTSALTWERTDDDLITFTGVMMFQDNQKGLR 152
Db 318 -----LEQAREIDEATRSLEALHKKHSELVKQKTWEDFS-----RDTFARSLT 364
QY 153 DELAEMTAELKIY-----VIQSEINQVLSAANSQTKTNFNLMDYKLYGYESL 201

Db 365 EKSKDLEEKIRVYEGKLAACGOSLSLQEELDQ--SSAENELLADTNNQIKIKI- 419
QY 202 AKFMGEFELLKSMFSDSQVTKAQQDFTNAKNELENTVTSLNPKIOAEAKTDYERKKA 261
Db 420 EGYLDSEKETAIEKL--NQKTEAKOLITKLKSH-ENVIEHKRQVLEASGVAD-TRKVE 475
QY 262 IFEEIVETQIITLTKTFLESDLKKSGAMSGIEAEYKYDKDNKNGFNSTSVSRPLNDL 321
Db 476 VEEALL--KLNTLESTIEELEKENGDLAEVNI-----KLQKLANQSGSDDDFOAKLSVL 528
QY 322 VSEK-----TARLNDVSSRYNAAIEAL-----NRFIQKYDYSIMRDL 358
Db 529 EAEKYQQAQKELQITIEDLTQKLTSERLRSQISSLEEEKNQVNEIYQSTKNELV 583

RESULT 6
T18372
repeat organellar protein - Plasmodium chabaudi
C:Species: Plasmodium chabaudi
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18372
R:Werner, E.B.; Taylor, W.R.; Holder, A.A.
Mol. Biochem. Parasitol. 94, 185-196, 1998
A:Title: A Plasmodium chabaudi protein contains a repetitive region with a predicted sp
A:Reference number: Z18922; MUID:98418765; PMID:9747969
A:Accession: T18372
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1939 <WER>
A:Cross-references: UNIPROT:Q25662; UNIPARC:UPI00000823AB; EMBL:U43145; NID:g1151157; P

Query Match 7.1%; Score 128.5; DB 2; Length 1939;
Best Local Similarity 21.8%; Pred. No. 8.2;
Matches 59; Conservative 46; Mismatches 103; Indels 63; Gaps 11;
QY 119 LLSALTMTERTDDDLITFTGVMMFQDNQKRLDELAETAELKIYGVITQSEINQVLSA 178
Db 193 MSLDKLTCE-----VQEKDNLEK-INKKVIEKENNLRELKEPMKEKNEIES 239
QY 179 ASNQTKTNFNLMDYKLYGVESLAKMEGFEKLLSKMFSDSQVTKAQQDFTN--AKNEL 236
Db 240 LDG-TINDKKNAYEKLSEFEKKRIEMLDLKLIEK-----EENFANKQAKLEK 289
QY 237 ENVTSTSLNPKIOAEAKTDYERKKAIFEEIVETQIITLTKTFLESDLKKSGAMSGI----- 291
Db 289 ENIIIEKLDIESREK-DFKSEKFPAS-MENELNTLK-----SDLSKNACQMEVYKLEI 342
QY 292 -----EAEYKYDKDNKNGFNSTSVSDR-----SRPLNDLVSEKT 326
Db 343 KQLSQSLVEKEREIFEIKNEYDDKINNKEKLSINDKIGDINTVLHSEEEKINKLLEKE 402
QY 327 ARLNDVSSRYNAAIEAL--NRFIQKYDYSIMRD 356
Db 403 TELNEIHKYNNLEIETIKNELNEKEBELEKN 433

RESULT 7
B42771
reticulocyte-binding protein 2 - Plasmodium vivax (fragment)
C:Species: Plasmodium vivax
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Sep-1997
C:Accession: B42771
R:Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.
Cell 69, 1213-1226, 1992
A:Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.
A:Reference number: A42771; MUID:92315338; PMID:1617731
A:Accession: B42771
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1252 <GAL>
A:Cross-references: UNIPARC:UPI000017B645; GB:M88098; NID:g160627; PID:g160628
A:Experimental source: strain Belem, merozoites

C;Genetics:
A;Gene: RBP2

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Query Match          6.8%; Score 124; DB 2; Length 1252;
Best Local Similarity 20.2%; Pred. No. 8.;
Matches 76; Conservative 74; Mismatches 138; Indels 88; Gaps 17;

QY 21 QALNTLPNGKNPKLTVELLKGKTTI---SADSTALSKE-OLEKLLAAYLTPASING 76
Db 841 EAVSVKIGNVKKHSEL-----SKITCSKSYNIITALEKQTLQNLRSFTQKTNNTS 895

QY 77 GWAMGQFKGGQDA---AIAAIKGYI-----ERGAQTQPPVTHWTIPEFMLSLSA 123
Db 896 DSKLEKIKTDFSLKNAKLTLEGEVNAKASSDNHEHVQSKSEPVNP-----ALSE 946

QY 124 LTWERDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAASQNT 183
Db 947 IEKEETDIDSLNALDELL-----KKG-----RTCEVSRYLKIDTWTKEISDDTELI 994

QY 184 FKTNFNLMYKLY---GYESLAKFMEGGEFKLSKMFSDQVTKAQ-QDFTNAKNELENV 239
Db 995 NTIEKNVKAVALIKKNYEDTVQ-----DVLTLNEHFNTPQVSNHPTNFDKSNKSEEL 1049

QY 240 TSTSLNPKIOAEAKTYERKAIFEIFVETQIITLKTFLFSLDKKSGAMSGIEAAYKYDK 299
Db 1050 T-----KAVTDSKTIISKLGVIIEVNE--TEMNTIESSAKE-----IEALY---- 1090

QY 300 DNNKLGNFSTVSDRSRPLNDL---VSEKTAFLNDVSSRYNAAIE-----ALN 344
Db 1091 --NELKNKKTSLNEIYQTSNEVKLQEMKNADKYIDVSKIFNVLTQKSNIVTNQHSIN 1148

QY 345 RFIQKYDSIMRDLGA 360
Db 1149 NVKDKLKGKQLQELIDA 1164

RESULT 8
rhoptry protein - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28677; C45521
R;Keen, J.; Sinha, K.; Brown, K.; Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
A;Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii.
A;Reference number: Z20508; MUID:95021522; PMID:7935623
A;Accession: T28677
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2269 <KEE>
A;Cross-references: UNIPROT:Q26223; UNIPARC:UPI0000080871; EMBL:L27838; NID:g457145; PID
R;Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple co
A;Reference number: A45521; MUID:91101660; PMID:2270106
A;Accession: C45521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 2131-2269 <KE2>
A;Cross-references: UNIPARC:UPI0000178646; GB:M34283
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Query Match          6.8%; Score 123.5; DB 2; Length 2269;
Best Local Similarity 21.6%; Pred. No. 21;
Matches 80; Conservative 55; Mismatches 103; Indels 133; Gaps 17;

QY 35 TELVELLKGKTIISA---DSSTALSKE-----QLEKLLA 65
Db 1656 TTTAETLKIKTDYSKFIESATKFSKEFLKYIGDTSNLSNLDIATILQKYDLHQINKYVT 1715

QY 66 AYLTPASINGWAMGQFKGGDAATAIKGV-----IERGAQTQPPV----- 108
Db 1716 SKLSDATDNNNLIEKEATEQ-----AIKNLTKLFTDSSNIDANALHNNKIOMVYFNS 1770
```

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QY 109 -THWTIPE-----FMLSLSALTMTERTDDDLITFTGVMFQDNQKGLRDELA 157
Db 1771 ELHKSIESIKQLYKQKHVFKLLNIGQINGKYP--DISKOFDNLILQOE-----SE 1818

QY 158 MTAEI-----KIYGVIOSEINQVLSAASQNTFKTNFNLMDYKLYGYESLAKFMEGGFKL 213
Db 1819 LTANLNDLKEIGKISDKKNKFLHAL-NETPIPNFN-----TL 1855

QY 214 SKMFSDQVTKAQDFTNAKNELENVTS-----TSLNPKIOA--EAKTDYER 258
Db 1856 KIIYHDIVVKRQID-----BIENITSEENENITLYIDITIKLKEKVQSIILNFVTYEN 1909

QY 259 KKAIFEEIV---ETQII---TLKTFLESDLKKSGAMSGIEAAYKYDKDNNKLGNFST 310
Db 1910 DSNIIKQHIQDNTENDVSKIESLTKTQSFQIILNKINGIKAQF---YDNNNNINNT 1966

QY 311 VSDRSRPLNDL 321
Db 1967 ISTISQDVNDV 1977

RESULT 9
G70163
hypothetical protein BB0512 - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70163
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: G70163
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-2166 <KLE>
A;Cross-references: UNIPROT:O51465; UNIPARC:UPI00000574E8; GB:AE001153; GB:AE000783; NIT
A;Experimental source: strain B31
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Query Match          6.7%; Score 121.5; DB 2; Length 2166;
Best Local Similarity 19.2%; Pred. No. 26;
Matches 77; Conservative 79; Mismatches 113; Indels 131; Gaps 21;

QY 29 NK-NPKLTVELLKGK-ITISADSTALSKEQLEKLLAAYLTPASINGWAMGQFKGG 86
Db 644 NKTNEEFLSLIQIQKDGIELSESVFNDLSDHQIKKAI-----DMHGSW----- 687

QY 87 ODAATAAIKGVIERCAKQTPPVTHWTIP-----EFMLL---S 120
Db 688 KDELIALNKSLLDIKVSSEELSSATLKIESLKVDNRMEXVLTKGTGIESLVIEKYKE 747

QY 121 ISALTMTERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 748 LKDMYSQSDEAIL---GIKEFINRQTEIITKDKSVFMLEDL----- 785

QY 181 NQTF--KTNFNL-----MDYKLYGYE-----SLAKFMEGGEFKLSKMFSDQ 221
Db 786 NKKFDQKNFVISKIEECYDKLKQFKIESEDILNNFKSLDNBEFIE-SKLQIVSNITKSDNQ 844

QY 222 -----VTKAQDFTNAKNELENVTSLSNP-----KIQ---AEAKTDYERKKAI 262
Db 845 KQIDDFLRISKDILNRKDSINNEVDSKLSQWQSKLNITVKIENLSSGKVLDL----L 900

QY 263 FEEIVETQIITLKTFLFSLDKKSGAMSGIEAAY--KYDKDNNKLGNFSTVSDRSRPLND 320
Db 901 IDSEVTTIKELKFSIES-----LESYLEKIDEFNRQGAISDEL-----LQD 944

QY 321 LV---SEKTAFLND-VSSRYNAAIEALNRFITQKYDSIMRD 356
Db 945 IMNHFNKETRELENLSKFAAVLNNSSEFVKEDVSLIQD 984
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C;Genetics:
A;Gene: CESP:Y6B3B.3
A;Map position: 1
A;Introns: 365/2; 800/2; 936/3

Query Match 6.6%; Score 120.5; DB 2; Length 995;
Best Local Similarity 20.8%; Pred. No. 11;
Matches 75; Conservative 51; Mismatches 127; Indels 107; Gaps 13;

Qy 17 WLVDQALNTLPNGKN-PKLTVELVLLKGK-TISADSSSTALSKEQLEKLLAAYLTDPASI 74
Db 5 WSRVGDLSKLDPDKATFKKLGDLKSLNLGTATIDVDS-----IISKLDD---- 48

Qy 75 NGWAMGQFKGGQDAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLLSLSALTWERTDDDL- 133
Db 49 -----GSDKSAVAANTTLEEFPAKGIATVT-----SALDKTSMETLE 85

Qy 134 ----ITTFCTVMFQDNOR-----KGLRDELAEMTAELKIYGVIOSEINQVLS 177
Db 86 TLPITNYAKLFQYDINSQAIYKAAATDDDIKGLDNLSTIKTIPNSNSTLFSDKMLTT 145

Qy 178 AASNQTFKTNFLMDYKLYGYESLAKPMEGEFKLLSKM-----FSDEQVTKAQ 226
Db 146 ETSSLIRQHTSLWN-----GYHDFSLLKDKINKFFLRIILRVFFHFTCFPSHAGMSUDE 201

Qy 227 QDFTNAKNELENTVTSNLNPKIOAEAKTDYERKKAIA---FEEIVETQIITLKTFLSDLK 283
Db 202 EDFADAGEFLE-----CDLKRNGIPISFEERI---FVSPSKFLKSEEF 242

Qy 284 KSGAMSGIEAEYKYDKNNKLGNFSTSDRSRPLNDLVSEKTLARLNDVSSRYNAAIKAL 343
Db 243 KSSMRSIIET-----SIDATLNNRMKKLEDKIAELTEDLTKOKRLDLALVEL 290

RESULT 15
A82889
hypothetical protein UU443 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82889
R;Glass, J.I.; Leikowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A;Reference number: A82870
A;Accession: A82889
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-628 <GLA>
A;Cross-references: UNIPARC:UPI00000C1C6D; GB:AE002141; GB:AF222894; NID:G6899434; PIDN
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU443
A;Genetic code: SGC3

Query Match 6.6%; Score 120; DB 2; Length 628;
Best Local Similarity 23.3%; Pred. No. 6.2;
Matches 60; Conservative 48; Mismatches 114; Indels 36; Gaps 10;

Qy 118 LLSLSALTWERTDDDLITFTGVMMFQDNORKGLRDELAEMTAELKIYGVIOSEINQVLS 177
Db 13 LMSISAIPLAT---IITACAKV-----DTQKAKEELQSSLNKAVALKEIVDQSSYEDFK 65

Qy 178 AASNQTFKTNF-----NLMDYKLYGYESLAKFM-----EGGEFKLLSKMFSQ---EQV 222
Db 66 KIYNQTLKSNLEINIKLSEQKLKQEQOTIKNLITQVSVLNELDSIKNMSDLIDVVELENT 125

Qy 223 TKAQDFTNAKNELENTVTSNLNPKIOAEAKTDYERKKAIFEEIVETQIITLKTFLSDLK 282
Db 126 KQQLQDPLNQYEKLLN---QASVDTTIDKUSDAHQRLHTKALIQKTIIDLANKIKNL 183

Qy 283 KKSAMSG-----IEAEYKYDKNNKLGNFSTSDRSRPLNDLVSEKTLARLNDVSSRYNAA 339
Db 184 KTSGSKNKNIVEISDIOKLVNNTKANFKKLYEDFK-----LIYTK---LNDINDLNKE 235

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GenCore version 5.1.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:53:15 ; Search time 283.517 Seconds
(without alignments)
1177.815 Million cell updates/sec

Title: US-10-813-908A-8
Perfect score: 1816
Sequence: 1 MSTIPDNTNPGAFVGHLDV.....ALNRFQKYSIMRDLGAI 361

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	361	2	Q70WN7_AERSA
2	1804	99.3	361	2	Q5ISV9_AERSA
3	1799	99.1	361	2	Q5ISW0_AERSA
4	1790	98.6	361	2	Q5ISV8_AERSA
5	1615	88.9	361	2	Q5ISV7_9GAMM
6	1512.5	83.3	374	2	Q5ISV5_9GAMM
7	1481.5	81.6	362	2	Q5ISV6_9GAMM
8	1386	76.3	361	2	Q699K0_AERHY
9	1384.5	76.2	362	2	Q5CC97_AERSO
10	1196.5	65.9	312	2	Q5XL04_AERHY
11	625	34.4	304	2	Q7N0X1_PHOLL
12	605.5	33.3	325	2	Q84GV5_PHOLL
13	570.5	31.4	334	2	Q56896_YEREN
14	569.5	31.4	333	2	Q84GT5_YEREN
15	569.5	31.4	334	2	Q56853_YEREN
16	567	31.2	325	2	Q56880_YEREN
17	564	31.1	324	2	Q93K04_YEREN
18	564	31.1	326	1	LCRV_YERPS
19	561	30.9	324	2	Q56846_YEREN
20	561	30.9	324	2	Q56879_YEREN
21	560	30.8	324	2	Q87495_YEREN
22	558	30.7	324	2	Q56882_YEREN
23	557	30.7	326	1	LCRV_YERPE
24	491.5	27.1	367	2	Q5ISV4_AERHY
25	488.5	26.9	367	2	Q6TLM2_AERHY
26	474	26.1	294	2	Q30527_PSEAE
27	281	15.5	607	2	Q87P59_VIBPA
28	253	13.9	605	2	Q6QV52_VIBPA
29	159	8.8	1813	2	Q513P3_ENTHI
30	138.5	7.6	1612	2	Q5ESB7_VIBF1
31	133.5	7.4	624	2	Q49548_MYCHO

32	133	7.3	965	2	Q7QJ14_ANOGA	Q7qji4 anopheles g
33	131.5	7.2	820	2	Q500S4_ENTHI	Q50qs4 entamoeba h
34	131.5	7.2	1398	2	Q6FKE6_CANGA	Q6fke6 candida gla
35	130.5	7.2	775	2	Q4A7M2_MYCH7	Q4a7m2 mycoplasma
36	130	7.2	1128	2	Q3D3M0_STRAG	Q3d3m0 streptococc
37	130	7.2	1913	2	Q4AA31_MYCHU	Q4aa31 mycoplasma
38	130	7.2	1975	2	Q600Y2_MYCHU	Q600y2 mycoplasma
39	129.5	7.1	775	2	Q4A917_MYCHU	Q4a917 mycoplasma
40	129.5	7.1	2162	2	Q661A9_BORGA	Q661a9 borrelia ga
41	129	7.1	699	2	Q56WB1_ARATH	Q56wb1 arabidopsis
42	129	7.1	841	2	Q230J7_ARATH	Q230j7 arabidopsis
43	129	7.1	1404	2	Q8RJN9_MYCHO	Q8rjn9 mycoplasma
44	129	7.1	2013	2	Q9VK10_DROME	Q9vki0 drosophila
45	129	7.1	2244	2	Q9NCG0_DROME	Q9ncg0 drosophila

ALIGNMENTS

RESULT 1
Q70WN7_AERSA
ID Q70WN7_AERSA PRELIMINARY; PRT; 361 AA.
AC Q70WN7;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Acrv protein.
GN Name=acrv;
OS Aeromonas salmonicida subsp. salmonicida.
OG Plasmid pASvira.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=JF2267; PLASMID=pASvira;
RX MEDLINE=22957181; PubMed=14594831;
RA DOI=10.1128/JB.185.22.6583-6591.2003;
RA Burr S.E., Stuber K., Frey J.;
RT "The ADP-ribosylating toxin, AexT, from Aeromonas salmonicida subsp. salmonicida is translocated via a type III secretion pathway.";
RL J. Bacteriol. 185:6583-6591(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RA Burr S.E., Pugovkin D., Wahli T., Segner H., Frey J.;
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";
RL Microbiol. 151:2111-2118(2005).
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CC
CC EMBL; AJ516009; CAD56769.1; -; Genomic DNA.
DR EMBL; AY649419; AAV67428.1; -; Genomic DNA.
DR EMBL; AY649420; AAV67429.1; -; Genomic DNA.
DR EMBL; AJ616218; CAB83108.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; Lcrv; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
KW Plasmid.
SQ SEQUENCE 361 AA; 40165 MW; 66FBEE940891510 CRC64;
Query Match 100.0%; Score 1816; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 6.3e-100;

Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSTIPDYNTPGAFVGLWDVQALNTPGNKNPKLTTELVELLKGKITISADSTALSKEQL 60
Db 1 MSTIPDYNTPGAFVGLWDVQALNTPGNKNPKLTTELVELLKGKITISADSTALSKEQL 60

QY 61 EKLLAAYLTPDASINGGWAMGQFGGQDAAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120
Db 61 EKLLAAYLTPDASINGGWAMGQFGGQDAAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120

QY 121 LSALTMTERTDDDLITFTGVMVFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 121 LSALTMTERTDDDLITFTGVMVFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180

QY 181 NOTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENYT 240
Db 181 NOTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENYT 240

QY 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLTFTFLESDLKKSAMSGIAEYKYDKD 300
Db 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLTFTFLESDLKKSAMSGIAEYKYDKD 300

QY 301 NNKLGNFSTSVSDRSRPLNDLVSEKTAARLNDVSSRYNAAEALNRFIOKYDSIMRDLGA 360
Db 301 NNKLGNFSTSVSDRSRPLNDLVSEKTAARLNDVSSRYNAAEALNRFIOKYDSIMRDLGA 360

QY 361 I 361
Db 361 I 361
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RESULT 2

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Q5ISV9 AERSA
ID Q5ISV9 AERSA PRELIMINARY; PRT; 361 AA.
AC Q5ISV9;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE AcrV.
GN Name=acrV;
OS Aeromonas salmonicida subsp. masoucida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=197700;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R3;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY649422; AAV67431.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; Lcrv; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
SQ SEQUENCE 361 AA; 40194 MW; 7D76B652308C1510 CRC64;
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Query Match 99.3%; Score 1804; DB 2; Length 361;
Best Local Similarity 99.4%; Pred. No. 3.3e-99;
Matches 359; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MSTIPDYNTPGAFVGLWDVQALNTPGNKNPKLTTELVELLKGKITISADSTALSKEQL 60
Db 1 MSTIPDYNTPGAFVGLWDVQALNTPGNKNPKLTTELVELLKGKITISADSTALSKEQL 60

QY 61 EKLLAAYLTPDASINGGWAMGQFGGQDAAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120
Db 61 EKLLAAYLTPDASINGGWAMGQFGGQDAAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120
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QY 121 LSALTMTERTDDDLITFTGVMVFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 121 LSALTMTERTDDDLITFTGVMVFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180

QY 181 NOTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENYT 240
Db 181 NOTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENYT 240

QY 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLTFTFLESDLKKSAMSGIAEYKYDKD 300
Db 241 STSLNPKIOAEAKTDYERKKAIFEEIVETQIITLTFTFLESDLKKSAMSGIAEYKYDKD 300

QY 301 NNKLGNFSTSVSDRSRPLNDLVSEKTAARLNDVSSRYNAAEALNRFIOKYDSIMRDLGA 360
Db 301 NNKLGNFSTSVSDRSRPLNDLVSEKTAARLNDVSSRYNAAEALNRFIOKYDSIMRDLGA 360

QY 361 I 361
Db 361 I 361
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RESULT 3

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Q5ISW0 AERSA
ID Q5ISW0 AERSA PRELIMINARY; PRT; 361 AA.
AC Q5ISW0;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE AcrV.
GN Name=acrV;
OS Aeromonas salmonicida subsp. achromogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=113288;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R2;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY649421; AAV67430.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; Lcrv; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
SQ SEQUENCE 361 AA; 40164 MW; 7D76B64F86576510 CRC64;
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Query Match 99.1%; Score 1799; DB 2; Length 361;
Best Local Similarity 99.2%; Pred. No. 6.5e-99;
Matches 358; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 EKLLAAYLTPDASINGGWAMGQFGGQDAAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120
Db 61 EKLLAAYLTPDASINGGWAMGQFGGQDAAIAAIAKGVIERGAKQTPPVTHWTIPFEMLLS 120

QY 121 LSALTMTERTDDDLITFTGVMVFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
Db 121 LSALTMTERTDDDLITFTGVMVFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180

QY 181 NOTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENYT 240
Db 181 NOTFKTNFNLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENYT 240
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QY 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGAMSGIEABYKYDKD 300
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Db |
QY 301 NNKLGNFSTVS DRSRPLNDLVSEKTLARLNDVSSRYNAAIEALNRFIQKYDSIMRDLILGA 360
Db |
QY 361 I 361
Db |
QY 361 I 361
Db |

RESULT 4
Q5ISV8_AERSA
ID Q5ISV8_AERSA PRELIMINARY; PRT; 361 AA.
AC Q5ISV8;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE AcrV.
GN Name=acrV;
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=R722;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AY649423; AAV67432.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
SQ SEQUENCE 361 AA; 40210 MW; 7D6AA68109E469E2 CRC64;

Query Match 98.6%; Score 1790; DB 2; Length 361;
Best Local Similarity 98.9%; Pred. No. 2.2e-98;
Matches 357; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db |
QY 61 EKLLAAYLTDPASINGGWAMGQFGGQDAAIAAIKGVIERGAKOTPPVTHWTIPEFMLLS 120
Db |
QY 121 LSALTMTERTDDDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NOTFKTNFLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENTV 240
Db |
QY 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGAMSGIEABYKYDKD 300
Db |
QY 361 I 361
Db |

RESULT 5
Q5ISV7_9GAMM
ID Q5ISV7_9GAMM PRELIMINARY; PRT; 361 AA.
AC Q5ISV7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE AcrV.
GN Name=acrV;
OS Aeromonas veronii bv. Sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=114517;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=R735;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AY649424; AAV67433.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
SQ SEQUENCE 361 AA; 39860 MW; F71CC3A15E644648 CRC64;

Query Match 88.9%; Score 1615; DB 2; Length 361;
Best Local Similarity 88.1%; Pred. No. 5.7e-88;
Matches 318; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 MSTIPDYNTPGAFVGVGLDQVQALNTLPGNKNPKLTTELVELLKGKITTISADSSTALSKEQL 60
Db |
QY 61 EKLLAAYLTDPASINGGWAMGQFGGQDAAIAAIKGVIERGAKOTPPVTHWTIPEFMLLS 120
Db |
QY 121 LSALTMTERTDDDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NOTFKTNFLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENTV 240
Db |
QY 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGAMSGIEABYKYDKD 300
Db |
QY 361 I 361
Db |

RESULT 6
Q5ISV5_9GAMM
ID Q5ISV5_9GAMM PRELIMINARY; PRT; 374 AA.
AC Q5ISV5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
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Db |
QY 361 I 361
Db |

RESULT 5
Q5ISV7_9GAMM
ID Q5ISV7_9GAMM PRELIMINARY; PRT; 361 AA.
AC Q5ISV7;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE AcrV.
GN Name=acrV;
OS Aeromonas veronii bv. Sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=114517;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=R735;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL; AY649424; AAV67433.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
SQ SEQUENCE 361 AA; 39860 MW; F71CC3A15E644648 CRC64;

Query Match 88.9%; Score 1615; DB 2; Length 361;
Best Local Similarity 88.1%; Pred. No. 5.7e-88;
Matches 318; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 MSTIPDYNTPGAFVGVGLDQVQALNTLPGNKNPKLTTELVELLKGKITTISADSSTALSKEQL 60
Db |
QY 61 EKLLAAYLTDPASINGGWAMGQFGGQDAAIAAIKGVIERGAKOTPPVTHWTIPEFMLLS 120
Db |
QY 121 LSALTMTERTDDDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NOTFKTNFLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQQDFTNAKNELENTV 240
Db |
QY 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKSGAMSGIEABYKYDKD 300
Db |
QY 361 I 361
Db |

RESULT 6
Q5ISV5_9GAMM
ID Q5ISV5_9GAMM PRELIMINARY; PRT; 374 AA.
AC Q5ISV5;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
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DT 15-FEB-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Acrv.
GN Name=acrv;
OS Aeromonas veronii bv. Sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=114517;
RN [1]_TaxID=114517;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R739;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY649426; AAV67435.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 374 AA; 41603 MW; F284B0914D81BEA8 CRC64;
Query Match 83.3%; Score 1512.5; DB 2; Length 374;
Best Local Similarity 80.7%; Pred. No. 7.4e-82;
Matches 302; Conservative 25; Mismatches 34; Indels 13; Gaps 2;
QY 1 MSTIPDYNTPGAFVGLDQALNTLPGNKPKLTVELLKGKITISADSTALSKEQL 60
DB 1 MSTIPDYNTPGAFVGLDQALDLPGHKPKLTVELLKGKITISADSTALSKEQL 60
QY 61 EKLLAAYLTPASINGWAMGQFGQDAAIAAIGKVIERGAKTPPVTHWTPIPEFMLS 120
DB 61 EKLLAAYLTPASINGWAMGQFGQDAAIAAIGKVIERGAKTPPVTHWTPIPEFMLS 120
QY 121 LSALTWERTDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
DB 121 LSALTMDRIDDDLIITFTGVMAFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NOTKTFNFMNDYKLYGYESLAKFMGEGFLLSKMFSDEQVTKAQDFTNAKNELENV- 239
DB 181 SQTFTNFNLMYKLYGYQSQAKEGAEYKLLSKMFTNEQVKKAQDFSEAESNLNEII 240
QY 240 -----TSTSLN-PKIQAEAKTDYERKKAIFEEIVETQITLTKTFLESCLKKSGA 287
DB 241 KNQQRHAGISTGIDINFESYSELQAVYDYSKKAILEQVAKQKITVKEFLESQKSGA 300
QY 288 MSGIEAEYKYDKNKNGFNSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRPI 347
DB 301 MTNIEASYDKNKNGFNSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRPI 360
QY 348 QKYDSIMRDILGAI 361
DB 361 QKYDSIMRDILGAI 374
RESULT 7
QSISV6_9GAMM PRELIMINARY; PRT; 362 AA.
AC QSISV6;
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Acrv.
GN Name=acrv;
OS Aeromonas veronii bv. Sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=114517;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R737;
RA Fan W., MacIntyre S.;
RT "Cross reactivity of V-antigen from different Aeromonas species.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY649425; AAV67434.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 362 AA; 39991 MW; 0F1A2FFBE93BFF4B CRC64;
Query Match 81.6%; Score 1481.5; DB 2; Length 362;
Best Local Similarity 82.3%; Pred. No. 5e-80;
Matches 298; Conservative 19; Mismatches 44; Indels 1; Gaps 1;
QY 1 MSTIPDYNTPGAFVGLDQALNTLPGNKPKLTVELLKGKITISADSTALSKEQL 60
DB 1 MSTIPDYNTPGAFVGLDQALGALPGHKNPKLTVELLKGKITISADPTPLTKAQL 60
QY 61 EKLLAAYLTPASINGWAMGQFGQDAAIAAIGKVIERGAKTPPVTHWTPIPEFMLS 120
DB 61 EKLLAAYLTPDSINGWAAQFGQDAAIAAIGKVIERGAKTPPVTHWTPIPEFMLS 120
QY 121 LSALTWERTDLITFTGVMMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
DB 121 LSALTWERIDDDLIITFTGVMAFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAAS 180
QY 181 NO-TKTFNFMNDYKLYGYESLAKFMGEGFLLSKMFSDEQVTKAQDFTNAKNELENV 239
DB 181 DKPTFTNFNLDYKLYGYESLAKFLDCAEFLLSKMFTDLDLVXNALQSFNTAKNALEKV 240
QY 240 TSTSLNPKIQAEAKTDYERKKAIFEEIVETQITLTKTFLESCLKKSGAMSGEAEYKYDK 299
DB 241 KSASLDSKTLGASAAERKKAANLQIVATQIVTKTFLESQKSGAMENAEYSYKK 300
QY 300 DNNKLGNFSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAIAEALNRFIQKYSIMRDILG 359
DB 301 DDNKLGNFSTSVSDRSRPLNDVSEKTLARLNDVSSRYNAIAEALNRFIQKYSIMRDILG 360
QY 360 AI 361
DB 361 AI 362
RESULT 8
QS99R0_AERHY PRELIMINARY; PRT; 361 AA.
AC QS99R0;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Acrv.
GN Name=acrv;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]_TaxID=644;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpulli G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
CC -----
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CC -----
DR EMBL; AY528667; AAS91819.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005413; P:pathogenesis; IEA.
DR Pfam; PF04792; LcrV_1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 361 AA; 40149 MW; FAD8542D4A1C0103 CRC64;

Query Match 76.3%; Score 1386; DB 2; Length 361;
Best Local Similarity 76.2%; Pred. No. 2.4e-74;
Matches 275; Conservative 27; Mismatches 59; Indels 0; Gaps 0;

Qy 1 MSTIPDYNTNPGAFVGMWLDVQALNTLPGNKPKLTVELLKGKITISADSSTALSKEQL 60
Db 1 MSVIPDYNPNPAGFVGMWLDVQALNTLPCHNNPKLAELLALLEGKITISTDQPTVLSKAQL 60

Qy 61 EKLLAAYLTDPASINGWAMQFGGQDAAIAIKGVIERGAKQTPPVTHWTIPFEMLLS 120
Db 61 EKLLAKYLTDPATVGTGWSWPTDQFLRGQEAATAIKGLIEQEKREPKVTSWTSVEFMLLS 120

Qy 121 LSAITMERTDDDLTTFTGVMMFQDNORKGLRDELAEMTAELKTYGVIOSEINQVLSAAS 180
Db 121 FSAITMDRIODDIINVTGVMAFQDNORKKALGNELKMDTAELKTYGVIOSEINKVLSAAS 180

Qy 181 NOTFTNFMNDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQODFTNAKNELENVT 240
Db 181 SQTFTNFMNDYKLYGYESLAKFMDCGAEFKLLSKMFTDVQVKAQODFTNAKNELEKVK 240

Qy 241 STSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGSGAMGIEAEYKYDK 300
Db 241 SASLDPKTLEENADYEEKKALIEKSVKQSIITVKSFLESDQKSGAMKIEASYSYDKD 300

Qy 301 NNKLGNFSTVSRSRPLNDVSEKTLRLNDVSSRYNAALRNFTQKYDSIMRDILGA 360
Db 301 NNKLGNFSTVSRSRPLNDVSEKTLRLNDVSSRYNAALRNFTQKYDSIMRDILGA 360

Qy 361 I 361
Db 361 I 361

RESULT 9
Q5CC97 AERSO PRELIMINARY; PRT; 362 AA.
AC Q5CC97;
DT 12-APR-2005, integrated into UniProtKB/TREMBL.
DT 12-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE AcrV protein.
GN Name=acrV;
OS Aeromonas sobria.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=646;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2635;
RX PubMed=15752274; DOI=10.1111/j.1365-2761.2005.00608.x;
RA Wahli T., Burr S.E., Pugovkin D., Mueller O., Frey J.;
RT "Aeromonas sobria, a causative agent of disease in farmed perch, *Perca fluviatilis*,"
RL J. Fish Dis. 28:141-150 (2005).
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CC -----
DR EMBL; AJ749609; CAG44558.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR SQ SEQUENCE 361 AA; 40149 MW; FAD8542D4A1C0103 CRC64;

Query Match 76.2%; Score 1384.5; DB 2; Length 362;
Best Local Similarity 76.5%; Pred. No. 2.9e-74;
Matches 277; Conservative 29; Mismatches 55; Indels 1; Gaps 1;

Qy 1 MSTIPDYNTNPGAFVGMWLDVQALNTLPGNKPKLTVELLKGKITISADSSTALSKEQL 60
Db 1 MSTIPDYNNAAGFVGMWLDGQADALPGHKNLKLNEILLTLLDGKITISADKPILTRQL 60

Qy 61 EKLLAAYLTDPASINGWAMQFGGQDAAIAIKGVIERGAKQTPPVTHWTIPFEMLLS 120
Db 61 EKLLAQYLTDPATVGTGWSWPTDQFLRGQEAATAIKGLIEQEKREPKVTSWTSVEFMLLS 120

Qy 121 LSAITMERTDDDLTTFTGVMMFQDNORKGLRDELAEMTAELKTYGVIOSEINQVLSAAS 180
Db 121 LSAITMDRIODDIINVTGVMAFQDNORKKALGNELKMDTAELKTYGVIOSEINKVLSAAS 180

Qy 181 NQ-TFTNFMNDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQODFTNAKNELENV 239
Db 181 DKPTNFMNDYKLYGYESLAKFMGAEFKLLSKMFTVDVYNKAQODFTNAKNELEKV 240

Qy 240 TSLSNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGSGAMGIEAEYKYDK 299
Db 241 KSNLDPKILEAAKADYEEKKALIEKSVKQSIITVKAFLSDQKSGAMGIEAEYKYDK 300

Qy 300 DNKLGNFSTVSRSRPLNDVSEKTLRLNDVSSRYNAALRNFTQKYDSIMRDILG 359
Db 301 DNKLGNFSTVSRSRPLNDVSEKTLRLNDVSSRYNAALRNFTQKYDSIMRDILG 360

Qy 360 AI 361
Db 361 AI 362

RESULT 10
Q5XL04 AERHY PRELIMINARY; PRT; 312 AA.
AC Q5XL04;
DT 23-NOV-2004, integrated into UniProtKB/TREMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE AcrV.
GN Name=acrV;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Brova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the Virulence of *Aeromonas hydrophila*,"
RL Infect. Immun. 73:6446-6457 (2005).
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CC -----
DR EMBL; AY763611; AAV30233.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV_1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 312 AA; 34342 MW; A759ED1E0A7BA07E CRC64;

Query Match 65.9%; Score 1196.5; DB 2; Length 312;
Best Local Similarity 67.9%; Pred. No. 3.7e-63;
Matches 245; Conservative 26; Mismatches 41; Indels 49; Gaps 2;

DR Pfam; PF04792; LcrV_1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 362 AA; 40549 MW; 54F4C6F476D952F7 CRC64;

Query Match 76.2%; Score 1384.5; DB 2; Length 362;
Best Local Similarity 76.5%; Pred. No. 2.9e-74;
Matches 277; Conservative 29; Mismatches 55; Indels 1; Gaps 1;

Qy 1 MSTIPDYNTNPGAFVGMWLDVQALNTLPGNKPKLTVELLKGKITISADSSTALSKEQL 60
Db 1 MSTIPDYNNAAGFVGMWLDGQADALPGHKNLKLNEILLTLLDGKITISADKPILTRQL 60

Qy 61 EKLLAAYLTDPASINGWAMQFGGQDAAIAIKGVIERGAKQTPPVTHWTIPFEMLLS 120
Db 61 EKLLAQYLTDPATVGTGWSWPTDQFLRGQEAATAIKGLIEQEKREPKVTSWTSVEFMLLS 120

Qy 121 LSAITMERTDDDLTTFTGVMMFQDNORKGLRDELAEMTAELKTYGVIOSEINQVLSAAS 180
Db 121 LSAITMDRIODDIINVTGVMAFQDNORKKALGNELKMDTAELKTYGVIOSEINKVLSAAS 180

Qy 181 NQ-TFTNFMNDYKLYGYESLAKFMEGGFKLLSKMFSDEQVTKAQODFTNAKNELENV 239
Db 181 DKPTNFMNDYKLYGYESLAKFMGAEFKLLSKMFTVDVYNKAQODFTNAKNELEKV 240

Qy 240 TSLSNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGSGAMGIEAEYKYDK 299
Db 241 KSNLDPKILEAAKADYEEKKALIEKSVKQSIITVKAFLSDQKSGAMGIEAEYKYDK 300

Qy 300 DNKLGNFSTVSRSRPLNDVSEKTLRLNDVSSRYNAALRNFTQKYDSIMRDILG 359
Db 301 DNKLGNFSTVSRSRPLNDVSEKTLRLNDVSSRYNAALRNFTQKYDSIMRDILG 360

Qy 360 AI 361
Db 361 AI 362

RESULT 10
Q5XL04 AERHY PRELIMINARY; PRT; 312 AA.
AC Q5XL04;
DT 23-NOV-2004, integrated into UniProtKB/TREMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE AcrV.
GN Name=acrV;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Brova T.E., Chopra A.K.;
RT "The Type III Secretion System and Cytotoxic Enterotoxin Alter the Virulence of *Aeromonas hydrophila*,"
RL Infect. Immun. 73:6446-6457 (2005).
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CC -----
DR EMBL; AY763611; AAV30233.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV_1.
DR PRINTS; PR01592; LCRVANTIGEN.
DR SQ SEQUENCE 312 AA; 34342 MW; A759ED1E0A7BA07E CRC64;

Query Match 65.9%; Score 1196.5; DB 2; Length 312;
Best Local Similarity 67.9%; Pred. No. 3.7e-63;
Matches 245; Conservative 26; Mismatches 41; Indels 49; Gaps 2;

QY 1 MSTIPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVLLKGLKGLTISADSTALSKEOL 60
 DB 1 MSTIPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVLLKGLKGLTISADSTALSKEOL 60
 QY 61 EKLLAAYLTDPASINGWAMGQFGGQDAIAAIAKGVIERGAKQTPPVTHWTIPPEFMLS 120
 DB 61 EKLLAAYLTDPASINGWAMGQFGGQDAIAAIAKGVIERGAKQTPPVTHWTIPPEFMLS 120
 QY 121 LSAWERTDDDLITFTGVMMFQDNQKRLRDLAEMTAELKIYGVIOSEINQVLSAAS 180
 DB 121 LSAWERTDDDLITFTGVMMFQDNQKRLRDLAEMTAELKIYGVIOSEINQVLSAAS 180
 QY 181 NOTFKTNFLMDYKLYGYESLAKFMGEGFKLLSKMFSDEQVTKAQQDTNKNLELNV 240
 DB 181 NOTFKTNFLMDYKLYGYESLAKFMGEGFKLLSKMFSDEQVTKAQQDTNKNLELNV 240
 QY 241 STSLNPKIOAEAKTDYERKKAIFEIVETQIITLKTFFLESDLKKGSGAMSGIEAEYKYDK 300
 DB 241 STSLNPKIOAEAKTDYERKKAIFEIVETQIITLKTFFLESDLKKGSGAMSGIEAEYKYDK 300
 QY 301 NNKLGNFSTVSDRSPRLNDLVSEKTRALNDVSSRYNAAIEALNRFIQYDSIMRDLGA 360
 DB 301 NNKLGNFSTVSDRSPRLNDLVSEKTRALNDVSSRYNAAIEALNRFIQYDSIMRDLGA 360
 QY 361 I 361
 DB 361 I 361

RESULT 11

Q7NOX1_PHOLL
 ID Q7NOX1_PHOLL PRELIMINARY; PRT; 304 AA.
 AC Q7NOX1;
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 11.
 DE Similar to the virulence-associated V antigen.
 GN OrderedLocName=plu3758;
 OS Photorhabdus luminescens subsp. laumondii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 OX NCBI_TaxID=141679;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
 RA Duchaud E., Ruenik C., Frangeul L., Buchrieser C., Givaudan A.,
 RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
 RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
 RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
 RA Zouline M., Glaeser P., Boemare N., Danchin A., Kunst F.,
 RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
 luminescens.";
 RT Nat. Biotechnol. 21:1307-1313(2003).
 CC -----
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 CC EMBL; BX571871; CAE16130.1; -; Genomic DNA.
 DR PhotoList; plu3758;
 DR BioCyc; PLUM243265:PLU3758-MONOMER; -;
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 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR005413; LCRV_antigen.
 DR Pfam; PF04792; LcrV; 1.
 DR PRINTS; PRO1592; LCRVANTIGEN.
 KW Complete proteome.
 SQ SEQUENCE 304 AA; 34067 MW; EC9144A374B02FF1 CRC64;

Query Match 34.4%; Score 625; DB 2; Length 304;
 Best Local Similarity 41.8%; Pred. No. 3.5e-29;
 Matches 151; Conservative 47; Mismatches 101; Indels 62; Gaps 6;

QY 4 IPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVLLKGLKGLTISADSTALSKEOL 61
 DB 3 IRPYQNDPQLFLADLEKVSALQOQSGSSELDRLNLIFDKGKIKITSDSVVTKELLK 62
 QY 62 KLLAAYLTDPASINGWAMGQFGGQDAIAAIAKGVIERGAKQTPPVTHWTIPPEFMLS 121
 DB 63 KLIAYFLPADAVVEGGHLSQIKNG-----INNLESPLNSTLKT-----WTLKDFLAHV 113
 QY 122 SALTWERTDDDLITFTGVMMFQDNQKRLRDLAEMTAELKIYGVIOSEINQVLSAAS 181
 DB 114 FNLTDPRLDDDDITFTGVMSGHDKKRLRDLAEMTAELKIYGVIOSEINAKLAANGE 173
 QY 182 QTFKTNFLMDYKLYGYESLAKFMGEGFKLLSKMFSDEQVTKAQQDTNKNLELNV 240
 DB 174 LKIDNSFNLLDHHKYGFSQDQTFEKSABYKULRKISGSE----- 214
 QY 241 STSLNPKIOAEAKTDYERKKAIFEIVETQIITLKTFFLESDLKKGSGAMSGIEAEYKYDK 300
 DB 215 -----ISIKTFLESSNKQSGAMAGLENSYEYDKE 243
 QY 301 NNKLGNFSTVSDRSPRLNDLVSEKTRALNDVSSRYNAAIEALNRFIQYDSIMRDLGA 360
 DB 244 NNRLANFSTVSDRSPRLNLTVEKTRALNEASSRYNAAIEALNRFIQYDSIMRDLGA 303
 QY 361 I 361
 DB 304 I 304

RESULT 12

Q84GY5_PHOLU
 ID Q84GY5_PHOLU PRELIMINARY; PRT; 325 AA.
 AC Q84GY5;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE LcrV.
 GN Name=lcrV;
 OS Photorhabdus luminescens (Xenorhabdus luminescens).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 OX NCBI_TaxID=29488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=H4;
 RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
 RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
 RT "Genomic islands in Photorhabdus.";
 RL Trends Microbiol. 10:541-545(2002).
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 CC -----
 CC EMBL; AY144116; AAO18053.1; -; Genomic DNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR005413; LCRV_antigen.
 DR Pfam; PF04792; LcrV; 1.
 DR PRINTS; PRO1592; LCRVANTIGEN.
 SQ SEQUENCE 325 AA; 36997 MW; E413A4C51615B22C CRC64;

Query Match 33.3%; Score 605.5; DB 2; Length 325;
 Best Local Similarity 40.8%; Pred. No. 5.4e-28;
 Matches 155; Conservative 44; Mismatches 102; Indels 79; Gaps 9;

QY 4 IPDYNTPGAFVGLWDVQALNTLPGNKNPKLTSLVLLKGLKGLTISADSTALSKEOL 58
 DB 3 IRPYQNDPQLFLADLEKVSALQOQSGSSELDRLNLIFDKGKIKITSDSVVTKELLK 62
 QY 59 -----OLEKLLAAYLTDPASINGWAMGQFGGQDAIAAIAKGVIERGAKQTP 106
 DB 63 QVITQDGRDDKGLLKKLIAYFLPADAVVEGGHLSQIKNG-----IKNLKSLF-----NSP 113

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Qy 166 GVIOSEINOVLSAASNQ-----TFKTNFNLMYKLYGYESLAKFMEGGFEKLLSKWFSDEQ 221
Db 174 SVIOSEINAKUSAGKQKLDISISFDLRHKKYGFSDTAFKDSAEYALLKKMF----- 229
Qy 222 VTQAQODFTNAKNELENVTSLNPKIOAEAKTDYERKKAIFEIVETQIITTLTKTFLES 281
Db 230 -----PKLE-----ER-----VSICKFLESP 245
Qy 282 LKSGGAMSGTAEYKYDKNNKLNFTSVSDRPRPLNDLVSEKTLARLNDVSSRYNAAE 341
Db 246 NKQSGAMTGLENSEYEDKNNKLANFSTVNDRVNPLNNTVQKTRTLNEASSRYNAAE 305
Qy 342 ALNRFIOKYSIMRDIILGAI 361
Db 306 ALNRFIOKYSIMRNILGAI 325

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ID Q56896.YEREN PRELIMINARY; PRT; 334 AA.
AC Q56896;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE V antigen (fragment).
OS Yersinia enterocolitica (type 0:8).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=34054;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NTCC;
RA MEDLINE=97162308; PubMed=9009295;
RA Roggenkamp A., Geiger A.M., Leitritz L., Kessler A., Heesemann J.;
RT "Passive immunity to infection with Yersinia spp. mediated by anti-
RT recombinant V antigen is dependent on polymorphism of V antigen.";
RL Infect. Immun. 65:446-451(1997).
CC -----
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CC -----
CC EMBL; X96797; CAA65589.1; -; Genomic_DNA.
DR SMR; Q56896; 40-331.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
FT NON TER 334.
FT SEQUENCE 334 AA; 38227 MW; 43AC0567D7CCE2FA CRC64;

Query Match 31.4%; Score 570.5; DB 2; Length 334;
Best Local Similarity 38.5%; Pred. No. 6.8e-26;
Matches 141; Conservative 62; Mismatches 108; Indels 55; Gaps 9;

Qy 7 YNTNPGAFVGLVDVQALNTLPGNKNPKLTVELVLLKG-KITIS-----ADSSALSK-- 57
Db 5 YEONPOHFIEDLEKRVVDLTGHGSSVLEELVQLVKDKIDISIKYDPKDKSEVFAERVI 64
Qy 58 ----EOLKLLAAYLTDPASINGWAMGQFKGQDAIAAIAKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSNTOWEL 115
Qy 114 PEFMLLSALMTERTDDDLITTTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173
Db 116 RAFMAVMHFSLTADRIDDDILKIVDSMNHGDAKSLRELAELTAEIKIYSVIOAEIN 175
Qy 174 QVLSAASN-QTFKTNFNLMYKLYGYESLAKFMEGGFEKLLSKWFSDEQVTKAQQDFTNA 232
Db 176 KHLSSSGTINIHEKSLNMDKNLYGYTDEIFKASAEYKILKKM-----POTTIK 225
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Db 226 DDELHEV-----GVIAAG-----EKQIVSIKNFLESENKRTGALGNLK 263
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Qy 293 AEYKYDKNNKLNFTSVSDRPRPLNDLVSEKTLARLNDVSSRYNAAEALNRFIOKYDS 352
Db 264 DSYNKKNNELSHFATACSKSRPLNDLVSQKTLQSLDITSRENSAIEALNRFIOKYDS 323
Qy 353 IMRDIL 358
Db 324 VMORLL 329

RESULT 14
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ID Q84GT5.YEREN PRELIMINARY; PRT; 333 AA.
AC Q84GT5;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE LcrV.
GN Name=lcrV;
OS Yersinia enterocolitica.
OG Plasmid pYVal27/90.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A127/90;
RA Fouldier B.G.F., Bernard A., Putnelle B., Cornelis G.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; AY150843; AAN37531.1; -; Genomic_DNA.
DR SMR; Q84GT5; 40-331.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR005413; LCRV_antigen.
DR Pfam; PF04792; LcrV; 1.
DR PRINTS; PR01592; LCRVANTIGEN.
KW Plasmid.
SQ SEQUENCE 333 AA; 38128 MW; CC4067923952FA8F CRC64;

Query Match 31.4%; Score 569.5; DB 2; Length 333;
Best Local Similarity 38.5%; Pred. No. 7.8e-26;
Matches 141; Conservative 61; Mismatches 109; Indels 55; Gaps 9;

Qy 7 YNTNPGAFVGLVDVQALNTLPGNKNPKLTVELVLLKG-KITIS-----ADSSALSK-- 57
Db 5 YEONPOHFIEDLEKRVVEQLTGHGSSVLEELVQLVKDKIDISIKYDPKDKSEVFAERVI 64
Qy 58 ----EOLKLLAAYLTDPASINGWAMGQFKGQDAIAAIAKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKKILAYFLPEDAILKGGHYDNQLONG-----IKRVKEFLE-----SSNTOWEL 115
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Db 116 RAFMAVMHFSLTADRIDDDILKIVDSMNHGDAKSLRELAELTAEIKIYSVIOAEIN 175
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 66.6236 Seconds
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Title: US-10-813-908A-8
Perfect score: 1816
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Scoring table: BLOSUM62

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 5: /EMC_Celerra_SID33/ptodata/2/iaa/PCTUS COMB.pep:*
 - 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE COMB.pep:*
 - 7: /EMC_Celerra_SID33/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	557	30.7	480	1	US-08-913-477-17
4	557	30.7	501	1	US-08-913-477-23
5	474	26.1	297	2	US-09-252-991A-30058
6	253	13.9	142	2	US-09-248-588-36
7	127	7.0	367	2	US-09-861-451A-46
8	127	7.0	646	2	US-09-543-681A-6840
9	121	6.7	366	2	US-09-716-964B-144
10	120	6.6	630	2	US-09-248-796A-20275
11	119.5	6.6	885	2	US-09-710-279-1660
12	119	6.6	10182	2	US-09-134-001C-3159
13	117.5	6.5	478	2	US-08-772-270A-5
14	117.5	6.5	478	2	US-09-062-126-5
15	117.5	6.5	899	2	US-09-248-796A-19542
16	117	6.4	935	2	US-09-914-259-25
17	115.5	6.4	1211	2	US-09-134-001C-4820
18	114.5	6.3	456	2	US-09-808-701A-24
19	114.5	6.3	810	2	US-09-248-796A-20281
20	113.5	6.2	436	2	US-09-543-681A-4941
21	113.5	6.2	461	1	US-08-392-625-24
22	113.5	6.2	461	1	US-08-466-961A-24
23	113.5	6.2	461	1	US-08-645-193B-26
24	113	6.2	2733	2	US-09-949-016-11433
25	112	6.2	450	2	US-09-248-796A-15183
26	112	6.2	839	2	US-09-758-282B-130

27	112	6.2	839	2	US-09-758-282B-136	Sequence 136, App
28	112	6.2	839	2	US-09-577-304A-130	Sequence 130, App
29	112	6.2	839	2	US-09-577-304A-136	Sequence 136, App
30	112	6.2	1561	2	US-08-894-017-23	Sequence 23, Appl
31	112	6.2	1561	2	US-09-456-474-23	Sequence 23, Appl
32	111.5	6.1	2125	2	US-09-919-172-29	Sequence 29, Appl
33	111	6.1	471	2	US-09-248-796A-18841	Sequence 18841, A
34	111	6.1	839	2	US-09-758-282B-118	Sequence 118, App
35	111	6.1	839	2	US-09-758-282B-127	Sequence 127, App
36	111	6.1	839	2	US-09-758-282B-142	Sequence 142, App
37	111	6.1	839	2	US-09-577-304A-118	Sequence 118, App
38	111	6.1	839	2	US-09-577-304A-127	Sequence 127, App
39	111	6.1	839	2	US-09-577-304A-142	Sequence 142, App
40	111	6.1	2662	2	US-09-595-684B-31	Sequence 31, Appl
41	111	6.1	2663	2	US-09-538-092-1252	Sequence 1252, Ap
42	110.5	6.1	506	2	US-09-328-352-7166	Sequence 7166, Ap
43	110.5	6.1	1111	2	US-09-914-259-28	Sequence 28, Appl
44	110.5	6.1	1281	2	US-09-902-540-9864	Sequence 9864, Ap
45	110.5	6.1	2704	2	US-09-538-092-1260	Sequence 1260, Ap

ALIGNMENTS

RESULT 1
US-08-913-477-2
; Sequence 2, Application US/08913477
; Patent No. 5985285
; GENERAL INFORMATION:
; APPLICANT: Titball, Richard W.
; APPLICANT: Williamson, Ethel D.
; APPLICANT: Leary, Sophie E.C.
; APPLICANT: Oyston, Petra C.F.
; APPLICANT: Bennett, Alice M.
; TITLE OF INVENTION: VACCINES FOR PLAGUE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 5985285th Giebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,477
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00571
; FILING DATE: 13-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505059.7
; FILING DATE: 13-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9518946.0
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9524825.8
; FILING DATE: 05-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 124-599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

[illegible]

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,477
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00571
; FILING DATE: 13-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505059.7
; FILING DATE: 13-MAR-1995
; APPLICATION DATA:
; APPLICATION NUMBER: GB 9518946.0
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9524825.8
; FILING DATE: 05-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 124-599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-477-17

Query Match 30.7%; Score 557; DB 1; Length 480;
Best Local Similarity 37.4%; Pred. No. 5.9e-41;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

Qy 7 YNTNPGAFVGLDQVALNTLPGKNPKLTTELVELLKGK-ITIS-----ADSSSTLSK-- 57
Db 159 YEONPQHFIEDLEKRVVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSVFANRVI 218
Qy 58 -----EQLEKLLAAYLTDPASINGCWAMGQFKGGODAAIAIKGVIERGAKQTPPVTHWTI 113
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Qy 114 PEFMLLSLSALTWERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173
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RESULT 4
US-08-913-477-23
; Sequence 23, Application US/08913477
; Patent No. 5985285
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; GENERAL INFORMATION:
; APPLICANT: Titball, Richard W.
; APPLICANT: Williamson, Ethel D.
; APPLICANT: Leary, Sophie E.C.
; APPLICANT: Oyston, Petra C.F.
; APPLICANT: Bennett, Alice M.
; TITLE OF INVENTION: VACCINES FOR PLAGUE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 No. 5985285th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,477
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00571
; FILING DATE: 13-MAR-1996
; PRIOR APPLICATION DATA:
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; FILING DATE: 13-MAR-1995
; APPLICATION DATA:
; APPLICATION NUMBER: GB 9518946.0
; FILING DATE: 15-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9524825.8
; FILING DATE: 05-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 124-599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-913-477-23

Query Match 30.7%; Score 557; DB 1; Length 501;
Best Local Similarity 37.4%; Pred. No. 6.3e-41;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

Qy 7 YNTNPGAFVGLDQVALNTLPGKNPKLTTELVELLKGK-ITIS-----ADSSSTLSK-- 57
Db 180 YEONPQHFIEDLEKRVVEQLTGHGSSVLEELVQLVKDKNIDISIKYDPRKDSVFANRVI 239
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Qy 114 PEFMLLSLSALTWERTDDDLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEIN 173
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; Sequence 23, Application US/08913477
; Patent No. 5985285
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QY 293 AEYKDKNNKLGNFSTVSRSRPLNDLVSEKTLARLNDVSSRYNAIEALNRFIOKYDS 352
Db 430 NSSYKNNKLNELSHFATTCDSKRPLNDLVSQTKTQLSDITSRFSNAIEALNRFIOKYDS 489
QY 353 IMRDIL 358
Db 490 VMQRLL 495

RESULT 5
US-09-252-991A-30058
; Sequence 30058, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30058
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30058

Query Match 26.1%; Score 474; DB 2; Length 297;
Best Local Similarity 36.0%; Pred. No. 6.8e-34;
Matches 118; Conservative 50; Mismatches 94; Indels 66; Gaps 7;

QY 36 ELVELLKGITTSADSTALSKEQLEKLLAAVLTDPASINGGWMQGFKGQDAAIAATK 95
Db 34 ELUALLRSRIVLAHAGPLSEAOVLKALAWLLAANPSAPPG-----QGLEVLR 82
QY 96 GVIERGAKPTPVVHTWITPEFMLLSLGALTMERTDDDLITFTGVMMFQDNORKGLRDEL 155
Db 83 EVLQ---ARRQPGAQWDLREFLVSAFSL-HGRLEDVIGVKDVLQTDQGRKALLDEL 138
QY 156 AEMTAEKLYGVITQSEINQVLSAASQTKT-NFNLMYKLYGYE-SLAKFMEGGEFKLL 213
Db 139 KALTAEKLYSVIQSQINAAKQIRIDAGGIDLVDPTLYGAVGDPRWKDSPEYALL 198
QY 214 SKMFSDEQVTKAQODFTNAKNELENVTSTSLNPKIQAEAKTDYERKKAIFEEIVETQIIT 273
Db 199 SNL-----DTFSCK-----LS 209
QY 274 LKTFLESDLKKGAMSGIEAEYKYDKNNKLGNFSTVSRSRPLNDLVSEKTLARLNDV 333
Db 210 IKDFLSCPSQSGELKGLRDEYVPEFEDNNPVGNFATTVSDRSRPLNDKVNKXTLLINDTS 269
QY 334 SRYNAIEALNRFIOKYDSIMRDILGAI 361
Db 270 SRYNSAVEALNRFIOKYDSVLRDILSAI 297

RESULT 6
US-09-248-588-36
; Sequence 36, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; TITLE OF INVENTION: their Derivatives
; FILE REFERENCE: SYN-101 4564/69529
; CURRENT APPLICATION NUMBER: US/09/248,588
; CURRENT FILING DATE: 1999-02-11
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; EARLIER APPLICATION NUMBER: 60/074537
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Versinia pectis
; PUBLICATION INFORMATION:
; AUTHORS: Hill, J.
; AUTHORS: et al.,
; JOURNAL: Infect. Immun.
; VOLUME: 65
; ISSUE: 11
; PAGES: 4476-
; DATE: (1997)
; US-09-248-588-36

Query Match 13.9%; Score 253; DB 2; Length 142;
Best Local Similarity 33.9%; Pred. No. 9.7e-15;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITTTGVMMFQDNORKGLRDELAEMTAEKLYGVIOSEINQVLSAASN-QTFKTNFNL 190
Db 1 DILKIVIVDSMNHHGDARSKLRELAELTAEKLYSVIOAEINKHLSSTGTINIHDKSINL 60
QY 191 MDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEIFKASAEYKILEKM---PQTT-----IQV 93
QY 251 EAKTDYERKKAIFEEIVETQIITLTKTFLESDLKKGAMSGIEAEYKYDKNNKLGNFST 310
Db 94 DGS-----EKKIVSIKDFLGSENKRTGALGNKLSYNNKDNELSHFATT 139
QY 311 VSD 313
Db 140 CSD 142

RESULT 7
US-09-861-451A-46
; Sequence 46, Application US/09861451A
; Patent No. 6759516
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific & Industrial Research Orga
; TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences
; FILE REFERENCE: FF34033/01
; CURRENT APPLICATION NUMBER: US/09/861,451A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PP7273
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein
; OTHER INFORMATION: sequence from clone pad922
US-09-861-451A-46

Query Match 7.0%; Score 127; DB 2; Length 367;
Best Local Similarity 24.0%; Pred. No. 0.0063;
Matches 63; Conservative 46; Mismatches 90; Indels 64; Gaps 13;

QY 132 DLITTTGVMMFQDNORKGLRDELAEMTAEKLYGVIOSEINQVLSA-----ASNQT 183
Db 21 DLEMLEKGNFQDFINFQWSRIEKENLAQISTDKITEAKINEFFNSYLLYFEKLQKL 80
QY 184 FKTENLMDYKLYGYESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENVTST 243
Db 81 FSSSYNL-----GYENVAKLYD--YFVEVQKIYRQKQAKVFEFDRSAKKDYEDQLK-- 130
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Search completed: June 16, 2006, 19:28:54
Job time : 68.6236 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.
OM protein - protein search, using sw model
Run on: June 16, 2006, 20:12:36 ; Search time 201.925 Seconds
(without alignments)
828.131 Million cell updates/sec
Title: US-10-813-908A-8
Perfect score: 1816
Sequence: 1 MSTIPDYNTNPGAFVGLDV.....ALNRFIOKYSIMRDLGAI 361
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pbp.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pbp.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pbp.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pbp.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1816	100.0	361	5	US-10-813-908-8
2	557	30.7	326	5	US-10-987-533-1
3	253	13.9	142	3	US-09-930-915A-11
4	253	13.9	142	4	US-10-082-014-33
5	253	13.9	142	4	US-10-372-076-34
6	253	13.9	142	4	US-10-732-862A-48
7	253	13.9	142	4	US-10-806-006-11
8	253	13.9	142	4	US-10-677-074-34
9	253	13.9	142	4	US-10-805-913-11
10	132	7.3	506	4	US-10-424-539-238728
11	129	7.1	459	4	US-10-702-305A-18
12	129	7.1	1404	5	US-10-732-923-3304
13	129	7.1	2013	6	US-11-097-143-13758
14	128.5	7.1	1939	5	US-10-732-923-3340
15	127	7.0	367	3	US-09-861-451A-46
16	127	7.0	2539	5	US-10-831-070-6
17	125	6.9	643	4	US-10-282-122A-68817
18	121.5	6.7	1196	4	US-10-282-122A-52737
19	121	6.7	366	3	US-09-906-179A-179
20	121	6.7	366	4	US-10-671-403-144
21	121	6.7	366	4	US-10-671-419-144
22	121	6.7	366	4	US-10-670-844-144
23	121	6.7	366	4	US-10-671-134-144
24	121	6.7	366	4	US-10-673-098-144
25	121	6.7	366	4	US-10-672-638-144
26	121	6.7	366	4	US-10-673-127-144
27	121	6.7	366	4	US-10-670-817-144

28	121	6.7	366	4	US-10-673-119-144	Sequence 144, App
29	121	6.7	366	4	US-10-671-207-144	Sequence 144, App
30	121	6.7	366	5	US-10-673-120-144	Sequence 144, App
31	121	6.7	366	5	US-10-671-412-144	Sequence 144, App
32	121	6.7	366	5	US-10-671-859-144	Sequence 144, App
33	121	6.7	366	5	US-10-671-106-144	Sequence 144, App
34	121	6.7	366	5	US-10-671-106-144	Sequence 144, App
35	121	6.7	616	4	US-10-282-122A-76864	Sequence 76864, A
36	121	6.7	832	3	US-09-864-636A-446	Sequence 446, App
37	121	6.7	832	3	US-09-864-426A-446	Sequence 446, App
38	120.5	6.6	980	4	US-10-084-839-446	Sequence 446, App
39	120.5	6.6	989	5	US-10-211-462-145	Sequence 145, App
40	120	6.6	835	3	US-10-821-234-975	Sequence 975, App
41	120	6.6	835	3	US-09-864-636A-450	Sequence 450, App
42	120	6.6	835	4	US-09-864-426A-450	Sequence 450, App
43	120	6.6	1095	4	US-10-084-839-450	Sequence 450, App
44	120	6.6	1277	4	US-10-128-714-8039	Sequence 3039, Ap
45	119.5	6.6	815	4	US-10-128-714-8039	Sequence 8039, Ap
					US-10-437-963-191043	Sequence 191043,

ALIGNMENTS

RESULT 1

US-10-813-908-8
; Sequence 8, Application US/10813908
; Publication No. US20050058662A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and
; FILE REFERENCE: MIC01/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813,908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
; US-10-813-908-8

Query Match		100.0%;	Score 1816;	DB 5;	Length 361;
Best Local Similarity		100.0%;	Pred. No. 2.1e-131;		
Matches 361;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSTIPDYNTNPGAFVGLDV	VOALNTLPGNKNPKLT	TELVELLKGKITIS	ADSSTALSKEQL 60
Db	1	MSTIPDYNTNPGAFVGLDV	VOALNTLPGNKNPKLT	TELVELLKGKITIS	ADSSTALSKEQL 60
Qy	61	EKLLAAYLTDPASINGWANGOKG	GODAAIAIKGVI	ERGAKOTPPVHTT	PEFMLS 120
Db	61	EKLLAAYLTDPASINGWANGOKG	GODAAIAIKGVI	ERGAKOTPPVHTT	PEFMLS 120
Qy	121	LSALTWERTDDDLITFTGVMMFQ	DNQKRLRDELAEMT	AELKIYGVIOSEIN	OVLSAAS 180
Db	121	LSALTWERTDDDLITFTGVMMFQ	DNQKRLRDELAEMT	AELKIYGVIOSEIN	OVLSAAS 180
Qy	181	NOTFKTNFNLMYKLYGYESLAKF	MEGGEPKLLSKNFS	DEQVTKAQODFTN	AKNELENTV 240
Db	181	NOTFKTNFNLMYKLYGYESLAKF	MEGGEPKLLSKNFS	DEQVTKAQODFTN	AKNELENTV 240
Qy	241	STSLNPKIOAEAKTDYERKKAIF	EETIVETQIITLKT	PLESDLKSGMSGIE	AEYKYDKD 300
Db	241	STSLNPKIOAEAKTDYERKKAIF	EETIVETQIITLKT	PLESDLKSGMSGIE	AEYKYDKD 300
Qy	301	NNKLGNFSTSVSDRSRPLNDLV	SEKTLARLNDVSR	RYNAALNRRFIQK	YDYSIMRDLGA 360
Db	301	NNKLGNFSTSVSDRSRPLNDLV	SEKTLARLNDVSR	RYNAALNRRFIQK	YDYSIMRDLGA 360

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QY 361 I 361
Db 361 I 361

RESULT 2
US-10-987-533-1
; Sequence 1, Application US/10987533
; Publication No. US2005022079A1
; GENERAL INFORMATION:
; APPLICANT: Chanh, Tran C.
; APPLICANT: Andrews, Gerard P.
; APPLICANT: Adamovics, Jeffrey J.
; APPLICANT: Powell, Bradford S.
; TITLE OF INVENTION: Prophylactic and Therapeutic Monoclonal Antibodies
; FILE REFERENCE: 003/307/SAP
; CURRENT APPLICATION NUMBER: US/10/987,533
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/519,384
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word XP
; SEQ ID NO 1
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Yersinia Pestis
; FEATURE:
; OTHER INFORMATION: V antigen
US-10-987-533-1

Query Match 30.7%; Score 557; DB 5; Length 326;
Best Local Similarity 37.4%; Pred. No. 1.7e-34;
Matches 137; Conservative 61; Mismatches 104; Indels 64; Gaps 9;

QY 7 YNTNPGAFWGLDVQALNTLPGNNPKLTVELLKGK-ITIS-----ADSTALSK-- 57
Db 5 YEQNPQHFIEDLEKVRVEQLTGHSSVLELVQLVKDKNIDISIKYDPRKDSVFANRVI 64
QY 58 -----EOLKLLAAYLTPASINGWAMGQPKGQDAAIAIKGVIERGAKQTPPVTHWTI 113
Db 65 TDDIELLKKLALVLPEDALLKGHHVDNLQNG-----IKRVKFLE-----SSPQWEL 115
QY 114 PEFMLLSLSALTMTERTDDDLITFTGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEIN 173
Db 116 RAFMAVHPSLTADRIDDDILKIVDSMNHGHDARSKLREELAEALTAELKIYSVIOAEIN 175
QY 174 QVLASAASN-QTFKTNFNMDYKLYGESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNA 232
Db 176 KHLSSSGTINIHDKSIINLMDKNLYGYTDEEIFKASAEYKILEKM---PQTT----- 223
QY 233 KNELENVVTSTSLNPKIOAEAKTDYERKKAIFEIVETQIITLKTFLSGLKSGAMSGIE 292
Db 224 -----IQVDS-----EKKIVSIKDFLGSNKRTGALGNLJK 254
QY 293 AEYKDKNNKLNFGSTVSRSRPLNDLVSEKTLARLNDVSSRYNAALRNRFIOKYS 352
Db 255 NSYSYKNNKNNELSHFATCTCDKSRPLNDLVSOXTTLQSDITSRFSNAIEALNRFIOKYS 314
QY 353 IMRDIL 358
Db 315 VMQRLL 320

RESULT 3
US-09-930-915A-11
; Sequence 11, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; STABILITY
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
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; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-09-930-915A-11

Query Match 13.9%; Score 253; DB 3; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITFTGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190
Db 1 DILKIVDSMNHGHDARSKLREELAEALTAELKIYSVIOAEINKHLSSSGTINIHDKSIINL 60
QY 191 MDYKLYGESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENVVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93
QY 251 EAKTDYERKKAIFEIVETQIITLKTFLSGLKSGAMSGIEAEYKYDKNNKLNFGST 310
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKNNELSHFATT 139
QY 311 VSD 313
Db 140 CSD 142

RESULT 4
US-10-082-014-33
; Sequence 33, Application US/10082014
; Publication No. US2003018585A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL C
; FILE REFERENCE: ICC-130.0 4564/85124
; CURRENT APPLICATION NUMBER: US/10/082,014
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-082-014-33

Query Match 13.9%; Score 253; DB 4; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITFTGVMMFQDNQRKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190
Db 1 DILKIVDSMNHGHDARSKLREELAEALTAELKIYSVIOAEINKHLSSSGTINIHDKSIINL 60
QY 191 MDYKLYGESLAKFMEGGEFKLLSKMFSDEQVTKAQODFTNAKNELENVVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEEIFKASAEYKILEKM---PQTT-----IQV 93
QY 251 EAKTDYERKKAIFEIVETQIITLKTFLSGLKSGAMSGIEAEYKYDKNNKLNFGST 310
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKNNELSHFATT 139
QY 311 VSD 313
Db 140 CSD 142
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RESULT 5
US-10-372-076-34
; Sequence 34, Application US/10372076
; Publication No. US20030198645A1
; GENERAL INFORMATION:
; APPLICANT: Page, Mark
; APPLICANT: Friede, Martin
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; TITLE OF INVENTION: CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/372,076
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-372-076-34

Query Match 13.9%; Score 253; DB 4; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

Qy 132 DLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEELTAELKIYSVIOAEINKHLSGGTINIHDKSINL 60
Qy 191 MDYKLYGYESLAKFMEGEPEKLLSKMPSDEOVTKAQODFTNAKNELENVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEEIKFASAEYKILEKM---PQTT-----IQV 93
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEAEYKYDKONKLNLFNSTS 310
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139
Qy 311 VSD 313
Db 140 CSD 142

RESULT 6
US-10-732-862A-48
; Sequence 48, Application US/10732862A
; Publication No. US20040146524A1
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: Lyons, Katelynne J.
; TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICC-136.0 (4564-88881)
; CURRENT APPLICATION NUMBER: US/10/732,862A
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,123
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis

US-10-732-862A-48

Query Match 13.9%; Score 253; DB 4; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

Qy 132 DLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEELTAELKIYSVIOAEINKHLSGGTINIHDKSINL 60
Qy 191 MDYKLYGYESLAKFMEGEPEKLLSKMPSDEOVTKAQODFTNAKNELENVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEEIKFASAEYKILEKM---PQTT-----IQV 93
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEAEYKYDKONKLNLFNSTS 310
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139
Qy 311 VSD 313
Db 140 CSD 142

RESULT 7

US-10-806-006-11
; Sequence 11, Application US/10806006
; Publication No. US20040152876A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/91644 ICC-102.2 DV I
; CURRENT APPLICATION NUMBER: US/10/806,006
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/41759
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-806-006-11

Query Match 13.9%; Score 253; DB 4; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

Qy 132 DLITFTGVMFQDNQKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-OTFKTNFNL 190
Db 1 DILKVIIVDSNMNHHGDARSKLREELAEELTAELKIYSVIOAEINKHLSGGTINIHDKSINL 60
Qy 191 MDYKLYGYESLAKFMEGEPEKLLSKMPSDEOVTKAQODFTNAKNELENVTSTSLNPKIOA 250
Db 61 MDKNLYGYTDEEIKFASAEYKILEKM---PQTT-----IQV 93
Qy 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKGAMSGIEAEYKYDKONKLNLFNSTS 310
Db 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKONNELSHFATT 139
Qy 311 VSD 313
Db 140 CSD 142

RESULT 8

US-10-677-074-34

; Sequence 34, Application US/10677074
; Publication No. US20040156863A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Schmidt, Annette Elisabeth
; APPLICANT: Stober, Detlef
; TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
; TITLE OF INVENTION: CHRONIC HEPATITIS
; FILE REFERENCE: 4564/87179
; CURRENT APPLICATION NUMBER: US/10/677,074
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 10/372,076
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-677-074-34

Query Match 13.9%; Score 253; DB 4; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITFTGVMMFQDNORKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190
DB 1 DILKVIIVDSNMNHCDAKRLRELAELTAELKIYVIOAEINKHLSSSGTINIHDKSINL 60

QY 191 MDYKLYGYESLAKPMEGEGFKLSKMFSDQVTKAQOQDFTNAKNELENVTSTSLNPKIQ 250
DB 61 MDKNLYGYTDEEIFKASAEVKILEKM---PQTT-----IQV 93

QY 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKSAGMSGIEAEYKYDKNNKLGNFSTS 310
DB 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKDNLSHPATT 139

QY 311 VSD 313
DB 140 CSD 142

RESULT 9
US-10-805-913-11
; Sequence 11, Application US/10805913
; Publication No. US20040156864A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; TITLE OF INVENTION: STABILITY
; FILE REFERENCE: 4564/91645 ICC-102.2 DV II
; CURRENT APPLICATION NUMBER: US/10/805,913
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/930,915
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: PCT/US01/41759
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-805-913-11

Query Match 13.9%; Score 253; DB 4; Length 142;
Best Local Similarity 33.9%; Pred. No. 1.4e-11;
Matches 62; Conservative 28; Mismatches 51; Indels 42; Gaps 4;

QY 132 DLITFTGVMMFQDNORKGLRDELAEMTAELKIYGVIOSEINQVLSAASN-QTFKTNFNL 190
DB 1 DILKVIIVDSNMNHCDAKRLRELAELTAELKIYVIOAEINKHLSSSGTINIHDKSINL 60

QY 191 MDYKLYGYESLAKPMEGEGFKLSKMFSDQVTKAQOQDFTNAKNELENVTSTSLNPKIQ 250
DB 61 MDKNLYGYTDEEIFKASAEVKILEKM---PQTT-----IQV 93

QY 251 EAKTDYERKKAIFEEIVETQIITLKTFLSDLKKSAGMSGIEAEYKYDKNNKLGNFSTS 310
DB 94 DGS-----EKKIVSIKDFLGSNKRTGALGNLKNYSYNKDNLSHPATT 139

QY 311 VSD 313
DB 140 CSD 142

RESULT 10
US-10-424-599-238728
; Sequence 238728, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 238728
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(506)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_57597C.1.pap
US-10-424-599-238728

Query Match 7.3%; Score 132; DB 4; Length 506;
Best Local Similarity 23.1%; Pred. No. 0.17;
Matches 85; Conservative 73; Mismatches 132; Indels 78; Gaps 18;

QY 33 KLTELVELLKGKITTISADSSSTALSKEQLEKLLAA-----YLTDPASINGGWMGQFKG 85
DB 30 KYSELESVLEAEKYSQNSLNOIS--TLEEKRGASEGQANKYLDVDSNUTS--ELEAIQA 85

QY 86 QODAAIAAKGVIERGAKQTPPVTHWTIPEFMLLSLSLTMBERTD--DDLITTTGYMMFQ 144
DB 86 RASTLETTLQAAANERKGELED-----SLNAVTEEKKNLEDAISINLEKLAEK 132

QY 145 DNQRKGLRDE-----LAEMTAELKIYGVIOSEINQVLSAASNQTF-----KTNFNL 190
DB 133 ENLLEILRDDNLMTQDKLQSTEDLREAEPLRESEIEIKLKASEENLVVRGRDIEETAARH 192

QY 191 MDYKLYGYESLA-----KFMEGGE-----FKLLSKM-FSDEQVTKAQOQDFTNAKNE 235
DB 193 SELQLL-HESUTRDESEKQFQEAIEKFNKNDSEVQSLEKILEEQIAKAGEQSTSLKNE 251

QY 236 LENVTSTSLNPKIQAEAKTDYERKKAIFEEIVETQIITLKTFLSDLKKSAGMSGIEAEY 295
DB 252 FEE-----SLSKLASLESENEIDLKRG-----ILEAEKSSQSPSENELLVG---TNIQLKT 299

QY 296 KYDKNNKLGNFSTSVDSRPLNDLVSEKTA--RLNDV---SSRYNAIAEALNRFIOKY 350
Db 300 KIDELESLNH---ALSEKEAAQELVSHKNSITSLNDLQSKSSBIOQANEAL---ILKV 353
QY 351 DSIMRDIL 358
Db 354 ESQLEAL 361

RESULT 11

US-10-702-305A-18
; Sequence 18, Application US/10702305A
; Publication No. US20040213803A1
; GENERAL INFORMATION:
; APPLICANT: Michael C. Chen
; APPLICANT: Chuang-Jiun Chiou
; APPLICANT: Zhongming Li
; APPLICANT: Dong-Sheng Chen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING OR
; TITLE OF INVENTION: PREVENTING PNEUMOCOCCAL INFECTION
; FILE REFERENCE: 12844-002001
; CURRENT APPLICATION NUMBER: US/10/702,305A
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 60/424,497
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: polypeptide of pSA-60 PspA insert sequence
US-10-702-305A-18

Query Match
Best Local Similarity 7.1%; Score 129; DB 4; Length 459;
Matches 80; Conservative 63; Mismatches 127; Indels 82; Gaps 15;
QY 19 DVQALNTLPGNKPKLTTEL-VLLKGGKITISADSSSTALSKEQ---LEKLLAAYLTDP--- 71
Db 154 DYATLKVALAKVEAKELEIEKLQYEIS-TLEQVAIAQHVDNLNKKLAG--ADPDG 210
QY 72 -----ASINGWANGQFGGQDAALAAIKGVIERGAKOTPPVTHWTIPEFMLLSALTM 126
Db 211 TKVTEAKLN-----KGAEALNAKQAEALAKKQTELEKLLSLD--PE 249
QY 127 ERTDDDLITFTGVMMFODNOKGLRDELAEMTAELKIYGVIOSEINQVLSAASNQTFKT 186
Db 250 GKTDQLDKKAAEAL--DKKADLQNKVADLEKGIAPYQIKVAELNKEITA-----RL 300
QY 187 NFNLMYKLYGYESLAKFMGEGFKLLSK-----MFSDEQVTKAQDFTNAKNELENTST 242
Db 301 QSDLKDAEENNVEDIK--EGLEQAIADKKAELATTQKNIDKTQKDLDAELEKVLAT 358
QY 243 SLNPKIOAEAKTYDERKKAIFEIVEVETIITLK-----TFLESCLKSGAMSGIE 292
Db 359 -LDPEGTQDELKAEAEADANIERALQNKVADLNKVAELDKVEVTRLQSDLK-----D 409
QY 293 AEYKYDKNNKLGNFSTSVDSRPLNDLVSEKTAARNDVSSRYNAIAEALN 344
Db 410 AEENNVEDYVKEG-----LDKALTDDKKVLLNNTQKALDTTQAKALD 449

RESULT 12

US-10-732-923-3304
; Sequence 3304, Application US/10732923
; Publication No. US2005010879A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3304
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-10-732-923-3304

Query Match
Best Local Similarity 7.1%; Score 129; DB 5; Length 1404;
Matches 88; Conservative 57; Mismatches 136; Indels 108; Gaps 18;
QY 29 NKNPKLTVELLKGK-----ITISADSSSTALSKEQ-LEKLLAAYLTDPASING----- 76
Db 598 NTNPNYATLIQKLOAKLDAKNSITKSSNKSIDIATNQALQALAEKTEKESANSQNAV 657
QY 77 ----GWANGQPK-----GGQDAALAAIKGVIERGAKOTPPVTHWTIPEFMLLSLS 122
Db 658 KNTLNETIGKAKELDKNLTDSDGEIQQAKAELTNEIEK-ANQT-----IASNN 704
QY 123 ALTWERTDDDLITFTGVMMFQD---NORKGLRDELAEMTAELKIYGVIOSEINQVLSAA 179
Db 705 TALMENSNTSLNKISEVQNKLDKFNNDKKAEFNKLOE-----LNKIDDFEKN 754
QY 180 SNOTFKTNFN---LMDYKLYGYESLAKFMGEGFK-----LLSKMFSDEQ 221
Db 755 KNEIYKFNDELINLKVQIKNSLGSINSSNKKDIDVANKKQDALNELQAKM--AEI 812
QY 222 VTQAQDFTNAKNELENTSTSLNPKIOAEAKTYDERKKAIFEIVEVETIITLKTFLES 281
Db 813 HKKTFQEFNEHKNELENL---IKKEDAKEVGTD-EANTAI-----TNND 852
QY 282 LKXSGAMSGI-----EAERYKYD-KNNKLGNFSTSVDSRPLNDLVSEKTAARNDV 332
Db 853 VKENSIEETTKATKALDEAKSLDKQKINTQKATELSLNESEKELNLI---TSSNQV 909
QY 333 S-----SRYNAAIEALNRFIOKYDSIMRDI 357
Db 910 SAEISKAKKVLBEINNLNNDSSIKSL 938

RESULT 13

US-11-097-143-13758
; Sequence 13758, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13758

; LENGTH: 2013

; TYPE: PRT

; ORGANISM: DROSOPHILA

US-11-097-143-13758

Query Match

Best Local Similarity 7.1%; Score 129; DB 6; Length 2013;

Matches 83; Conservative 78; Mismatches 138; Indels 94; Gaps 17;

Qy 33 KLTELVELLKGKI-----TISADSTSLKSEQLKLAAYLTPASINGWAMQFGQGD 88

Db 1251 KLNQLLNAAKDELHDVRRIKDDEISALRMEFLLIQIETNEKENQAKFYA--ELQETKDRYE 1308

Qy 89 AATAAKGVIERGAKQTPPTHWTIPFMLL-----SLSALTWERTDDDLITFTGVMM 142

Db 1309 SNVAELKEKLQVEETLSSVTVRQAELEALKSAHNISQAVEER--NNLIVQHOAEM- 1365

Qy 143 FQDNQRKGLRDLAE-MTAEKIVGVIOSEINQVLSAASNOTFTKN-----FNLMDYK 194

Db 1366 --ETIRETLKNLAESTQSKMEDAFRAINEVRATLMEQLNOTKEDRDKGASKLEEVK 1423

Qy 195 LYGVESLAKPMEGEFKLLSKMFSDEQVTKAQODF-----TNAKNEL 236

Db 1424 ---KTLQOMINGG--RVMSDTIAELEKTKAEQDLAVNKLTKDNIELEKQCSKTQBOLOM 1477

Qy 237 ENVTSTSLNPKIOAEK-----TDYERKKAI-FEEIVETQIITL-----KTFLESCLK 284

Db 1478 ESLTRDQISFEIHAHTKLELIVASSKKRIIELEKCDQOVLELDKCRLEKLSLESEIQ 1537

Qy 285 SGA-----MSGIEAEYKYDKN-----KLGNFSTSVSRSRPL----- 318

Db 1538 ANSEHSCMEKLQLOAEKVLNRNEKEKCFETKLETFPKITLDEVLKEAQHKVIL 1597

Qy 319 -NDLVSEK-----TARLNDVSSRYNAEALN 344

Db 1598 YDDLVSQHERLKICLAENELSSLNQKVMSLH 1630

RESULT 14

US-10-732-923-3340

; Sequence 3340, Application US/10732923

; Publication No. US20050108791A1

; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154

; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149

; SEQ ID NO 3340

; LENGTH: 1939

; TYPE: PRT

; ORGANISM: Plasmodium chabaudi

US-10-732-923-3340

Query Match

Best Local Similarity 7.1%; Score 128.5; DB 5; Length 1939;

Matches 59; Conservative 46; Mismatches 103; Indels 63; Gaps 11;

Qy 119 LLSALTWERTDDDLITFTGVMMFQDNQRKGLRDLAEWTAELKIVGVIOSEINQVLSA 178

Db 193 MSLDKLTCE-----VOEKDNLK-INKKVIKENNLRELKFMKEKNIEIES 239

Qy 179 ASNOTFTKNFNLMDYKLYGVESLAKFMEGEFKLLSKMFSDEQVTKAQODFTN--AKNEL 236

Db 240 LDG-TINDKKNAYEKLKLEISFEERKKMIEMLDLSKLEK-----EENFANKQAKLEK 288

Qy 237 ENVTSTSLNPKIOAEKTDYERKKAI-FEEIVETQIITLKTFLSCLKKSGMSGI----- 291

Db 289 ENEIIIEKLDIESREK-DFKSKEEKFAS-MENELNTLK-----SDLSKNACOMEVYKLEI 342

Qy 292 -----EAEYKYDKDNKNGNFSTSVSDR-----SRPLNDLYSEKT 326

Db 343 KOLSQSLVEKEREIFEIKNEYDDKINNKKKUSSINDKIDNTVILHSEBEKINKLLKEKE 402

Qy 327 ARLNDVSSRYNAEAL-NRFIOKYVDSIMRD 356

Db 403 TELNEIHKYKYNLEIETIKNELNEKEEELKN 433

RESULT 15

US-09-861-451A-46

; Sequence 46, Application US/09861451A

; Patent No. US20020068289A1

; GENERAL INFORMATION:

; APPLICANT: Commonwealth Scientific & Industrial Research Orga

; TITLE OF INVENTION: Methods of Identifying Antigen Gene Sequences

; FILE REFERENCE: PF34033/01

; CURRENT APPLICATION NUMBER: US/09/861,451A

; CURRENT FILING DATE: 2001-05-21

; PRIOR APPLICATION NUMBER: PF7273

; PRIOR FILING DATE: 1998-11-20

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 46

; LENGTH: 367

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Deduced protein

; OTHER INFORMATION: sequence from clone PAD922

US-09-861-451A-46

Query Match

Best Local Similarity 7.0%; Score 127; DB 3; Length 367;

Matches 63; Conservative 46; Mismatches 90; Indels 64; Gaps 13;

Qy 132 DLITFTGVMMFQD--NORKGLRDLAEWTAELKIVGVIOSEINQVLSA-----ASNQT 183

Db 21 DLEMLEKGNFEFQDFINFWQSRIEKIEENLAQISTDKITEAKINEFFNYSILLYFEKLQKL 80

Qy 184 FKTNFNLMDYKLYGVESLAKFMEGGEFFKLLSKMFSDEQVTKAQODFTNAKNELENVTSTS 243

Db 81 FSSSYNL-----GYENVAKLYD--YFYEYQKIYRQKQAKVEFDYRSAKKDVEDQLK-- 130

Qy 244 LNPKIQAEAKTDYERKKAI-FEEIVETQIITLKTFLSCLKKSGMSGI-----EAEYKY 297

Db 131 ---KIKQE-----KAFFIKTLNVKALNLKKEAQLKIDKFTAQNNLLTSYIDFNFY 179

Qy 298 DKDNKK-----LGNFS-----TSVSDRSRPLNDLVSEKT--ARLNDVSSRYN 337

Db 180 KIANNKALVTTDLKNYSFPFKQAIINKEIAKFLDRR---NILLEKNLFSFLN--ISEIE 234

Qy 338 AAIEALNRF-----IQKYDSIMRD 356

Db 235 KLFEIMNPNFKSQIEKYKSLTFD 257

Search completed: June 16, 2006, 20:24:51

Job time : 203.925 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:13:41 ; Search time 15.5553 Seconds
(without alignments)
523.484 Million cell updates/sec

Title: US-10-813-908A-8
Perfect score: 1816
Sequence: 1 MSTIPDYNTNPGAFVGLDV.....ALNRFIQYDSIMRDLGAI 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pap:
2: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pap:
3: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pap:
4: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pap:
5: /EMC Celleria_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pap:
6: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pap:
7: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pap:
8: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.5	6.6	980	7	US-11-289-102-296
2	117.5	6.5	9535	6	US-10-471-571A-4496
3	113.5	6.2	515	6	US-10-953-349-17060
4	113.5	6.2	541	6	US-10-953-349-17059
5	109	6.0	2478	6	US-10-471-571A-2278
6	107.5	5.9	720	6	US-10-449-902-51542
7	106.5	5.9	1169	6	US-10-527-411-20
8	106	5.8	686	6	US-10-449-902-45659
9	105	5.8	2871	6	US-10-505-928-100
10	104.5	5.8	972	6	US-10-480-962-4
11	104.5	5.8	1234	7	US-11-327-900-6
12	104	5.7	578	6	US-10-471-571A-1920
13	103.5	5.7	1224	6	US-10-449-902-41406
14	103	5.7	872	6	US-10-449-902-53872
15	103	5.7	971	6	US-10-449-902-45697
16	102	5.6	888	6	US-10-527-411-112
17	102	5.6	1056	6	US-10-449-902-45516
18	101.5	5.6	432	6	US-10-449-902-50904
19	101.5	5.6	677	7	US-11-165-586-44
20	101.5	5.6	844	6	US-10-449-902-56744
21	101.5	5.6	880	6	US-10-449-902-56394
22	101	5.6	311	6	US-10-953-349-17061
23	100.5	5.5	491	6	US-10-449-902-44584
24	100.5	5.5	561	6	US-10-953-349-20041
25	99.5	5.5	432	6	US-10-449-902-31206

26	99	5.5	466	6	US-10-953-349-33042	Sequence 33042, A
27	99	5.5	496	6	US-10-953-349-33041	Sequence 33041, A
28	99	5.5	562	6	US-10-953-349-33040	Sequence 33040, A
29	99	5.5	858	6	US-10-527-411-22	Sequence 22, Appl
30	99	5.5	860	6	US-10-527-411-175	Sequence 175, Appl
31	99	5.5	862	6	US-10-527-411-94	Sequence 94, Appl
32	99	5.5	862	6	US-10-527-411-171	Sequence 171, Appl
33	99	5.5	862	6	US-10-527-411-173	Sequence 173, Appl
34	99	5.5	864	6	US-10-527-411-102	Sequence 102, Appl
35	99	5.5	865	6	US-10-527-411-100	Sequence 100, Appl
36	99	5.5	866	6	US-10-527-411-88	Sequence 88, Appl
37	99	5.5	866	6	US-10-527-411-104	Sequence 104, Appl
38	99	5.5	867	6	US-10-527-411-80	Sequence 80, Appl
39	99	5.5	867	6	US-10-527-411-96	Sequence 96, Appl
40	99	5.5	867	6	US-10-527-411-98	Sequence 98, Appl
41	99	5.5	870	6	US-10-527-411-92	Sequence 92, Appl
42	99	5.5	871	6	US-10-527-411-84	Sequence 84, Appl
43	99	5.5	871	6	US-10-527-411-86	Sequence 86, Appl
44	99	5.5	871	6	US-10-527-411-90	Sequence 90, Appl
45	99	5.5	876	6	US-10-527-411-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1

US-11-289-102-296
; Sequence 296, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 296
; LENGTH: 980
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-296

Query Match	6.6%	Score 120.5;	DB 7;	Length 980;
Best Local Similarity	20.2%	Pred. No. 1.1;		
Matches	79;	Conservative	67;	Mismatches 151; Indels 95; Gaps 16;
QY	36	ELVELLKGKTTISADSTALSKEQLEKLLAAYLTDPASINGWAMGQFGQDAAIAIK	95	
Db	347	DLUSLQAKVA-----SLTHNKLQDKLQA---KSPKEADISFDSYHSTQ-----TDLG	395	
QY	96	GVIERGAKQPPVTHWTIPFELLSLSALMTERTDD-----LITTTGVMMFQDNQ	147	
Db	396	PSLGKPGTSPDPSK-SSPSVLHSLGKST---TDNVRIQQLQQLQLEILQKRLSEAE	451	
QY	148	RKGLRDLBMTAELKIYGVIOSEINQVLSAANQTKTNFNL-----MDYK	194	
Db	452	RKQLOVELOSRRAELVCLN--NTEISENSDDLSQLKTSQKYEAMKEVLVSQKQMKLG	509	
QY	195	LYGVESLAKFMEGEGFKLLSKMFSDEQVTKAQODFTNAKNE-----LENV	239	
Db	510	LVSPEMDNYSHFHELRV-----TEBEINVKLQDLQNALEESERNKEKVRLEEKLVRE	564	
QY	240	TSTSLNPKIO--AAAKTDY-----ERKKAIFEEIVETQ--IITLTFLESDLKKSQA	287	
Db	565	KGVIVKPPVEYEEMKSSYCVIENNNKKAFLFEKYQEAQBEIMKLKDTLKSQMTQE--	622	
QY	288	MSGIEAEYKYDKNNKLGNFSTSVSRPLNDLVSE-----KTARLNDVSSRY-----	336	

Db 263 LKQFELALGEASKSQI-VIADLSQERDDLKEALDNE--SSKVHKLQELQVTLLENLAKS 319
QY 289 SGIEAEY-----KYDKNNKLGNFSTVSDDR-SRPLND-----LVSEKT-- 326
Db 320 RNESAELNLLTSLNKLCKELEVSLSSELTEVNESLQRLDDAKHAEMLASLTTA 379
QY 327 -----ARLNDVSSRYNAIAEALNRFIQYDSIMRDIL 358
Db 380 KEHLKEAQELQGVSKELTALE-----KNDLSQKELV 412

RESULT 5

US-10-471-571A-2278
; Sequence 2278, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2278
; LENGTH: 2478
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(2478)
; OTHER INFORMATION: FmtB protein [Staphylococcus
US-10-471-571A-2278

Query Match 6.0%; Score 109; DB 6; Length 2478;
Best Local Similarity 19.3%; Pred. No. 23;
Matches 90; Conservative 64; Mismatches 146; Indels 166; Gaps 20;
QY 6 DYNTPGAFVGLDVQALNTLPG-----NKNPKLTVEL-----LKGKIT 46
Db 454 QNANKVTFTS-----QGVTTARGTHKEVLPDPDKSLKSYKVNVANIDTPKNIDFNEKLT 509
QY 47 ISADSSTALSKEQLEKLLAAYLTDPASINGWAMQFGGQDAIAIAKGVIERGAKQTP 106
Db 510 YRTASDVVINNAQPEVTLTA---DPFSV-----AVENMKDALQOQVNSQV 551
QY 107 PVTHWT---IPEFMLLSLSALTMERTD-----DDLITFTGVMMFQDNO- 147
Db 552 DNSHYTTASTAEYNKLLKQADTLINEDANHVKTANRASQADIDGLVTKLQAALI--DNQA 609
QY 148 -----RKGLRDE-----LAEMTAEKLYGV----- 167
Db 610 AIAELDTKAQEKVTAAGQSKVQDVEAALVTKINNDKNAIAEINKQTTAQGVTEKDN 669
QY 168 -----IQSEINQVLGAASNQTFKTNFNLMDYKLYGVESLAKMEGGEF 210
Db 670 GIAVLQDVITPVPKQAKQDIIQAVTTKQKQIKKSNASLQDEKDVANDKIGKI-----ET 725
QY 211 KLSKMFSEQVTKAQDQF--TNAKNELENVTSTSLNPKIOAEAKTDYERKKAFFESIVE 268
Db 726 KAIKDI--DAATTNAQVEAIKTKAINDINQTF-----PATTKAAALEE-----FDEWVQ 773
QY 269 TQI-----ITLKTFLSEDLKKSQA--MSGIEA-----EYKDYKDNKNKLGNFST 309
Db 774 AQIDQAPLNPDTTNEEVAEAIERINAAKVSQVKAIEATTTAQDLERKVNKEISKIENTID 833
QY 310 SVSDRSRPLNDLVSEKTAR-----LNDVSSRYNAIAEALNR 345
Db 834 STQTKMDAYNEVKQAAATARKAQATNSATNEEVAEADAADVAQAQ 879

RESULT 6

US-10-449-902-51542
; Sequence 51542, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51542
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-51542

Query Match 5.9%; Score 107.5; DB 6; Length 720;
Best Local Similarity 21.0%; Pred. No. 5.3;
Matches 85; Conservative 72; Mismatches 130; Indels 117; Gaps 20;
QY 33 KLTELVELLKGKI--TISADSSTALSKEQLEKL-----LAAVLT 70
Db 148 KIGELETQLKKEIDSRITAESSASAKESVKELEGNLQRLSENSEKKAALKKLSYLQD 207
QY 71 PASINGWAMQFPK-----GGQDAA-----IAAIKGVIERGAKQTPPVTHWTIPEFM 117
Db 208 DTKLISIKLNAELERMELRALNSEDEAKLLNEQLEDLKKQDDESVERNEMEH-----R 261
QY 118 LLSLSALTMERTDDD-----LITPTGVMMFQDN--QRKGL 151
Db 262 LLMCSSLSYERTSPDDQKLIKLOEELRNYEKEYDEARLKSSTNTVELLKEKILEBQGC 321
QY 152 RDELAEMTAEKLYGVITQSEINQV--LSAASNQTFKTNFNLMDYKLYGVESLAKMEGGEF 210
Db 322 R-ERAEM--ELSKLOEIEAKQAQKLELASCALLS--NIPDVSSFGD----- 364
QY 211 KLSKMFSDSDQVTKAQDFTNAKNELENVTSTSLNPKI-----QAEAKTDYER 258
Db 365 --IPQKIADIQ---KQALTNL-NKYGEVTSQKELKVALEFADLSKQRAEGEATLAKER 417
QY 259 KKAIFBEIVETQIITLTKTFLESD-LKSGAMS-----GIEAEYK-YDKNNKLGNFSTSVS 312
Db 418 AESATREIKLELELLAALISEERDLRKDHAVSKSRDGDASSKNMESDLSRMEKVVTELE 477
QY 313 DRSRPLNDLVSEKTARLNDVSSRYNAIAEALNRFIQYDSIMRD 356
Db 478 STTDRQELISQOQTEHLNLMNEK--LSIES-----RKAKSLERD 514

RESULT 7

US-10-527-411-20
; Sequence 20, Application US/10527411
; Publication No. US20060110410A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130005
; CURRENT APPLICATION NUMBER: US/10/527,411
; CURRENT FILING DATE: 2005-03-11

; PRIOR APPLICATION NUMBER: PCT/GB2003/003824
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 10/241,596
; PRIOR FILING DATE: 2002-09-12
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-527-411-20

Query Match
Best Local Similarity 5.9%; Score 106.5; DB 6; Length 1169;
Matches 81; Conservative 59; Mismatches 135; Indels 93; Gaps 20;

QY 12 GAFVGLDVQALNTLPGNKPKLTVELLKGKITISADSSTALSKEQLEKLAAYLTD 71
Db 588 GLFAGW-----VKQIVNDFVIEANKSNTMDKIADISLIVPYIGLA 627

QY 72 ASINGWAMQPKGGODAAIAIKGVIERGAKQTPPVTHWTIPFEMLLSLSALTMERTD 131
Db 628 LNVGNETAKNFENAEIAGAST--LLE-----FIPELLIPVVGAPFLLESYID 673

QY 132 D---LITFTGVMMFQDNQKGLRDELAEMTAEIKYGVIOSEINQVLSAASNQ--TFKT 186
Db 674 NKNKIITKTI-----DNALTKNEKWSDM-----YGLI---VAQWLSTVNTQFYTIKE 717

QY 187 N-FNLMDYKLYGVESLAKFMGEGEFKLLSKMFSEQVTKAQDFT--NAK-NELENVTST 242
Db 718 GMYKALNYQAQALEERIKYR-----YNIYSEKEKSNINIDFNDINSKLNAGINQAI 769

QY 243 SLNPKIQAEAKTDYERKKAIF---FEIIVETQIITLAKTFL-----ESDLKXKSGAMSGIEAEV 295
Db 770 NINNFING--CSVYLKMKMIMPLAVEKLDLFDNTLKNLNYIDENKLYLIGS-----AEY 823

QY 296 KYDKONKKNLGNFSTSVDSRRLNDLVSEKTLARLNDVSRYNAAIEALNRFI---QKYDS 352
Db 824 EKSVMKYLKTIIMP--FDLSIYNTDII-----LIEMFNKYS--EILNIIILNRYKDN 873

QY 353 IMRDLIG 359
Db 874 NLIDLGS 880

RESULT 8
US-10-449-902-45659
; Sequence 45659, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45659
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45659

Query Match
Best Local Similarity 5.8%; Score 106; DB 6; Length 686;
Matches 79; Conservative 63; Mismatches 130; Indels 110; Gaps 17;

QY 6 DYTNPFGAFVGLDVQALN-----TLPGNKPKLTVELLKGKITISADSSTALSKEQ 59
Db 338 DGHSTQEQFTG-LDMQLLYDMAQIILPADQRPKLTRL-----ISMDRRQVTKATD 388

QY 60 LEKLLAAYLTDPSINGWAMQPKGGODAAIAIKGVIERGAKQTPPVTHWTIPFEMLL 119
Db 389 MEDLI-----ARLNQEVAVKEYLA---TKVKDLEVELEATKKDKKEILHQAV----- 432

QY 120 SLSALTMERTDDDLITFTGVMMFQDNQKGLRDEL-----AEWTAEIKYGVIOSEINQV 175
Db 433 -----LTEREKIT-----QLQWDKDELYRYKSEMESLNKIE---QNEKTRV 470

QY 176 LSAASNOTPKTFNL--MDYKLYGVESLAKFMGEGEFKLLSK-----MFSDE 220
Db 471 QSEKTTASEKEMLLEETKKEVESLQOHI--GEFEAKSKADIKVLVKEVKSRLNSQK 528

QY 221 QYTKAQDFTNAKNELENVTSTSLNPKIQAEAKTDYERKKAIFE----- 264
Db 529 EMKKVLNQYHEEKTELERI-----VNRQKORSTRARFSREKILHECRLRLRERLQECTAKFV 584

QY 265 -EIVETQIITLAKTFL-----SD-----LKSGAMSGIEAEYKYDKONKKNLGNFSTS 310
Db 585 ADEQDQTMITDLSLFDALDLVTSDNRIRLVAEQAQLSRDDEQGSDDGDGNSDGKSVT 644

QY 311 VSDRSRPLNDLVSEKTLARLNDV 332
Db 645 MSEDAYVTD--EETTKMLSDL 664

RESULT 9
US-10-505-928-100
; Sequence 100, Application US/10505928
; Publication No. US2006008832A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 100
; LENGTH: 2871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-100

Query Match 5.8%; Score 105; DB 6; Length 2871;
Best Local Similarity 22.6%; Pred. No. 54;
Matches 53; Conservative 42; Mismatches 96; Indels 44; Gaps 9;

QY 135 TTTFTGVMMFQDNQKGLRDELAEMTAEIKYGVIOSEI---NQVLSAASNQTFKTNFNL 191
Db 1219 TTIKEISMQKEDDSKNRLNQLDRLSREN---DLKDEIVRLNDSILQATEQRRRAEENAL 1275

QY 192 DYKLYGVESLAKFMGEGEFKLLSKMFSEQVTKAQDFTNAKNELENVTST----- 242
Db 1276 QQACGSGEIMQK-KQHLEIELKQVM-----QQRSEDNARHKQSLEEAATTIQDKNKEIE 1328

QY 243 SLNPKIQAEAKTDYERKKAIF-----EEIV-----ETQI--ITLKTFLSDLKXSGAM 288
Db 1329 RLKAEFQAEAKRWEYENELSKVRNNYDEEIIISLKNQFETENITKTTTHQLTMQKEEDT 1388

QY 289 SGIEAEY-----KYDKONKKNLGNFSTSVDSRRLNDLVSEKTLARLNDVSSR 335
Db 1389 SCYRAQIDNLTRENSLSLEEIKRLKNTLTOTTENLRRVEEDIQQKATGSEVSQR 1443

RESULT 10
US-10-480-962-4

```
; Sequence 4, Application US/10480962
; Publication No. US20060115813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Junming; EMERLING, Brooke M.;
; APPLICANT: TANG, Y. Tom; BAUGHN, Mariah R.;
; APPLICANT: LEE, Ernestine A.; RAMKUMAR, Jayalaxmi;
; APPLICANT: YUE, Henry; GRIFFIN, Jennifer A.;
; APPLICANT: CHAWLA, Narinder K.; TRAN, Bao
; APPLICANT: NGUYEN, Dannel B.; KHAN, Farrah A.;
; APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
; APPLICANT: SWARNAKER, Anita; GURURAJAN, Rajagopal;
; APPLICANT: POLICKY, Jennifer L.; YAO, Monique G.;
; APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.;
; APPLICANT: ELLIOTT, Vicki S.; LEE, Soo Yeun;
; APPLICANT: SANJANWALA, Bharati; HONCHELL, Cynthia D.;
; APPLICANT: FORSYTHE, Ian J.; GORVAD, Ann E.;
; APPLICANT: RICHARDSON, Thomas W.; LEE, Sally;
; APPLICANT: BARROSO, Ines
; TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-1002 USN
; CURRENT APPLICATION NUMBER: US/10/480,962
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/US02/17955
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/297,010
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/298,706
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/299,998
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,377
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,871
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/303,349
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: US 60/303,403
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/351,927
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3418524CD1
US-10-480-962-4

Query Match      5.8%; Score 104.5; DB 6; Length 972;
Best Local Similarity 21.3%; Pred. No. 13;
Matches 81; Conservative 50; Mismatches 127; Indels 123; Gaps 18;

Qy      46  TISADSTALSKEOLEKLLAAYTD-----PASI-----NGG----- 77
Db      45  SVGGGSGKTLTSMENIQSLNAAYATSPGMYLSDHENVGSETPKSTMTLGRSGRLPYGVRM 104

Qy      78  WAMQOFKGGQDAATAAKGVIERGAKOTPPVT-HWTIPFPMLLSLSALTWTERTDDDLITT 136
Db      105  TAMGSSPNIASSGVAS--DTTAFGEHLLPPVSMASVTPHSL-----RQARDNTIMDLQIQ 157

Qy      137  FTGYMFMQDNQRKGL-----RDELAEMTAELKIYGV 167
Db      158  LKEVLRENDLLRKDVEKESKLSSMNSIKTFWSPELKKERALKRDEASKITIWKEQYRV 217

Qy      168  IQSE-----INQVLSAASH-----QTFKTNFNLMDYKUYGY 198
Db      218  VQEEENOHQMTQIALQDELRIQRDLNQLFQDSSSRTPGCPVAELTEENFORLHAE---H 274

Qy      199  ESLAKFMEGEFKLLSKWFSDEQV-TKAQODFTNAKNE-----LENTVSTSLNPKIQAEA 252
Db      728  QNRK--OLELKVTSLEELTDLRVEKESLEKNLSERKKSKSAQBSQAEEIDEIRK 781

Db      275  ERQAK-----ELFLRLKTLBEMELRIETQKOTLNARDESICKLLEMLQSKGLSAKATEE- 328
Qy      253  KTDYERKKAIFEEIVETQIITLKTFLFESDLKKGAMGIEAEYKYDK--DNKLGNFST- 309
Db      329  --DHETRRRLAE--AEMHVHLESLLLEQK-EKENSMLREEMHRRFENAPDSAKTKALQTV 383
Qy      310  -----SVSDRSRPLNDLVSE 324
Db      384  IEMKDSKISSMERGLRDLLEE 404

RESULT 11
US-11-327-900-6
; Sequence 6, Application US/11327900
; Publication No. US20060099174A1
; GENERAL INFORMATION:
; APPLICANT: PHARMA PACIFIC
; APPLICANT: Meritet, Jean Francois
; APPLICANT: Dron, Michel
; APPLICANT: Tovey, Michael Gerard
; TITLE OF INVENTION: INTERFERON-ALPHA INDUCED GENE
; FILE REFERENCE: 46658/250044
; CURRENT APPLICATION NUMBER: US/11/327,900
; CURRENT FILING DATE: 2006-01-09
; PRIOR APPLICATION NUMBER: US/10/203,311
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: GB 0002979.3
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: GB 0002980.1
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: GB 0002982.7
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: GB 0002981.9
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-327-900-6

Query Match      5.8%; Score 104.5; DB 7; Length 1234;
Best Local Similarity 18.8%; Pred. No. 18;
Matches 78; Conservative 71; Mismatches 150; Indels 117; Gaps 16;

Qy      19  DVQALNTLPCNKNPKLTVEL-----KEQLEKLLAAY---LTDPSASINGGWAMG 81
Db      404  EIEDVNTLQGGGQPVVTPSVQPSLQPAHPALPQMTSQAPQPSVTGLQAPSAALMQ---VS 460

Qy      48  SADSTALS-----KEQLEKLLAAY---LTDPSASINGGWAMG 81
Db      461  SLDSHSAVSGNAQSFQYAGQMAVAYPOASAVTSQLOVPVPLYPAPLSQPPHFGSGDMA 520

Qy      82  QFQGGQ-----DAAIAAKGVIERGAKOTPPVTHWTIPFPMLLSLSALTWTERTDDDL 133
Db      521  SFLMTEARQHTNIRMAVSKVADKMDHLMTKVEELQKHSAGNSMLIPSPMSVMTWE----- 574

Qy      134  ITTFTFGVM-----FQDNQKGLRDELAEMTAELKIYGVIOSEINQVLS--AASNOTFK 185
Db      575  -----TSMIMNSIQRIIOENER--LKOEILEKSNRIE-----EONDKISELIERNORYV 621

Qy      186  TPNFLMDYKLYGYESLAKFMEGEFKLLSKWFSDEQVTKAQODFTNAKNELENTVTS--TS 243
Db      622  EQSNLMWEK--RNNSLOTATENTQARVL-----HAEQEKAKVTEELAAATAQVSH 669

Qy      244  LNPKIQAEAKTDYERKKAIFEEIVETQI-----ITLKTFLFESDLKKGAMGIEAEYKYDK 299
Db      670  LQLKMTAHQKTELOMQLTESLKTDLRLGQLTKVQAKLSLQETSEQA--OSKPKSEK 727

Qy      300  DNKLGNFSTSVSDRSRPLNDLVSEKTLARLNDVSSRYNAEALNFIQKYDSEIMR 355
Db      728  QNRK--OLELKVTSLEELTDLRVEKESLEKNLSERKKSKSAQBSQAEEIDEIRK 781
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Qy      98 IERGAQTPPVTHWTIPFEMLLSLSALTWERTDDDLITTTCTVMFMFDONQRKGLRD---E 154
Db      460 LRSLSQSTEP---FDVP--MTDSVRAGSPKOIDDEVAKEWHEHTML-QDSMGKELNELNRQ   513
Qy      155 LAEMTAELKIYG-----VIQSEINQVLSA-----ASNQTFKTN 187
Db      514 LEQKESEMKGYSDDTVALKHQHFKKLLEBEKEKRAVQQERDLLAEVESLNADGQTHK-- 571
Qy      188 FNLMDYKLYGYEST-----AKFWGGGFELL-SKMFSDEQVTKAQOFTNAKNLEUNT 240
Db      572 --LRDAQIQUKUTLEAQILDLUKKQENOVQLLKEKQSDAEAAKLQEIHSTKAQ----- 624
Qy      241 STSLNPXIQAEB-----KTDYERKKAIFEETVETQIIILTKTLF 278
Db      625 KVQLQHKKIQEAEQFROWKATREKELLQURKEGRNEVERHK--LQALNQRKVLQRKT 682
Qy      279 ESDLKSGAMSG-TEAEKYDKDNKL-----GNPSTSVSRDRRPDLNDVEKSTARLNDV 332
Db      683 EEAAAMATRLKELLEARKSGSRDNSGMNGTPGSHMTEKSLOKWLEQDL--EVMVHVHVEV 740
Qy      333 SSRY 336
Db      741 RNEY 744

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RESULT 15

```

US-10-449-902-45697
; Sequence 45697, Application US/10449902
; Publication No. US20060123505A1
GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIORITY APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIORITY APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45697
; LENGTH: 971
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45697

```

Query Match	5.7%; Score 103; DB 6; Length 971;
Best Local Similarity	20.3%; Pred. No. 16;
Matches	86; Conservative 67; Mismatches 129; Indels 142; Gaps 22;
QY	21 QALNTLP-----GNKNP-----KUTELVELLKGITTSADSTLSK----- 57 : : :: : :: : Db 291 ETLNTLYKANRARNIQNPVNRPNVADEMKRMQRQIEYLQAEI-VSARGGVVLDDVOGL 349 -TDPA-----SINGGWAMQPKGGODAAIAIKGV 97 QY 58 -----EQLEKLLAAYL-----GDKL-----GDKL-----GDKL----- Db 350 RERISMLEQNEDLCRELYDLRNHYDTDPCEPELQKITGYTKGE-----G 395 QY 98 IERGAQTPTVHTWTFEEMLLSLALTMTERTDDDLITFTGVMMFODNORKGLRD--E 154 : : : : : : : : : : : : : Db 396 LKRSLOSTEP---FDVP--MTDSVRAGSPKDIDDEVAKWEHWTWL-QDSMGKELNELNRQ 449 - - - - -VTQSEINQVLSA-----ASNQTFKTN 187 QY 155 LAEMTAECLKTYG-----LKEEKRAVQOERDRLLAEVESLNADGOETHK-- 507 : : : : : : : : : : : : : Db 450 LEQKESMWMYSGSDTVALKQHFGKKLLEEEKRAVQOERDRLLAEVESLNADGOETHK-- 507 - - - - -SKMFSDSQVTKAQODFTNAKNEULENVT 240 QY 188 FNLMDYKLKYGESL-----AKMEWGEGFKLL-SKMFSDEQVTKAQODFTNAKNEULENVT 240 : : : : : : : : : : : : : Db 508 --LRDAQQLKLTLEAQILDKKKQENOVOLLAKOKSDSAANKLOBEHSIRKAO----- 560 : : : : : : : : : : : : :

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 18:52:40 ; Search time 105.354 Seconds
(without alignments)
690.032 Million cell updates/sec

Title: US-10-813-908A-9
Perfect score: 827
Sequence: 1 MQDTTITPVEAELEAFMA.....QADLAASAKVMLEAIAIRRD 159

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseqp2006s.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	827	100.0	159	5 ABB80777	Abb80777 A. salmon
2	596	72.1	168	6 ABM69523	Abm69523 Photorhab
3	549	66.4	167	6 ABU38392	Abu38392 Protein e
4	548	66.3	239	7 ABO81217	AbO81217 Pseudomon
5	177	21.4	171	6 ABU22325	Abu22325 Protein e
6	169.5	20.5	172	6 ABU40949	Abu40949 Protein e
7	167	20.2	161	3 AAB14112	Aab14112 Bordetell
8	166.5	20.1	165	6 ABU45583	Abu45583 Protein e
9	166.5	20.1	165	6 ABU48112	Abu48112 Protein e
10	166.5	20.1	165	9 ADW28241	Adw28241 Amino aci
11	165	20.0	151	7 ADC00814	Adc00814 Enterohae
12	163.5	19.8	182	7 ADF06293	Adf06293 Bacterial
13	151	18.3	156	6 ABM70111	Abm70111 Photorhab
14	125.5	15.2	157	3 AAY70581	Ray70581 Salmonell
15	125.5	15.2	157	6 ABU47399	Abu47399 Protein e
16	121.5	14.7	158	9 ABM94434	Abm94434 M. xanthu
17	118	14.3	144	3 AAY70582	Ray70582 Salmonell
18	116.5	14.1	154	9 ABM96865	Abm96865 M. xanthu
19	109	13.2	246	6 ABU27402	Abu27402 Protein e
20	107.5	13.0	163	4 AAG98281	Aag98281 Escherich
21	107.5	13.0	163	6 ABU14803	Abu14803 Protein e
22	107.5	13.0	227	10 AEB60329	Aee60329 Cat chlam
23	105	12.7	210	2 AAY35451	Aay35451 Chlamydia

24	105	12.7	231	6 ABU27062	Abu27062 Protein e
25	105	12.7	231	9 AEC95744	Aec95744 C. pneumo
26	101.5	12.3	234	2 AAY37634	Aay37634 Protein w
27	100	12.1	172	9 AEC95749	Aec95749 C. pneumo
28	100	12.1	191	2 AAY35677	Aay35677 Chlamydia
29	90	10.9	172	2 AAY37895	Aay37895 Amino aci
30	90	10.9	304	8 ADS29906	Ads29906 Bacterial
31	88.5	10.7	280	8 ADS22934	Ads22934 Bacterial
32	87	10.5	153	3 AAB14140	Aab14140 Bordetell
33	86	10.4	172	10 AEB60330	Aee60330 Cat chlam
34	86	10.4	264	3 AAG42356	Aag42356 Arabidops
35	86	10.4	341	3 AAG42355	Aag42355 Arabidops
36	86	10.4	342	3 AAG42354	Aag42354 Arabidops
37	84.5	10.2	1564	8 ADL12580	Adl12580 Human ste
38	83	10.0	639	9 ABM92892	Abm92892 M. xanthu
39	80.5	9.7	562	9 AEB27261	Aeb27261 Pinus rad
40	80.5	9.7	579	6 ABU20545	Abu20545 Protein e
41	80.5	9.7	676	8 ADN20615	Adn20615 Bacterial
42	80	9.7	458	2 AAR41781	Aar41781 Rabbit HB
43	79	9.6	315	4 AAB60367	Aab60367 Xenopus l
44	79	9.6	315	6 AAO30937	Aao30937 Frog aton
45	79	9.6	574	9 AEB27139	Aeb27139 Pinus rad

ALIGNMENTS

RESULT 1
ABB80777
ID ABB80777 standard; protein; 159 AA.
XX AC ABB80777;
XX DT 23-SEP-2002 (first entry)
XX DE A. salmonicida type III secretion protein acrH sequence.
XX KW Type III secretion protein; acr1; acr2; acr3; acr4; acrD; acrR; acrG;
XX KM acrV; acrH; antibiotic; vaccine; fish.
XX OS Aeromonas salmonicida.
XX PN WO200240514-A2.
XX PD 23-MAY-2002.
XX PF 15-NOV-2001; 2001WO-CA001589.
XX PR 15-NOV-2000; 2000US-0248864P.
XX (FREY/) FREY J.
PA (STUB/) STUBER K.
PA (THOR/) THORNTON J C.
PA (KUZY/) KUZYSK M A.
PA (BURI/) BURIAN J.
XX
PI Frey J, Stuber K, Thornton JC, Kuzyk MA, Burian J;
XX
DR WPI: 2002-537338/57.
DR N-PSDB; ABN86172.
XX
PT Novel protein from Aeromonas salmonicida and nucleic acid encoding the
PT protein, useful for reducing susceptibility of fish to infection by a
virulent strain of Aeromonas salmonicida.
XX
PS Claim 13; Page 29; 39pp; English.
XX
CC The invention relates to A. salmonicida type III secretion genes and
CC encoded proteins Acr1, Acr2, Acr3, Acr4, AcrD, AcrR, AcrG, AcrV or AcrH.
CC A. salmonicida type III secretion apparatus is useful for producing
CC selected products, especially Aext. AcrV in vaccine, epitope or epitopic
CC region of AcrV or any other protein of A. salmonicida type III secretion
CC apparatus is useful for reducing the susceptibility of fish to infection

Db	9	EXKELDOLANIYIVSIVONGASIKDSEIFDGMFEGIIYSFAYDFYQKGKLDSEAFKFLCL	68
QY	65	LDHYEPRYFLGLGACRQAMGBFETAVQSYSGFAMLDLKDPRFPFHAGECRLQOQDNLGAE	124
Db	69	YDFYNDYIMGLAAVNQLKKQQAIDLYALAYLNKNDYRPFVYAGQCNLSIGEKEKAK	128
QY	125	SGFH	128
Db	129	YCFH	132
RESULT 7			
AAB14112			
ID	AAB14112 standard; protein; 161 AA.		
XX	AAB14112;		
XX	02-FEB-2001 (first entry)		
XX	Bordetella pertussis class I gene protein BcrH.		
XX	BcrH; bacterial infection; anti-bacterial; vaccine; whooping cough;		
KW	type III secretion system; virulence factor; pathogenicity island.		
XX	Bordetella pertussis.		
XX	WO200037493-A2.		
XX	29-JUN-2000.		
XX	21-DEC-1999; 99WO-EP010297.		
XX	21-DEC-1998; 98GB-00028217.		
XX	(ULBR) UNIV LIBRE BRUXELLES.		
XX	Bollen A, Fauconnier A, Godfroid E;		
XX	WPI; 2000-452178/39.		
XX	N-PSDB; AAB64850, AAB64890.		
XX	Novel polypeptides derived from Bordetella pertussis, useful for treating		
PT	and diagnosing Bordetella infection.		
XX	Example 2; Page 87-88; 165pp; English.		
XX	Bordetella pertussis possesses a type III secretion system. Type III		
CC	secretion systems allow bacteria to target virulence factors directly at		
CC	host cells. The present sequence is the BcrH protein of B. pertussis. The		
CC	present protein is encoded by a Class I type gene and is involved in the		
CC	type III secretion system of B. pertussis i.e. a Bordetella pathogenicity		
CC	protein. The gene of the present protein is located within a		
CC	pathogenicity island (see AAB64890). A pathogenicity island is a compact,		
CC	distinct genetic unit carrying virulence genes. The present protein may		
CC	be used to treat or diagnose B. pertussis infection, e.g. as a vaccine.		
CC	Whooping cough is a disease caused by infection by B. pertussis		
XX	Sequence 161 AA;		
SQ			
Query Match 20.2%; Score 167; DB 3; Length 161;			
Best Local Similarity 30.5%; Pred. No. 2e-10;			
Matches 47; Conservative 24; Mismatches 81; Indels 2; Gaps 2;			
QY	2	QTDTTLTPEYAELEAFNADGGTGLAMLODISGDTLTLEQLYALAFSQYQAGKVEDAHKIFQA	61
Db	7	QGGSPASASHEA-LRHILDAGSMGGLQGLDEAQQQALYAIHGAYEQGRVADAKMFCL	65
QY	62	LCMLDHYEPRYFLGLGACRQAMGBFETAVQSYSGFAMLDLKDPRFPFHAGECRLQOQDNLN	121
Db	66	LVACDPLEARYLLALGAAQAQELGLYEHALQQYAAAAALQDLSRPLLHGAECVLALGRRR	125
QY	122	GAESGFHSARILLADTDPOADLAASAKVNLRAIA	155

Db	126	DALDTLDMVLELQGS-PERAAALRERAEILLRRSYA	158
RESULT 8			
ABU45583			
ID	ABU45583	standard; protein; 165 AA.	
XX	AC	ABU45583;	
XX	DT	19-JUN-2003 (first entry)	
XX	DE	Protein encoded by Prokaryotic essential gene #31110.	
XX	KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.	
XX	OS	Salmonella paratyphi.	
XX	FN	WO200277183-A2.	
XX	PD	03-OCT-2002.	
XX	XX	21-MAR-2002; 2002WO-US009107.	
XX	PR	21-MAR-2001; 2001US-00815242.	
XX	PR	06-SEP-2001; 2001US-00948993.	
XX	PR	25-OCT-2001; 2001US-0342923P.	
XX	PR	08-FEB-2002; 2002US-00072851.	
XX	PR	06-MAR-2002; 2002US-0362699P.	
XX	PA	(ELIT-) ELITRA PHARM INC.	
XX	PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;	
XX	PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	
XX	DR	WPI; 2003-029926/02.	
XX	DR	N-PSDB; ACA49453.	
XX	PT	New antisense nucleic acids, useful for identifying proteins or screening	
XX	PT	for homologous nucleic acids required for cellular proliferation to	
XX	PT	isolate candidate molecules for rational drug discovery programs.	
XX	FS	Claim 25; SEQ ID NO 73507; 1766pp; English.	
XX	CC	The invention relates to an isolated nucleic acid comprising any one of	
XX	CC	the 6213 antisense sequences given in the specification where expression	
XX	CC	of the nucleic acid inhibits proliferation of a cell. Also included are:	
XX	CC	(1) a vector comprising a promoter operably linked to the nucleic acid	
XX	CC	encoding a polypeptide whose expression is inhibited by the antisense	
XX	CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated	
XX	CC	polypeptide or its fragment whose expression is inhibited by the	
XX	CC	antisense nucleic acid; (4) an antibody capable of specifically binding	
XX	CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular	
XX	CC	proliferation or the activity of a gene in an operon required for	
XX	CC	proliferation; (7) identifying a compound that influences the activity of	
XX	CC	the gene product or that has an activity against a biological pathway	
XX	CC	required for proliferation, or that inhibits cellular proliferation; (8)	
XX	CC	identifying a gene required for cellular proliferation or the biological	
XX	CC	pathway in which a proliferation-required gene or its gene product lies	
XX	CC	or a gene on which the test compound that inhibits proliferation of an	
XX	CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a	
XX	CC	compound's activity; (11) a culture comprising strains in which the gene	
XX	CC	product is overexpressed or underexpressed; (12) determining the extent	
XX	CC	to which each of the strains is present in a culture or collection of	
XX	CC	strains; or (13) identifying the target of a compound that inhibits the	
XX	CC	proliferation of an organism. The antisense nucleic acids are useful for	
XX	CC	identifying proteins or screening for homologous nucleic acids required	
XX	CC	for cellular proliferation to isolate candidate molecules for rational	
XX	CC	drug discovery programs, or for screening homologous nucleic acids	
XX	CC	required for proliferation in cells other than S. aureus, S. typhimurium,	
XX	CC	K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of	
XX	CC	the target prokaryotic essential genes. Note: The sequence data for this	
XX	CC	patent did not form part of the printed specification, but was obtained	

CC	in electronic format directly from WIPO at																									
CC	ftp.wipo.int/pub/published_pct_sequences																									
XX																										
SQ	Sequence 165 AA;																									
Query Match 20.1%; Score 166.5; DB 6; Length 165;																										
Best Local Similarity 30.8%; Pred. No. 2.4e-10;																										
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;																										
QY	1	MQDTTLTPEYAEI--EAFMADGGTILAMLDISGDTLEQLYALAFSQYQAGKWEDAHKI	58																							
Db	1	MDYQNNVSEERVAEMIWDA-VSEGATLKDVHGIPODMMDGLYAHAYEFYNGRLDEAETF	59																							
QY	59	FOALCMLDHYEPRYFLGLGACRQMGFEFTAVQSYSGAMLDLKDPRFPFHAGECRLOQG	118																							
Db	60	FRFLCIYDFNPDTMTGLAAVCQKKQFKACDLYAVAFTLLKNDYRPVFTGCQQLMR	119																							
QY	119	DLNGAESGFHSARLLADTDPQADLAASAKVMLEAI	154																							
Db	120	KAAKARQCFE---LVNRTEDESLRAKALVYLEAL	151																							
RESULT 9																										
ABU48112																										
ID	ABU48112	standard; protein; 165 AA.																								
XX	AC	ABU48112;																								
XX																										
DT	19-JUN-2003	(first entry)																								
XX																										
DE	Protein encoded by Prokaryotic essential gene #33639.																									
XX	Antisense; prokaryotic essential gene; cell proliferation; drug design.																									
KW	Salmonella typhi.																									
XX																										
OS	WO200277183-A2.																									
XX																										
PN	03-OCT-2002.																									
PD																										
XX																										
PF	21-MAR-2002;	2002WO-US009107.																								
XX																										
PR	21-MAR-2001;	2001US-00815242.																								
PR	06-SEP-2001;	2001US-00948993.																								
PR	25-OCT-2001;	2001US-0342923P.																								
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XX																										
PA	(ELIT-) ELITRA PHARM INC.																									
XX																										
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;																									
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;																									
XX																										
DR	WPI; 2003-029926/02.																									
DR	N-PSDB; ACA51982.																									
XX																										
PT	New antisense nucleic acids, useful for identifying proteins or screening																									
PT	for homologous nucleic acids required for cellular proliferation to																									
PT	isolate candidate molecules for rational drug discovery programs.																									
XX																										
PS	Claim 25; SEQ ID NO 76036; 1766pp; English.																									
XX																										
CC	The invention relates to an isolated nucleic acid comprising any one of																									
CC	the 6213 antisense sequences given in the specification where expression																									
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:																									
CC	(1) a vector comprising a promoter operably linked to the nucleic acid																									
CC	encoding a polypeptide whose expression is inhibited by the antisense																									
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated																									
CC	polypeptide or its fragment whose expression is inhibited by the																									
CC	antisense nucleic acid; (4) an antibody capable of specifically binding																									
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular																									
CC	proliferation or the activity of a gene in an operon required for																									
CC	proliferation; (7) identifying a compound that influences the activity of																									
CC	the gene product or that has an activity against a biological pathway																									
CC	required for proliferation, or that inhibits cellular proliferation; (8)																									
CC	identifying a gene required for cellular proliferation or the biological																									
CC	pathway in which a proliferation-required gene or its gene product lies																									
CC	or a gene on which the test compound that inhibits proliferation of an																									
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a																									
CC	compound's activity; (11) a culture comprising strains in which the gene																									
CC	product is overexpressed or underexpressed; (12) determining the extent																									
CC	to which each of the strains is present in a culture or collection of																									
CC	strains; or (13) identifying the target of a compound that inhibits the																									
CC	proliferation of an organism. The antisense nucleic acids are useful for																									
CC	identifying proteins or screening for homologous nucleic acids required																									
CC	for cellular proliferation to isolate candidate molecules for rational																									
CC	drug discovery programs, or for screening homologous nucleic acids																									
CC	required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,																									
CC	<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of																									
CC	the target prokaryotic essential genes. Note: The sequence data for this																									
CC	patent did not form part of the printed specification, but was obtained																									
CC	in electronic format directly from WIPO at																									
CC	ftp.wipo.int/pub/published_pct_sequences																									
XX																										
SQ	Sequence 165 AA;																									
Query Match 20.1%; Score 166.5; DB 6; Length 165;																										
Best Local Similarity 30.8%; Pred. No. 2.4e-10;																										
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;																										
QY	1	MQDTTLTPEYAEI--EAFMADGGTILAMLDISGDTLEQLYALAFSQYQAGKWEDAHKI	58																							
Db	1	MDYQNNVSEERVAEMIWDA-VSEGATLKDVHGIPODMMDGLYAHAYEFYNGRLDEAETF	59																							
QY	59	FOALCMLDHYEPRYFLGLGACRQMGFEFTAVQSYSGAMLDLKDPRFPFHAGECRLOQG	118																							
Db	60	FRFLCIYDFNPDTMTGLAAVCQKKQFKACDLYAVAFTLLKNDYRPVFTGCQQLMR	119																							
QY	119	DLNGAESGFHSARLLADTDPQADLAASAKVMLEAI	154																							
Db	120	KAAKARQCFE---LVNRTEDESLRAKALVYLEAL	151																							
RESULT 10																										
ADW28241																										
ID	ADW28241	standard; protein; 165 AA.																								
XX																										
AC	ADW28241;																									
XX																										
DT	07-APR-2005	(first entry)																								
XX																										
DE	Amino acid sequence of Sica protein from <i>Salmonella typhimurium</i> .																									
XX																										
KW	gastrointestinal-Gen.; dermatological; cardiovascular-Gen.; vasotropic;																									
KW	vulnery; ophthalmological; neuroprotective; antiapoptotic;																									
KW	antiinflammatory; cardiant; antimicrobial;																									
KW	matrix metalloprotease inhibitor; elastase inhibitor;																									
KW	apoptosis inhibitor; cell damage; tissue damage; protective protein;																									
KW	cationic antimicrobial proteolysis; matrix metalloprotease; elastase;																									
KW	wound healing; corneal damage; keratitis; meningitis; apoptosis;																									

XX (EXPR-) EXPRESSIVE CONSTRUCTS INC.
XX Sanders MC, Ellis-Busby DL, Sebastian S, Havard JM, Colpas GJ;
XX WPI; 2005-091980/10.
XX N-PSDB; ADW28242.
XX Inhibiting cell or tissue damage comprises contacting the cell or tissue
XX with a protective protein, its active fragment, variant or derivative, or
XX a chimeric protein comprising a protective protein.
XX Disclosure; SEQ ID NO 3; 121pp; English.
XX The specification describes a method for inhibiting cell or tissue
XX damage. The method comprises contacting the cell or tissue with a
XX protective protein, an active fragment, variant or derivative of the
XX protective protein, or a chimeric protein comprising the protective
XX protein, where the contact inhibits damage to the cell or tissue. The
XX protective protein is from a class of small chaperone proteins, and is
XX selected from p26, SicA, and a crystallin protein. The contact decreases
XX or prevents cationic antimicrobial proteolysis, especially of a matrix
XX metalloprotease such as elastase. The method of the invention is useful
XX for inhibiting cell or tissue damage, protease activity in a cell or
XX tissue, virulence of a pathogen, or proteolysis of a cationic microbial
XX peptide in a cell or tissue. The cell or tissue damage condition is
XX selected from wound and wound healing, corneal damage (microbial
XX keratitis), meningitis, apoptosis, necrosis, burns, scars, inflammation,
XX damage to heart valve, varicose veins, rash, incisions, diabetic,
XX pressure, venous leg, corneal or peptic ulcers, valve stenosis,
XX gingivitis, endocarditis, and calcification of cardiac tissue. The
XX present sequence represents SicA, a protective protein of the invention.
XX Sequence 165 AA;

Query Match 20.1%; Score 166.5; DB 9; Length 165;
Best Local Similarity 30.8%; Pred. No. 2.4e-10;
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;
Qy 1 MQTDTTTPYEAE--EAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADHKI 58
Db 1 MDYQNVSEERVAEMIWDA-VSEGATLKDVHGIFQDMMDGLYAHAYFYNGRUDEATF 59
Qy 59 FQALCMLDHYEPYFLGLGACRQAMGEFETAVQSIFGAMLDLKDPRFPFHAGECRLQGG 118
Db 60 FRFLCIYDFYNDYTMGLAAVCQLKKQFKACDLYAVAFLLKNDYRPVFTGQCQLMR 119
Qy 119 DLNGAESGFHSARLLADTDPOQADLAASAKVMLEAI 154
Db 120 KAKARQCFE----LVNERTEDESLRKALVYLEAL 151

RESULT 11
ADCO0814
ID ADCO0814 standard; protein; 151 AA.
AC ADCO0814;
XX
XX 04-DEC-2003 (first entry)
XX
XX Enterohaemorrhagic E. coli 0157:H7-specific protein SEQ ID NO: 859.
XX enterohaemorrhagic; anti-bacterial.
XX Escherichia coli; 0157:H7.
XX JP2002355074-A.
XX
XX 10-DEC-2002.
XX
XX 24-JAN-2002; 2002JP-00015959.
XX
XX 24-JAN-2001; 2001JP-00112010.

XX (UYTS-) UNIV TSUKUBA.
XX WPI; 2003-451640/43.
XX Enterohaemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
XX and a polypeptide and its use, a polypeptide, a vector and a host cell.
XX Claim 3; SEQ ID NO 859; 2067pp; Japanese.
XX The invention relates to a novel enterohaemorrhagic Escherichia coli
XX O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
XX has anti-bacterial activity. The polypeptide can be used in detection
XX and/or treatment of O157:H7 infection. The nucleotide sequence of the
XX genome of Enterohaemorrhagic E coli O157:H7 was determined. The present
XX sequence represents an E. coli O157:H7-specific polypeptide of the
XX invention.
XX Sequence 151 AA;
Query Match 20.0%; Score 165; DB 7; Length 151;
Best Local Similarity 29.1%; Pred. No. 3.1e-10;
Matches 39; Conservative 27; Mismatches 68; Indels 0; Gaps 0;
Qy 18 FMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADHKI FQALCMLDHYEPYFLGLG 77
Db 14 FYQDGGTTLASLTNLTQODLNDLHSHYATAYQSGDVITARNL FHLTYLHWNVDYTLSLG 73
Qy 78 ACQAMGEFETAVQSIFGAMLDLKDPRFPFHAGECRLQGGDLNGAESGFHSARLLADTD 137
Db 74 LCHQLSNHDEAQLCFARCATLVMQDPRASYISGYSLLVGNKKMAKFAKACLIMWCNEK 133
Qy 138 PQQADLAASAKVML 151
Db 134 EKTYTYKENIKLL 147
RESULT 12
ADFO6293
ID ADFO6293 standard; protein; 182 AA.
XX
XX AC ADFO6293;
XX
XX 12-FEB-2004 (first entry)
XX
XX Bacterial polypeptide #2406.
XX
XX Proteus mirabilis infection; bacterial infection; antibacterial;
XX immunostimulant.
XX
XX Proteus mirabilis.
XX
XX US6605709-B1.
XX
XX 12-AUG-2003.
XX
XX 05-APR-2000; 2000US-00543681.
XX
XX 09-APR-1999; 99US-0128706P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton GL;
XX
XX WPI; 2003-895291/82.
XX N-PSDB; ADF02121.
XX
XX New Proteus mirabilis polypeptides and polynucleotides, useful as
XX reagents for diagnosis of bacterial disease, as components of
XX antibacterial vaccines, as targets for antibacterial drugs, or as
XX biocontrol agents for plants.
XX
XX Disclosure; SEQ ID NO 6578; 870pp; English.

XX The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
SQ Sequence 182 AA;

Query Match 19.8%; Score 163.5; DB 7; Length 182;
Best Local Similarity 29.8%; Pred. No. 6e-10;
Matches 37; Conservative 25; Mismatches 55; Indels 7; Gaps 1;

QY 12 EAELE-----AFMADGGTLMQLDISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCM 64
DB 19 EKELDQLANIVISIVQNGASIKDESEIPDGFMEGDYSFAYDFYQKGLDEAEAFKPLCL 78

QY 65 LDHYEPRYFLGACRCQAMGEFFETAVQSYSFGAMLDLKDPRFPFHAGECRLOQGDINGAE 124
DB 79 YDFYNDYIMGLAANVLKQYQAAIDLVALALNAKNDYRPFYAGQCNLSIGEKEKAK 138

QY 125 SGPH 128
DB 139 YCFH 142

RESULT 13
ABM70111
ID ABM70111 standard; protein; 156 AA.
XX
AC ABM70111;
XX
DT 20-NOV-2003 (first entry)
XX
XX Photorhabdus luminescens protein sequence #3208.
XX
DE Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.
XX
OS Photorhabdus luminescens.
XX
PN WO200294867-A2.
XX
PD 28-NOV-2002.
XX
PF 07-FEB-2002; 2002WO-IB003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
XX WPI; 2003-148459/14.
XX
XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
XX Claim 2; SEQ ID NO 3208; 1205pp; French.
XX
XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are

CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins
XX
SQ Sequence 156 AA;

Query Match 18.3%; Score 151; DB 6; Length 156;
Best Local Similarity 32.6%; Pred. No. 1.3e-08;
Matches 31; Conservative 17; Mismatches 47; Indels 0; Gaps 0;

QY 22 GGTLMQLDISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCMLDHYEPRYFLGACRCQ 81
DB 22 GATLKDINAIPDDMMDDIYSAYDFYNKGRIBEAEEVFFRFLCIYDFYNVDYIMGLAAIYQ 81

QY 82 AMGEFETAVQSYSFGAMLDLKDPRFPFHAGECRLO 116
DB 82 IKEQFQQAADLYAVAFALGKNDYTPVFTGQCQLR 116

RESULT 14
AAY70581
ID AAY70581 standard; protein; 157 AA.
XX
AC AAY70581;
XX
DT 04-JUL-2000 (first entry)
XX
XX Salmonella Pathogenicity Island 2 (SPI2) SsCA protein.
DE
XX Salmonella Pathogenicity Island 2 locus; SPI2 locus; antigen carrier;
KW attenuation; gram-negative cell; vaccine; cytostatic; virucide; tumour;
KW anti-arteriosclerotic; anti-Alzheimer's; bactericide; hepatotropic;
KW antiinflammatory; microbial infection; therapeutic; Salmonella infection;
KW Helicobacter pylori; stomach cancer; Herpes virus; Chlamydia pneumoniae;
KW Alzheimer's disease; arteriosclerosis; viral pathogen; Hepatitis virus;
KW cervical cancer; ssca; chaperon; type III secretion system.
XX
OS Salmonella typhimurium.
XX
XX WO200014240-A2.
XX
XX 16-MAR-2000.
XX
XX 03-SEP-1999; 99WO-EP006514.
XX
XX 04-SEP-1998; 98EP-00116827.
XX
XX (CREA-) CREATOGEN BIOSCIENCES GMBH.
XX
XX Hensel M, Guzman CA, Medina E, Apfel H, Hueck C;
PI
XX WPI; 2000-256988/22.
DR
DR N-PSDB; AA251993.
XX
XX Attenuated gram-negative Salmonella cells, comprising inactivated genes
PT in the SPI2 locus and useful for vaccinating against a range of disorders
PT associated with microbial infections such as stomach and cervical

PT cancers.
PS Claim 18; Fig 23H; 180pp; English.
XX
CC The patent discloses attenuated gram-negative cells, especially
CC Salmonella, in which at least 1 gene in the Salmonella Pathogenicity
CC Island 2 (SPI2) locus has been inactivated resulting in attenuation/
CC reduction of virulence compared to the wild type cell. The attenuated
CC cells are used as carriers for presenting bacterial, viral or tumour
CC antigens to a host and are capable of expressing the antigen in a target
CC cell, especially a macrophage. The cells may therefore be used for the
CC preparation of a prophylactic or therapeutic composition for the
CC treatment of a chronic disease caused by a bacterium or virus, e.g.
CC Salmonella infection or a tumour. The cells may also be used to vaccinate
CC against a range of bacterial and viral pathogens e.g. Helicobacter pylori
CC (associated with stomach cancer), Chlamydia pneumoniae (associated with
CC arteriosclerosis and Alzheimer's disease), Borrelia burgdorferi,
CC Nanobacteria (found in the chronically diseased kidneys of patients with
CC crystalline deposits), Hepatitis virus (causative agent of Hepatitis B
CC and C and associated with liver cancer), Human papilloma virus (HPV)
CC (associated with cervical cancer) or Herpes virus. The present sequence
CC is the SCA protein, a chaperon protein of type III secretion system,
CC from the SPI2 locus of Salmonella. Inactivation of the ssc gene is useful
CC for producing the attenuated cells
XX
SQ Sequence 157 AA;

Query Match 15.2%; Score 125.5; DB 3; Length 157;
Best Local Similarity 27.0%; Pred. No. 1.1e-05;
Matches 43; Conservative 28; Mismatches 83; Indels 5; Gaps 4;
Qy 1 MQTDTLTPEYAELEAFMADGGTLLAM-LQDISGDTLEQLYALAFSQYQAGKWEHAHIF 59
Db 1 MKKDDPTLQQAHD--MRFFRRGSLRMLLDDDDVTQPLNTLYRYATQLMEVKEFAGARLF 58
Qy 60 QALCMLDHYEPRYFLGIGACQAMGEFETAVQSYSFGMMLDLKDPFFPHAGECRLOQGD 119
Db 59 QLLTIYDAWSFDYFRLGECQAKHGEAIYAGRAAQIKIDAPQAPMAAECYLACDN 118
Qy 120 LNGAESGFHS-ARLLADTDPQADLAASAKVMLEAIAIR 157
Db 119 VCVAIKALKAVVRICGEVSEHQI-LRQRAEKMLQQLSDR 156

RESULT 15
ABU47399
ID ABU47399 standard; protein; 157 AA.
XX AC ABU47399;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #32926.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Salmonella typhimurium.
XX PN W0200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX DR N-PSDB; ACA51269.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
PS Claim 25; SEQ ID NO 75323; 1766pp; English.
XX

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 157 AA;
Query Match 15.2%; Score 125.5; DB 6; Length 157;
Best Local Similarity 27.0%; Pred. No. 1.1e-05;
Matches 43; Conservative 28; Mismatches 83; Indels 5; Gaps 4;
Qy 1 MQTDTLTPEYAELEAFMADGGTLLAM-LQDISGDTLEQLYALAFSQYQAGKWEHAHIF 59
Db 1 MKKDDPTLQQAHD--MRFFRRGSLRMLLDDDDVTQPLNTLYRYATQLMEVKEFAGARLF 58
Qy 60 QALCMLDHYEPRYFLGIGACQAMGEFETAVQSYSFGMMLDLKDPFFPHAGECRLOQGD 119
Db 59 QLLTIYDAWSFDYFRLGECQAKHGEAIYAGRAAQIKIDAPQAPMAAECYLACDN 118
Qy 120 LNGAESGFHS-ARLLADTDPQADLAASAKVMLEAIAIR 157
Db 119 VCVAIKALKAVVRICGEVSEHQI-LRQRAEKMLQQLSDR 156

Search completed: June 16, 2006, 19:06:50
Job time : 108.354 secs

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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:07:20 ; Search time 16.1585 Seconds
(without alignments)
946.773 Million cell updates/sec

Title: US-10-813-908A-9
Perfect score: 827
Sequence: 1 MQDTTTLTPEYEAELEAFMA.....QADLAASAKVMLEAIAIRRD 159

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	549	66.4	167 2 H83432	regulatory protein
2	517	62.5	168 2 C37314	regulatory protein
3	509	61.5	168 2 C33601	low calcium respon
4	166.5	20.1	165 2 A80851	hypothetical prote
5	166.5	20.1	165 2 S70217	sipE protein - Sal
6	166.5	20.1	165 2 A57357	sicA protein - Sal
7	165	20.0	151 2 H91200	type III secretion
8	165	20.0	151 2 D86047	cesD (imported) -
9	151	18.3	155 2 S15576	ippI protein - Shi
10	151	18.3	155 2 C34965	hypothetical 17K p
11	124.5	15.1	157 2 A80699	probable type III
12	116.5	14.1	172 2 F81723	type III secretion
13	115.5	14.0	163 2 H85937	hypothetical prote
14	115.5	14.0	163 2 D91092	hypothetical prote
15	114	13.8	596 2 G75457	tetratricopeptide
16	113	13.7	144 2 A10698	probable pathogeni
17	109	13.2	246 2 D81655	type III secretion
18	108	13.1	198 2 E71461	probable low calci
19	107.5	13.0	163 2 D65068	hypothetical prote
20	105	12.7	231 2 A86592	low calcium respon
21	105	12.7	231 2 H72031	type III secretion
22	103.5	12.5	232 2 B71497	probable low calci
23	100	12.1	172 2 B86618	low calcium respon
24	100	12.1	172 2 C72007	type III secretion
25	98	11.9	403 2 S42532	hypothetical prote
26	96.5	11.7	458 2 T29520	hypothetical prote
27	91.5	11.1	576 2 H87414	TPR domain protein
28	91	11.0	835 2 I55603	reduced hepatic gl
29	90	10.9	402 2 A12030	hypothetical prote

ALIGNMENTS									
RESULT 1									
H83432									
regulatory protein PcrH PA1707 [imported] - Pseudomonas aeruginosa (strain PA01)									
C;Species: Pseudomonas aeruginosa									
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004									
C;Accession: H83432									
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;									
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Liu									
; Lory, S.; Olson, M.V									
Nature 406, 959-964, 2000									
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat									
A;Reference number: A82950; MUID:20437337; PMID:10984043									
A;Accession: H83432									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-167 <STO>									
A;Cross-references: UNIPROT:Q9I325; UNIPARC:UPI000000C5455; GB:AE004091; GB:AE004091; N									
A;Experimental source: strain PA01									
C;Genetics:									
A;Gene: pcrH; PA1707									
Query Match 66.4%; Score 549; DB 2; Length 167;									
Best Local Similarity 64.8%; Pred. No. 1.7e-47;									
Matches 103; Conservative 21; Mismatches 35; Indels 0; Gaps 0;									
Qy	1	MQDTTTLTPEYEAELEAFMADGGT	LAMLQDITSGDTLEQLYALAFSOYQAGKWE	AHKIFQ	60				
Db	1	MNQTPSDTQQQALEAF	LRDGGTFLMRGLSEDTLEQLYALGFNQYQAGKWD	DAQKIFQ	60				
Qy	61	ALCMLDHVEPRYFLGLGACRQAMGEF	TAVQSYSGFAMLDLKDPRFPFHAGECRLQ	QCGDL	120				
Db	61	ALCMLDHYDARYFLGLGACRQSLGLY	EQALQSYSGALMDINEPRFPFHAECHLQ	LGDL	120				
Qy	121	NGAESGHSAKRLIADTDPPQADLA	ASAKVMLEAIAIRRD	159					
Db	121	DGAESGFYSARALAAQAPAEAL	AARAGAMLEAVTARKD	159					
RESULT 2									
C37314									
regulatory protein LcrH - Yersinia pseudotuberculosis									
C;Species: Yersinia pseudotuberculosis									
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004									
C;Accession: C37314									
R;Bergman, T.; Hakansson, S.; Forsberg, A.; Norlander, L.; Macellaro, A.; Baeckman, A.;									
J. Bacteriol. 173, 1607-1616, 1991									
A;Title: Analysis of the V antigen lcrGVH-yopBD operon of Yersinia pseudotuberculosis:									
A;Reference number: A37314; MUID:91154114; PMID:1705541									
A;Accession: C37314									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-168 <BER>									

glycine dehydrogen
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hsp 90-binding pro
hypothetical prote
conserved hypothet
hypothetical prote
probable pilus aas
hypothetical prote
tetratricopeptide
tetratricopeptide
hypothetical prote
peptidylprolyl iso

A;Cross-references: UNIPROT:P23995; UNIPARC:UPI0000000BC5; GB:M57893; NID:g155456; PIDN:
C;Superfamily: ippi protein

Query Match 62.5%; Score 517; DB 2; Length 168;
Best Local Similarity 58.5%; Pred. No. 2.6e-44;
Matches 93; Conservative 34; Mismatches 32; Indels 0; Gaps 0;

QY 1 MQTDTTLTPEYAELEAFMADGGTTLAMLODISGDTLEQLYALAFSQYQAGKWEADHKIFQ 60

DB 1 MQQETTTQEQVLAWESFLKGGGTIAMLNEISSDTLSQLSLAFNQYQSGKYEDAHKVFQ 60

QY 61 ALQMLDHYEPYRFLGLGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLOQGD 120

DB 61 ALCVLDHYDSRFFLGLGACRQAMQYDLATHSYSGAIMDIKEPRFFPFAAECLLQKGL 120

QY 121 NGAESGFHSARLLADTDPQADLAASAKVMLEAIAIRRD 159

DB 121 AEASGLFLAQELIADKTEPKELSTRVSSMLEAIKLKKE 159

RESULT 3

C33601 low calcium response protein H - Yersinia pestis plasmid pCD1

C;Species: Yersinia pestis

C;Date: 18-May-1990 #sequence revision 18-May-1990 #text_change 09-Jul-2004

C;Accession: C33601; T43595; T42890

R;Price, S.B.; Leung, K.Y.; Barve, S.S.; Straley, S.C.

J. Bacteriol. 171, 5646-5653, 1989

A;Title: Molecular analysis of lcrGVH, the V antigen operon of Yersinia pestis.

A;Reference number: A33601; MUID:9000806; PMID:2477361

A;Accession: C33601

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-168 <PRI>

A;Cross-references: UNIPROT:P21207; UNIPARC:UPI000012E2B5; GB:M26405; NID:g155448; PIDN:

R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker

J. Bacteriol. 180, 5192-5202, 1998

A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.

A;Reference number: Z22578; MUID:98422474; PMID:9748454

A;Accession: T43595

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-168 <HUP>

A;Cross-references: UNIPARC:UPI000012E2B5; EMBL:AF053946; NID:g2996222; PIDN:AAC62575.1;

A;Experimental source: strain KIM

R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.

Infect. Immun. 66, 4611-4623, 1998

A;Title: DNA sequencing and analysis of the low-Caz+-response plasmid pCD1 of Yersinia P

A;Reference number: Z22273; MUID:98427122; PMID:9746557

A;Accession: T42890

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-168 <PER>

A;Cross-references: UNIPARC:UPI000012E2B5; EMBL:AF074612; NID:g3822037; PIDN:AAC69800.1;

A;Experimental source: strain KIMS

C;Genetics:

A;Gene: lcrH

A;Genome: plasmid

A;Note: plasmid pCD1

C;Superfamily: ippi protein

Query Match 61.5%; Score 509; DB 2; Length 168;

Best Local Similarity 57.9%; Pred. No. 1.7e-43;

Matches 92; Conservative 34; Mismatches 33; Indels 0; Gaps 0;

QY 1 MQTDTTLTPEYAELEAFMADGGTTLAMLODISGDTLEQLYALAFSQYQAGKWEADHKIFQ 60

DB 1 MQQETTTQEQVLAWESFLKGGGTIAMLNEISSDTLSQLSLAFNQYQSGKYEDAHKVFQ 60

QY 61 ALQMLDHYEPYRFLGLGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLOQGD 120

DB 61 ALCVLDHYDSRFFLGLGACRQAMQYDLATHSYSGAIMDIKEPRFFPFAAECLLQKGL 120

QY 121 NGAESGFHSARLLADTDPQADLAASAKVMLEAIAIRRD 159

DB 121 AEASGLFLAQELIADKTEPKELSTRVSSMLEAIKLKKE 159

RESULT 4

AB0851

hypothetical protein spaT [imported] - Salmonella enterica subsp. enterica serovar Typh

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB0851

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AB0851

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-165 <PAR>

A;Cross-references: UNIPROT:P40703; UNIPARC:UPI000005A36D; GB:AL513382; PIDN:CAD05993.1

C;Genetics:

A;Gene: spaT

C;Superfamily: ippi protein

Query Match 20.1%; Score 166.5; DB 2; Length 165;

Best Local Similarity 30.8%; Pred. No. 2.6e-09;

Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 1 MQTDTTLTPEYAELE--EAFMADGGTTLAMLODISGDTLSQLYALAFSQYQAGKWEADHKI 58

DB 1 MDYQNNVSEERVAEMTWDA-VSEGATLKDVHGIPQDMMDGLYAHAYEFYVNOGRLDEAETF 59

QY 59 FOALCMLDHYEPYRFLGLGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLOQG 118

DB 60 FRPLCIYDFYNDYTNGLAAVQLKQKQACDLYAVFTLLKNDYRPFVFTQCQLLMR 119

QY 119 DLNGAESGFHSARLLADTDPQADLAASAKVMLEAI 154

DB 120 KAAKARQCFE---LVNERTEDESLRKALVLEAL 151

RESULT 5

S70217

siPE protein - Salmonella typhi

C;Species: Salmonella typhi

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004

C;Accession: S70217

R;Hermant, D.; Menard, R.; Arricau, N.; Parsot, C.; Popoff, M.Y.

Mol. Microbiol. 17, 781-789, 1995

A;Title: Functional conservation of the Salmonella and Shigella effectors of entry into

A;Reference number: S70215; MUID:96111497; PMID:8801431

A;Accession: S70217

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-165 <HER>

A;Cross-references: UNIPROT:P40703; UNIPARC:UPI000005A36D; EMBL:X82670; NID:g1009001; P:

C;Genetics:

A;Gene: siPE

C;Superfamily: ippi protein

Query Match 20.1%; Score 166.5; DB 2; Length 165;

Best Local Similarity 30.8%; Pred. No. 2.6e-09;

Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 1 MQTDTTLTPEYAELE--EAFMADGGTTLAMLODISGDTLSQLYALAFSQYQAGKWEADHKI 58

DB 1 MDYQNNVSEERVAEMTWDA-VSEGATLKDVHGIPQDMMDGLYAHAYEFYVNOGRLDEAETF 59

QY 59 FOALCMLDHYEPYRFLGLGACRQAMGEFETAVQSYSGFAMLDLKDPRFPFHAGECRLOQG 118

Db 60 FRFLCIYDFYNDYTMGLAAVCQLKKQFKACDLVAVFTLLKNDYRVPVFTGQCQLLMR 119
Qy 119 DLNGAESGFHSGARLLADTDPOQADLAASAKVMLEAI 154
Db 120 KAARARQCFE---LVNERTEDSLRAKALVYLEAL 151
RESULT 6
A57357
sica protein - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: A57357; S37357
R:Kaniga, K.; Tucker, S.; Trollinger, D.; Galan, J.E.
J. Bacteriol. 177, 3965-3971, 1995
A:Title: Homologs of the Shigella IpaB and IpaC invasins are required for Salmonella ty
A:Reference number: A57357; MUID:95332200; PMID:7608068
A:Accession: A57357
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-165 <RES>
A:Cross-references: UNIPROT:P40703; UNIPARC:UPI000005A36D; EMBL:U25631; NID:g975293; PID
EMBO J. 12, 3779-3787, 1993
R:Groisman, E.A.; Ochman, H.
A:Title: Cognate gene clusters govern invasion of host epithelial cells by Salmonella ty
A:Reference number: S37304; MUID:94008985; PMID:8404849
A:Accession: S37357
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-32 <GRO>
A:Cross-references: UNIPARC:UPI00001703EB; EMBL:X73525; NID:g404286; PIDN:CAAS1928.1; PI
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993
C:Genetics:
A:Gene: sicaA; spat
C:Superfamily: ippi protein
Query Match 20.1%; Score 166.5; DB 2; Length 165;
Best Local Similarity 30.8%; Pred. No. 2.6e-09;
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3;
Qy 1 MQDTTLTPEYAEEL--EAFWADGGTGLMLQDISGDTLEQLYALAFSQYQAGKWEADAKI 58
Db 1 MDYQNVSERVAEMINDA-VSEGATLKDVGHIQDMMDGLYAHAYFYNQRLDEATF 59
Qy 59 FOALCMLDHYEPRYFLGLGACRQAMGEFTAVQSYSFGAMLDLKDPRFPFHAGECRLQQG 118
Db 60 FRFLCIYDFYNDYTMGLAAVCQLKKQFKACDLVAVFTLLKNDYRVPVFTGQCQLLMR 119
Qy 119 DLNGAESGFHSGARLLADTDPOQADLAASAKVMLEAI 154
Db 120 KAARARQCFE---LVNERTEDSLRAKALVYLEAL 151
RESULT 7
H91200
type III secretion system CesD protein [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H91200
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91200
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <HAY>
A:Cross-references: UNIPROT:O52134; UNIPARC:UPI000000D00B3; GB:BA000007; PIDN:BA837999.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs4576

Query Match 20.0%; Score 165; DB 2; Length 151;
Best Local Similarity 29.1%; Pred. No. 3.3e-09;
Matches 39; Conservative 27; Mismatches 68; Indels 0; Gaps 0;
Qy 18 FMADGGTGLMLQDISGDTLEQLYALAFSQYQAGKWEADAKI FOALCMLDHYEPRYFLGLG 77
Db 14 FYQDGGTGLASLTNL TQODLNDLHSA YATAYQSGDVITARNLFHLLTYLLEHWN YDTLSLG 73
Qy 78 ACROAMGEFTAVQSYSFGAMLDLKDPRFPFHAGECRLQQDGLNGAESGFHSGARLLADTD 137
Db 74 LCHQRLSNHEDAQLCFARCATLVNQDPRASYSGISYLLVGNKKWAKKAFACLMWCNEK 133
Qy 138 PQQADLAASAKVML 151
Db 134 EKVTYKENIKLL 147
RESULT 8
D86047
cesD [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D86047
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D86047
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <STO>
A:Cross-references: UNIPROT:O52134; UNIPARC:UPI000000D00B3; GB:AE005174; NID:gl2518467;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: cesD
Query Match 20.0%; Score 165; DB 2; Length 151;
Best Local Similarity 29.1%; Pred. No. 3.3e-09;
Matches 39; Conservative 27; Mismatches 68; Indels 0; Gaps 0;
Qy 18 FMADGGTGLMLQDISGDTLEQLYALAFSQYQAGKWEADAKI FOALCMLDHYEPRYFLGLG 77
Db 14 FYQDGGTGLASLTNL TQODLNDLHSA YATAYQSGDVITARNLFHLLTYLLEHWN YDTLSLG 73
Qy 78 ACROAMGEFTAVQSYSFGAMLDLKDPRFPFHAGECRLQQDGLNGAESGFHSGARLLADTD 137
Db 74 LCHQRLSNHEDAQLCFARCATLVNQDPRASYSGISYLLVGNKKWAKKAFACLMWCNEK 133
Qy 138 PQQADLAASAKVML 151
Db 134 EKVTYKENIKLL 147
RESULT 9
S15576
ippi protein - Shigella dysenteriae
C:Species: Shigella dysenteriae
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S15576
R:Yao, R.; Palchaudhuri, S.
submitted to the EMBL Data Library, June 1991
A:Description: Nucleotide sequence of the ipaBCD structure genes of Shigella dysenteria
A:Reference number: S15575
A:Accession: S15576
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <YAO>
A:Cross-references: UNIPROT:P18008; UNIPARC:UPI000012D80A; EMBL:X60777; NID:g46932; PID
C:Superfamily: ippi protein
Query Match 18.3%; Score 151; DB 2; Length 155;

A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85937
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-163 <STO>
A:Cross-references: UNIPROT:O8X6H6; UNIPARC:UPI00000D088
A:Experimental source: strain Q157:H7, substrain EDL933
C:Genetics:
A:Gene: ygeG
C:Superfamily: ippi protein

Query Match	14.0%;	Score 115.5;	DB 2;	Length 163;
Best Local Similarity	22.8%;	Pred. No. 0.00032;		
Matches	31;	Conservative 33;	Mismatches 61;	Indels 11; Gaps 3;
Qy	1	MOTDT- - - - - TLTPEVEAELEAFMADGGTFLAMLDQISGDTLEQLYALAFSQVQAGKWEDAH	56	
Db	1	MDTETIIFNNSDSEAWQLKHALSGENLALLHGLTPTDLRIYAYAFDYHEKGNVTTDAE	60	
Qy	57	KIFQALCMLDHYEPRYFLGLGACRQAMGEPTAVQ- - - - -SYSGFAMLLDKDPRFPFHAGE	112	
Db	61	IYYKLLCIYAFENHEYLKGFASVCQSKKYYQAYDLYKLSYNS- - - - -PYDDYSVIYRMGQ	117	
Qy	113	CRLOQGDNLGAEISGFH	128	
Db	118	COIGAKNIDNAMOCFY	133	

RESULT 14

D91092
A:Title: Hypothetical protein ECs3708 [imported] - Escherichia coli (strain O157:H7, substrain R157)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: D91092
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a non-O157:H7 enterohemorrhagic E. coli strain
A:Reference number: A9629; MUID:21156231; PMID:11258796
A:Accession: D91092
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <RAY>
A:Cross-references: UNIPROT:Q9X6H6; UNIPARC:UPI000000D0B85; GB:BA000007; PIDN:BAE37131.1; A:Experimental source: strain O157:H7, substrain R157
C:Genetics:
A:Gene: ECs3708
C:Superfamily: ippI protein

Query Match	14.0%;	Score 115.5;	DB 2;	Length 163;
Best Local Similarity	22.8%;	Pred. No. 0.00032;		
Matches	31; Conservative	33; Mismatches	61; Indels	11; Gaps
	3;			
QY	1	MQTDT----	TLTPEYEAELEAFWADGGTLAMLDIISGDTLEQLYALAFSQVQAGKWEDAH	56
Db	1	MDTETIEIFNNSDEWANOLKHAUSKGENLALLHGLTPDILDRIVAYAFDYHEKGNVTDAE	60	
QY	57	KIFQALCMDHYEPFRYFLGACRQAMGFETAQV-----SYSGFAMDLDKDPFPFHAGE	112	
Db	61	IYYKLLCIYAFENHEYLKGFASVCQSKKKQQAYDLYKLSYNYS--PYDDYSVIYRMQG	117	
QY	113	CRLQOQDLNGAESGFH	128	
Db	118	COIGAKNIDNAMOCFY	133	

RESULT 15

G75457
tetraatricopeptide repeat family protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: G75457
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID: 20036896; PMID:10567266
A:Accession: G75457
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-596 <WHI>
A:Cross-references: UNIPROT:Q9RVT5; UNIPARC:UPI000000D3D8B; GB:AE001946; GB:AE000513; NI
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0937
A:Map position: 1

	Query Match	13.8%;	Score 114;	DB 2;	Length 596;
	Best Local Similarity	26.5%;	Pred. No. 0.0021;		
	Matches	41;	Conservative	26;	Mismatches 72; Indels 16; Gaps 4
Qy	3	TDTTLTPEYAELEAFMADGGTGLAMLQDISDITLEQLYALAFSQVQAGKWEDAHKIFQAL	62		
Dd	114	TQTTPPAGEAPATRPVTVPVLTAEO-----QQLLQAQAQPAAGRYPOARNEFEAL	166		
Qy	63	CMLDHDEPRYFLGIGACRQAMGEPTAVQSYSFGAMLDLKDPF--PFHAGECRLOQGDL	120		
Dd	167	IVRNYNPNPEHFGLLGALYLQGLDRGA--TFEQGFQMFQARYEGPYNLGVIATREGY	224		
Qy	121	NGAESGPHSARLLIADTDPQQADLAASAKVMLEAIA	155		
Dd	225	PDALRLYGELTILTAQSAP-----PAARQVLLLRALA	254		

Search completed: June 16, 2006, 19:25:08
Job time : 17.1585 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.
OM protein - protein search, using sw model
Run on: June 16, 2006, 18:53:15 ; Search time 124.873 Seconds
(without alignments)
1177.815 Million cell updates/sec
Title: US-10-813-908A-9
Perfect score: 827
Sequence: 1 MQDTTTLTPYEAELEAFMA.....QADLAASAKVMLEAIRRD 159

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827	100.0	167	2	Q70WN6 aeromonas s
2	780	94.3	167	2	Q699Q9 AERHY
3	769	93.0	167	2	Q5XL03 AERHY
4	596	72.1	167	2	Q7N0X2 PHOLH
5	587	71.0	168	2	Q84GV4 PHOTRABDU
6	549	66.4	167	2	Q91325 PSEAE
7	548	66.3	168	2	Q30528 PSEAE
8	537	64.9	165	2	Q6TLM1 AERHY
9	518	62.6	168	2	Q87496 YEREN
10	517	62.5	168	1	LCRH YERPS
11	517	62.5	168	2	Q7BFE3 YEREN
12	517	62.5	168	2	Q84GT6 YEREN
13	509	61.5	168	1	LCRH YERPE
14	390.5	47.2	162	2	Q87P60 VIBPA
15	382	46.2	163	2	Q6QV83 VIBHA
16	247	29.9	186	2	Q2SH37 9GAMM
17	245	29.6	166	2	Q2W10 DESVH
18	245	29.6	172	2	Q2SC45 9GAMM
19	185	22.4	161	2	Q7NUW9 CHRVO
20	181	21.9	183	2	Q2NVH7 SODGL
21	179	21.6	166	2	Q3JL21 BURPL
22	177	21.4	171	2	Q6K3K3 BURPS
23	175	21.2	190	2	Q6MBE1 PARUM
24	173	20.9	171	2	Q2T712 BURTH
25	172.5	20.9	156	2	Q62B06 BURMA
26	170	20.6	151	2	Q9AJ22 ECOLI
27	168.5	20.4	161	2	Q7WLX5 BORBR
28	167	20.2	161	2	Q84CS6 BORPE
29	167	20.2	167	2	Q7NU57 CHRVO
30	166.5	20.1	165	1	SICA_SALDU
31	166.5	20.1	165	1	SICA_SALTI

32	166.5	20.1	165	1	SICA_SALTY	P69066 salmonella
33	166.5	20.1	165	2	Q57KN8 SALCH	P69066 salmonella
34	166.5	20.1	165	2	Q5PEB9 SALPA	Q5PEB9 salmonella
35	166	20.1	151	2	Q93FL5 ENTR	Q93FL5 citrobacter
36	165	20.0	151	2	Q52134 ECOLI	Q52134 escherichia
37	165	20.0	151	2	Q7DB63 ECOS7	Q7DB63 escherichia
38	164	19.8	155	2	Q4G4C9 EDWTA	Q4G4C9 edwardsiella
39	163.5	19.8	161	2	Q7W8B7 BORPA	Q7W8B7 bordetella
40	158.5	19.2	163	2	Q3Q839 9GAMM	Q3Q839 shewanella
41	158	19.1	169	2	Q93284 YEREN	Q93284 yersinia en
42	156	18.9	179	2	Q6MB00 PARUM	Q6MB00 parachlamyd
43	151	18.3	130	2	Q45P2 SHIDY	Q45P2 shigella dy
44	151	18.3	155	1	IPGC_SHIDY	P04205 shigella dy
45	151	18.3	155	1	IPGC_SHIFL	P04204 shigella fl

ALIGNMENTS

RESULT 1
Q70WN6_AERSA
ID Q70WN6_AERSA PRELIMINARY; PRT; 167 AA.
AC Q70WN6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE AcRH protein.
GN Name=acrh;
OS Aeromonas salmonicida subsp. salmonicida.
OG Plasmid pASvira.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=29491;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267; PLASMID=pASvira;
RX MEDLINE=22957181; PubMed=14594831;
RA DOI=10.1128/JB.185.22.6583-6591.2003;
RA Burr S.E., Stuber K., Frey J.;
RT "The ADP-ribosylating toxin, AexT, from Aeromonas salmonicida subsp. salmonicida is translocated via a type III secretion pathway.";
RT J. Bacteriol. 185:6583-6591(2003).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=JF2267;
RA Burr S.E., Pughovkin D., Wahli T., Segner H., Frey J.;
RT "Attenuated virulence of an Aeromonas salmonicida subsp. salmonicida type -III secretion mutant in a rainbow trout model.";
RL Microbiol. 151:2111-2118(2005).
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CC -----
DR EMBL; AJ516009; CAD56770.1; -; Genomic DNA.
DR EMBL; AJ616218; CAE83109.1; -; Genomic DNA.
DR GO; GO:0005488; F.binding; IEA.
DR GO; GO:0006950; P.response to stress; IEA.
DR InterPro; IPR005415; Syncd chap.
DR InterPro; IPR011990; TPR_Ilike_helical.
DR InterPro; IPR011716; TPR_3.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07720; TPR_3; 2.
DR PRINTS; PR01595; SYCDCHAPRONE.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Plasmid
SQ SEQUENCE 167 AA; 18566 MW; 569510660770E101 CRC64;

Query Match 100.0%; Score 827; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.3e-78;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQDTTTLTPYEAELEAFMADGGTTLMLQDISDITLEQLYALFASQYQACKWEDAHKIFQ 60
|||||

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Db 1 MQTDTTLTPEYAEAEAFNADGGTTLAMQLDISGDTLEQLYALAFSQYQAGKWEADAKIFQ 60
Qy 61 ALCMLDHYEPYFLGLGACRQAMGEFETAVQSYSFGAMLDLKDPFPFHAGSCRLOQGD 120
Db 61 ALCMLDHYEPYFLGLGACRQAMGEFETAVQSYSFGAMLDLKDPFPFPFHAGSCRLOQGD 120
Qy 121 NGAESGFHSARLLADTPQQAADLAASAKVWLEAIAIRRD 159
Db 121 NGAESGFHSARLLADTPQQAADLAASAKVWLEAIAIRRD 159

RESULT 2
Q699Q9 AERHY
ID Q699Q9 AERHY PRELIMINARY; PRT; 167 AA.
AC Q699Q9;
DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE ACRH.
GN Name=acrH;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH3;
RX PubMed=15528564; DOI=10.1128/AEM.70.11.6914-6919.2004;
RA Vilches S., Urgell C., Merino S., Chacon M.R., Soler L.,
RA Castro-Escarpull G., Figueras M.J., Tomas J.M.;
RT "Complete type III secretion system of a mesophilic Aeromonas
RT hydrophila strain.";
RL Appl. Environ. Microbiol. 70:6914-6919(2004).
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CC -----
DR EMBL; AY528667; AAS91820.1; -; Genomic_DNA.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR005415; SyCD_chap.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07720; TPR 3; 2.
DR PRINTS; PR01595; SYCDCHAPRONE.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 167 AA; 18533 MW; C6A9DEBEC335B8DD CRC64;

Query Match 94.3%; Score 780; DB 2; Length 167;
Best Local Similarity 93.1%; Pred. No. 1.1e-73;
Matches 148; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MQTDTTLTPEYAEAEAFNADGGTTLAMQLDISGDTLEQLYALAFSQYQAGKWEADAKIFQ 60
Db 1 MQTDTTLTPEYAEAEAFNADGGTTLAMQLDISGDTLEQLYALAFSQYQAGKWEADAKIFQ 60
Qy 61 ALCMLDHYEPYFLGLGACRQAMGEFETAVQSYSFGAMLDLKDPFPFHAGSCRLOQGD 120
Db 61 ALCMLDHYEPYFLGLGACRQAMGEFETAVQSYSFGAMLDLKDPFPFPFHAGSCRLOQGD 120
Qy 121 NGAESGFHSARLLADTPQQAADLAASAKVWLEAIAIRRD 159
Db 121 NGAESGFHSARLLADTPQQAADLAASAKVWLEAIAIRRD 159

RESULT 3
Q5XL03 AERHY
ID Q5XL03 AERHY PRELIMINARY; PRT; 167 AA.
AC Q5XL03;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
CC
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DE ACRH.
GN Name=acrH;
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSU;
RX PubMed=16177316; DOI=10.1128/IAI.73.10.6446-6457.2005;
RA Sha J., Pillai L., Fadl A.A., Galindo C.L., Erova T.E., Chopra A.K.;
RA "The Type III Secretion System and Cytotoxic Enterotoxin Alter the
RT Virulence of Aeromonas hydrophila.";
RL Infect. Immun. 73:6446-6457(2005).
CC
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CC -----
DR EMBL; AY763611; AAV30234.1; -; Genomic_DNA.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR005415; SyCD_chap.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR011716; TPR 3.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07720; TPR 3; 2.
DR PRINTS; PR01595; SYCDCHAPRONE.
DR PROSITE; PS50293; TPR_REGION; 1.
SQ SEQUENCE 167 AA; 18586 MW; 451FCF1DC6ED4211 CRC64;

Query Match 93.0%; Score 769; DB 2; Length 167;
Best Local Similarity 93.1%; Pred. No. 1.6e-72;
Matches 148; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MQTDTTLTPEYAEAEAFNADGGTTLAMQLDISGDTLEQLYALAFSQYQAGKWEADAKIFQ 60
Db 1 MQTDTTLTPEYAEAEAFNADGGTTLAMQLDISGDTLEQLYALAFSQYQAGKWEADAKIFQ 60
Qy 61 ALCMLDHYEPYFLGLGACRQAMGEFETAVQSYSFGAMLDLKDPFPFHAGSCRLOQGD 120
Db 61 ALCMLDHYEPYFLGLGACRQAMGEFETAVQSYSFGAMLDLKDPFPFPFHAGSCRLOQGD 120
Qy 121 NGAESGFHSARLLADTPQQAADLAASAKVWLEAIAIRRD 159
Db 121 NGAESGFHSARLLADTPQQAADLAASAKVWLEAIAIRRD 159

RESULT 4
Q7NOX2 PHOLL
ID Q7NOX2 PHOLL PRELIMINARY; PRT; 167 AA.
AC Q7NOX2;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Similar to low calcium response locus protein H LcrH.
DE OrderedLocusNames=plu3757;
OS Photorhabdus luminescens subsp. laumondii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Rusnok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
CC
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CC -----
CC EMBL; BX571871; CAE16129.1; -; Genomic_DNA.
CC Photolista; plu3757; -.
CC BioCyc; PLUM243265; PLU3757-MONOMER; -.
CC GO; GO:0005488; F:binding; IEA.
CC GO; GO:0006950; P:response to stress; IEA.
CC InterPro; IPR005415; SycD_chap.
CC InterPro; IPR011990; TPR-like_helical.
CC InterPro; IPR011716; TPR_3.
CC InterPro; IPR013026; TPR_region.
CC Pfam; PF07720; TPR_3; 1.
CC PRINTS; PR01595; SYCDCHAPRONE.
CC PROSITE; PS0293; TPR_REGION; 1.
CC Complete proteome.
CC SEQUENCE 167 AA; 18364 MW; 7D48A0A5CD43DA9 CRC64;

Query Match 72.1%; Score 596; DB 2; Length 167;
Best Local Similarity 70.7%; Pred. No. 2.7e-54;
Matches 111; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 2 QTDTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADAKHIFQA 61
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 QETSTSDQVAQELSFHLDGGTFLMKDLSSTLEQLYSLAFNQYSGKWDADAKHIFQA 63
QY 62 LCMLDHYEPRYFLGLGACRQAMGEFETAVQSYSGAMLDLKDPRFPFHAGECRLQOQDGLN 121
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
64 LCMLDHYDSRFFFLGLGACRQAMGLEQIQSYSGAMLDINEPRFPFHAAECLQLGELD 123
QY 122 GAESGFHSARLLADTDPQADLAASAKVMLEAIRR 158
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
124 GAESGFYSAQQLAAALPEQALAAASSAMLEAITIKR 160

RESULT 5
Q84GY4_PHOLU
ID Q84GY4 PHOLU PRELIMINARY; PRT; 168 AA.
AC Q84GY4;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DE Lsh.
GN Name=Lsh;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., French-Constant R.H.;
RT "Genomic islands in Photorhabdus";
RL Trends Microbiol. 10:541-545(2002).
CC
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CC -----
CC EMBL; AY144116; AA018054.1; -; Genomic_DNA.
CC GO; GO:0005488; F:binding; IEA.
CC GO; GO:0006950; P:response to stress; IEA.
CC InterPro; IPR005415; SycD_chap.
CC InterPro; IPR011990; TPR-like_helical.
CC InterPro; IPR011716; TPR_3.
CC InterPro; IPR013026; TPR_region.
CC Pfam; PF07720; TPR_3; 2.
CC PRINTS; PR01595; SYCDCHAPRONE.
CC PROSITE; PS0293; TPR_REGION; 1.
CC Complete proteome.
CC SEQUENCE 168 AA; 18567 MW; 832198A9DB9C49A2 CRC64;

Query Match 71.0%; Score 587; DB 2; Length 168;
Best Local Similarity 69.4%; Pred. No. 2.4e-53;

QY 121 NGAESGFHSARLLADTDPQADLAASAKVMLEAIRRD 159
```

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Matches 109; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

QY 2 QTDTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADAKHIFQA 61
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 QETSTSDQVAQELSFHLDGGTFLMKDLSSTLEQLYSLAFNQYSGKWDADAKHIFQA 63
QY 62 LCMLDHYEPRYFLGLGACRQAMGEFETAVQSYSGAMLDLKDPRFPFHAGECRLQOQDGLN 121
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
64 LCMLDHYDSRFFFLGLGACRQAMGLEQIQSYSGAMLDINEPRFPFHAAECLQLGELD 123
QY 122 GAESGFHSARLLADTDPQADLAASAKVMLEAIRR 158
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
124 GAESGFYSAQQLAAALPEQALAAASSAMLEAITIKR 160

RESULT 6
Q91325_PSBAAE
ID Q91325_PSBAAE PRELIMINARY; PRT; 167 AA.
AC Q91325;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE Regulatory protein PcrH.
GN Name=pcrH; OrderedLocustNames=PA1707;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC
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CC -----
CC EMBL; AE004597; AAG05096.1; -; Genomic_DNA.
CC PIR; H83432; H83432.
CC BioCyc; PAER287; PA1707-MONOMER; -.
CC GO; GO:0005488; F:binding; IEA.
CC GO; GO:0006950; P:response to stress; IEA.
CC InterPro; IPR005415; SycD_chap.
CC InterPro; IPR011990; TPR-like_helical.
CC InterPro; IPR011716; TPR_3.
CC InterPro; IPR013026; TPR_region.
CC Pfam; PF07720; TPR_3; 1.
CC PRINTS; PR01595; SYCDCHAPRONE.
CC PROSITE; PS0293; TPR_REGION; 1.
CC Complete proteome.
CC SEQUENCE 167 AA; 18350 MW; 178118F12FBB559D CRC64;

Query Match 66.4%; Score 549; DB 2; Length 167;
Best Local Similarity 64.8%; Pred. No. 2.4e-49;
Matches 103; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 1 MQDTTTLTPEYAELEAFMADGGTTLAMLDISGDTLEQLYALAFSQYQAGKWEADAKHIFQ 60
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MNQPTPSDDTQQQALAEFLRDGGTTLAMLRGLSSTLEQLYALGFNQYQAGKWDADAKHIFQ 60
QY 61 ALCMLDHYEPRYFLGLGACRQAMGEFETAVQSYSGAMLDLKDPRFPFHAGECRLQOQDGL 120
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 ALCMLDHYDARYFLGLGACRQSLGLYEQALQSYSGALMDINEPRFPFHAAECLQLGDL 120
QY 121 NGAESGFHSARLLADTDPQADLAASAKVMLEAIRRD 159
```

iriarte M., Lambermont L., Korbourec C., Cornells G.R.;
 Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

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 EMBL; AF102990; AAD16814.1; -; Genomic DNA.

```
DR GO: 0005488; F:binding; IEA.
DR GO: 0006950; P:response to stress; IEA.
DR InterPro: IPR005415; SyCD chap.
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR011716; TPR 3.
DR InterPro: IPR013026; TPR_region.
DR Pfam: PF07720; TPR_3; 2_region.
DR PRINTS: PR01595; SYCDCHAPRONE.
DR PROSITE: PS50293; TPR_REGION; 1.
KW Plasmid.
SQ SEQUENCE 168 AA; 18995 MW; D7F631B140EB16AE CRC64;

Query Match          62.6%; Score 518; DB 2; Length 168;
Best Local Similarity 58.5%; Pred. No. 4.5e-46;
Matches 93; Conservative 34; Mismatches 32; Indels 0; Gaps 0;

QY 1 MQDTTLTPYEAELEAFMADGGTGLMLQDISGDTLEQLYALAFSQYQAGKWEAHKIFQ 60
DB 1 MQQETTDQEQYLAMESFLKGGGTIAMLNEISSDTLEQLYSLAFNQYQSGKYEDAHKVFQ 60
QY 61 ALCMLDHYEPYFYLGLACRAMGEFETAVOSYSGFAMLDLKDPRFPFHAGCECLQQGDL 120
DB 61 ALCVLDHYDSRFFLGLACRAMGQYDLAIHSYSYGAVMDIKPRFPFHAAECCLLQKGL 120
QY 121 NGAESGFHSARLLADTDPPQADLAASAKVMLEAIRRD 159
DB 121 AEASGLFLAQELIANKEPFKELSTRVSSMLEAIKLKKE 159

RESULT 10
LCRH YERPS
ID _LCRH YERPS STANDARD; PRT; 168 AA.
AC P23995; Q66310;
DT 01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-1992, sequence version 1.
DT 07-MAR-2006, entry version 38.
DE Low calcium response locus protein H.
GN Name=lcRH; OrderedLocusNames=PYV0056;
OS Yersinia pseudotuberculosis.
OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=YPIII / Serotype O:3; PLASMID=PIB1;
RX MEDLINE=91154114; PubMed=1705541;
RA Bergman T., Haakansson S., Forsberg A., Norlander L., Macellaro A.,
RA Baeckman A., Boelin I., Wolf-Watz H.;
RT "Analysis of the v antigen lcrGVH-yopBD operon of Yersinia
pseudotuberculosis: evidence for a regulatory role of LcrH and LcrV.";
RL J. Bacteriol. 173:1607-1616(1991).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I; PLASMID=pyV;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Darbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Mediates the negative regulation of the lcrGVH operon by
ATP or calcium. Acts as a modulator of the yop operon expression.
CC -!- SIMILARITY: Belongs to the lcrH/syCD chaperrone family.
CC
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CC -----
CC EMBL; M57893; AAA27646.1; -; Genomic DNA.
CC EMBL; BX936399; CAP25399.1; -; Genomic DNA.
CC
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DR PIR; C37314; C37314.
DR PDB; 1OOL; Model; A=32-165.
DR PDB; 1OOS; Model; A=1-168.
DR GenomeReviews; BX936399 GR; pyV0056.
DR InterPro: IPR005415; SyCD chap.
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR011716; TPR 3.
DR InterPro: IPR013026; TPR_region.
DR Pfam: PF07720; TPR_3; 2_region.
DR PRINTS: PR01595; SYCDCHAPRONE.
DR PROSITE: PS50293; TPR_REGION; 1.
KW 3D-structure; Chaperrone; Complete proteome; Plasmid.
FT CHAIN 1 168
/FTid=PRO_0000206486.

STRAND 34 35
HELIX 36 49
TURN 50 50
HELIX 52 65
TURN 66 68
HELIX 70 83
TURN 84 84
HELIX 86 99
TURN 101 102
TURN 104 104
HELIX 105 117
TURN 118 118
HELIX 121 133
TURN 135 136
HELIX 138 147
TURN 148 148
HELIX 150 150
TURN 151 155
STRAND 158 158
TURN 160 161
HELIX 162 164
SEQUENCE 168 AA; 19011 MW; 2CE06AF240EB0424 CRC64;

Query Match          62.5%; Score 517; DB 1; Length 168;
Best Local Similarity 58.5%; Pred. No. 5.8e-46;
Matches 93; Conservative 34; Mismatches 32; Indels 0; Gaps 0;

QY 1 MQDTTLTPYEAELEAFMADGGTGLMLQDISGDTLEQLYALAFSQYQAGKWEAHKIFQ 60
DB 1 MQQETTDQEQYLAMESFLKGGGTIAMLNEISSDTLEQLYSLAFNQYQSGKYEDAHKVFQ 60
QY 61 ALCMLDHYEPYFYLGLACRAMGEFETAVOSYSGFAMLDLKDPRFPFHAGCECLQQGDL 120
DB 61 ALCVLDHYDSRFFLGLACRAMGQYDLAIHSYSYGAVMDIKPRFPFHAAECCLLQKGL 120
QY 121 NGAESGFHSARLLADTDPPQADLAASAKVMLEAIRRD 159
DB 121 AEASGLFLAQELIANKEPFKELSTRVSSMLEAIKLKKE 159

RESULT 11
Q7BFB3 YEREN
ID Q7BFB3_YEREN PRELIMINARY; PRT; 168 AA.
AC Q7BFB3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE YopB/D chaperrone SyCD.
GN Name=syCD;
OS Yersinia enterocolitica.
OG Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX NCBI_TaxID=630;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8081;
RX MEDLINE=21295118; PubMed=11402007;
RX
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LN      Nature 413:523-527(2001).
[5]
RN
RP     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=91001 / Biovar Metaeavalis;
RX      PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA      Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA      Zhou D., Qin H., Pang X., Han S., Zhai J., Li M., Cui B., Qi Z.,
RA      Jin L., Bai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA      Yang H., Wang J., Huang P., Yang R.;
RT      "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT      avirulent to humans.";
RNA     DNARES_11-179-197(2004).
CC      -1- FUNCTION: Mediates the negative regulation of the lcrGVH operon by
CC      ATP or calcium. Acts as a modulator of the yop operon expression.
CC      -1- SIMILARITY: Belongs to the lcrH/sycD chaperone family.
CC
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CC      -----
DR      EMBL; M26405; AAA27642.1; -; Genomic_DNA.
DR      EMBL; AF074612; AAC69800.1; -; Genomic_DNA.
DR      EMBL; AF053946; AAC62575.1; -; Genomic_DNA.
DR      EMBL; AL117189; CAB54907.1; -; Genomic_DNA.
DR      EMBL; AE017043; AAS58572.1; -; Genomic_DNA.
DR      PIR; C33601; C33601.
DR      GenomeReviews; AE017043 GR; pCD53.
DR      GenomeReviews; AL117189 GR; YPCD1.30C.
DR      BioCyc; YPES229193:PCD53-MONOMER; -.
DR      BioCyc; YPES632.YPCD1_30C-MONOMER; -.
DR      InterPro; IPR005415; SYCD_chap.
DR      InterPro; IPR011990; TPR-like_helical.
DR      InterPro; IPR011716; TPR_3.
DR      InterPro; IPR013026; TPR_region.
DR      Pfam; PF07720; TPR_3; 2.
DR      PRINTS; PR01595; SYCDCHAPRONE.
DR      PROSITE; PS50293; TPR_REGION; 1.
KW      Chaperone; Complete proteome; Plasmid.
FT      CHAIN          1..168
FT                     Low calcium response locus protein H.
FT                     /FTID=PRO_0000206485.
SQ
Query Match           61.5%; Score 509; DB 1; Length 168;
Best Local Similarity 57.9%; Pred. NO. 4e-45;
Matches 92; Conservative 34; Mismatches 33; Indels 0; Gaps 0

Qy      1   MQDTTTLTPVEAELEAFMAGGGTIAMLQDTSGLDTLEQLYALAFSQYQAGKWEADAKTFQ 60
Db      1   MQGETTDTEQVQLAWESFLKGGGTIAMLINEISSDTLEQLYSIAFNQYSGKYEDAHKVQF 60

Qy      61  ALCLMDHYEPRYFLGLGACROAMGEFETAVQSFGAMLDLKDPRFPFHAGECRICQQGD 120
Db      61  ALCVLVDHSRFFLLGLGACROAMGOYDLAIHSYSYGAIMDKIEPRFPFHAECLLKQGL 120

Qy      121 NGAESGFHARKLLADTPDQQADLAASKVMLEAIAIRD 159
Db      121 AEASSGLFLAQELIADTKTEFKELSTRVSMSLEAIKLKKE 159

RESULT 14
Q87P60_VIBPA PRELIMINARY; PRT; 162 AA.
AC Q87P60;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Low calcium response locus protein H.
OS OrderedLocusNames=VP1658;
GN Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
[1]
RP     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
```

RC STRAIN=RMD 2210633 / Serotype O3:K6;
RA MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RX Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RA "genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
RT distinct from that of *V. cholerae*."; <http://www.uniprot.org/terms>
RL Lancet 361:743-749 (2003).
CC
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CC -----
DR ENML; BA000031; BAC59921.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR005415; SyncD chap.
DR InterPro; IPR011990; TPR-Like_helical.
DR InterPro; IPR011716; TPR_3.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07720; TPR_3; 2.
DR PRINTS; PR01595; SYCDCHAPRONE.
DR PROSITE; PS0293; TPR_REGION; 1.
KW Complete proteome.
SQ SEQUENCE 162 AA; 18128 MW; 94FB1967B5C9EC1F CRC64;

Query Match 47.2%; Score 390.5; DB 2; Length 162;
Best Local Similarity 47.5%; Pred. No. 1.2e-32;
Matches 75; Conservative 36; Mismatches 46; Indels 1; Gaps 1;

QY 2 QDTTTLTPEYEA-ELEAFMADGGTTLAMLQDISGDTLEQLYALAFSQYQAGKWEDAHKIFQ 60
DB 3 KTNATDPQMOABELL5FLBEGGTLKMLHDVSDATTHIYAVGVNFFQSGKIEQAQKVFQ 62

QY 61 ALCMLDHYBPRYFLGLGACQAMGEPTAVQSYSGAMLDLKQPRPFPHAGECRLOQGD 120
DB 63 LLSMLDHYQARFFIGLGAARQELGEYLOAIDAISYAALVDINDRPFPHSAECHKLEQL 122

QY 121 NGAESGFHSARLLADTPDQQAADLAASAKVMLEAIAIRR 158
DB 123 TEAESGFYSAKENSAGKSQYADLHORAGIMLEAVRNKR 160

RESULT 15
Q6QVS3 VIBHA
ID O6QVS3 VIBHA PRELIMINARY; PRT; 163 AA.
AC O6QVS3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 03-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE VcrH.
GN Name=vcrH;
OS *Vibrio harveyi*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
ON NCBI_TaxID=669;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Henke J.M., Basler B.L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR ENML; AY524044; AAS13308.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR005415; SyncD chap.
DR InterPro; IPR011990; TPR-Like_helical.
DR InterPro; IPR011716; TPR_3.
DR InterPro; IPR013026; TPR_region.
DR Pfam; PF07720; TPR_3; 2.
DR PRINTS; PR01595; SYCDCHAPRONE.
DR PROSITE; PS0293; TPR_REGION; 1.
KW Complete proteome.

SQ SEQUENCE 163 AA; 18212 MW; A605672027F1252A CRC64;
Query Match 46.2%; Score 382; DB 2; Length 163;
Best Local Similarity 49.0%; Pred.No. 9.2e-32;
Matches 71; Conservative 33; Mismatches 41; Indels 0; Gaps 0;
Qy 14 ELEAFMADGGT LAMLDISGDTLEQLYALAFSQVQAGKWEDAHKIFQALCMLDHYEPRYF 73
Db 17 ELLSFLEGGT LKMLHDVSDTIEHIYAVGVNFFQSGKIEQAQVFOQLLSMLDHYQARFF 76
Qy 74 LGLGACRQAMGE PETAVQSYSGFAMLDLKDPRPFPHAGECRLOQGD LNGAESGFHSARLL 133
Db 77 IGLGAARQELGEYLQALDAYAALVDVNDPRPFHSAECHLKLEQLTEAESGFYSAKEM 136
Qy 134 ADTDPQADLAASAKVMLEAIRR 158
Db 137 SAGKSEYADLHQ RAGIMLEAVRNKR 161

Search completed: June 16, 2006, 19:23:00
Job time : 125.873 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 19:23:31 ; Search time 29.3439 Seconds
(without alignments)
474.285 Million cell updates/sec

Title: US-10-813-908A-9
Perfect score: 827
Sequence: 1 MQDTTTLTPEYEAELEAFMA.....QADLAASAKVMLEAIRRD 159

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents AA.*
- 1: /EMC_Celerra_SIDS3/protdata/2/iaa/5_COMB.pep.*
 - 2: /EMC_Celerra_SIDS3/protdata/2/iaa/6_COMB.pep.*
 - 3: /EMC_Celerra_SIDS3/protdata/2/iaa/7_COMB.pep.*
 - 4: /EMC_Celerra_SIDS3/protdata/2/iaa/H_COMB.pep.*
 - 5: /EMC_Celerra_SIDS3/protdata/2/iaa/PCTUS_COMB.pep.*
 - 6: /EMC_Celerra_SIDS3/protdata/2/iaa/RE_COMB.pep.*
 - 7: /EMC_Celerra_SIDS3/protdata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	66.3	239	2	US-09-252-991A-29963 Sequence 29963, A
2	163.5	19.8	182	2	US-09-543-681A-6578 Sequence 6578, A
3	125.5	15.2	157	2	US-09-763-620-19 Sequence 19, Appl
4	121.5	14.7	158	2	US-09-902-540-13633 Sequence 13633, A
5	118	14.3	144	2	US-09-763-620-21 Sequence 21, Appl
6	116.5	14.1	154	2	US-09-902-540-16064 Sequence 16064, A
7	105	12.7	210	2	US-09-198-452A-869 Sequence 869, App
8	105	12.7	242	2	US-09-438-185A-813 Sequence 813, App
9	100	12.1	191	2	US-09-198-452A-1095 Sequence 1095, App
10	100	12.1	191	2	US-09-438-185A-1022 Sequence 1022, App
11	84.5	10.2	1564	2	US-09-976-594-309 Sequence 309, App
12	83	10.0	639	2	US-09-902-540-12091 Sequence 12091, A
13	80	9.7	458	1	US-09-336-618-24 Sequence 24, Appl
14	79	9.6	315	2	US-09-585-645A-42 Sequence 42, Appl
15	79	9.6	667	2	US-09-248-796A-18663 Sequence 18663, A
16	78.5	9.5	380	2	US-09-902-540-12056 Sequence 12056, A
17	78.5	9.5	526	2	US-09-902-540-16327 Sequence 16327, A
18	78.5	9.5	806	2	US-09-328-352-7160 Sequence 7160, App
19	78	9.4	211	2	US-09-205-258-263 Sequence 263, App
20	78	9.4	211	2	US-10-004-860-263 Sequence 263, App
21	78	9.4	261	2	US-09-205-258-505 Sequence 505, App
22	78	9.4	261	2	US-10-004-860-505 Sequence 505, App
23	78	9.4	308	1	US-08-807-050-1 Sequence 1, Appli
24	78	9.4	317	2	US-09-205-258-504 Sequence 504, App
25	78	9.4	317	2	US-10-004-860-504 Sequence 504, App
26	77.5	9.4	322	2	US-09-902-540-11744 Sequence 11744, A

27	77	9.3	1191	2	US-09-921-099A-2 Sequence 2, Appli
28	77	9.3	1191	2	US-09-921-099A-4 Sequence 4, Appli
29	76.5	9.3	528	2	US-09-252-991A-32995 Sequence 32995, A
30	75.5	9.1	1490	2	US-09-252-991A-28442 Sequence 28442, A
31	75	9.1	308	1	US-08-807-050-3 Sequence 3, Appli
32	75	9.1	600	2	US-09-252-991A-31546 Sequence 31546, A
33	75	9.1	981	1	US-08-649-046-2 Sequence 2, Appli
34	74.5	9.0	2472	2	US-09-538-092-1312 Sequence 1312, Ap
35	74	8.9	466	2	US-09-248-796A-19009 Sequence 19009, A
36	74	8.9	1087	2	US-09-252-991A-28584 Sequence 28584, A
37	73.5	8.9	410	2	US-09-248-796A-17607 Sequence 17607, A
38	72.5	8.8	369	2	US-09-902-540-12050 Sequence 12050, A
39	72.5	8.8	479	1	US-08-942-218A-2 Sequence 2, Appli
40	72.5	8.8	499	1	US-08-610-731A-2 Sequence 2, Appli
41	72.5	8.8	499	1	US-09-067-379-2 Sequence 2, Appli
42	72.5	8.8	499	2	US-09-067-506-2 Sequence 2, Appli
43	72.5	8.8	499	2	US-08-951-034B-2 Sequence 2, Appli
44	72.5	8.8	510	2	US-09-252-991A-19584 Sequence 19584, A
45	72.5	8.8	519	2	US-09-786-240-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-29963
; Sequence 29963, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23963
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29963

Query Match	66.3%;	Score 548;	DB 2;	Length 239;
Best Local Similarity	65.2%;	Pred. No. 5.5e-59;		
Matches	103;	Conservative 21;	Mismatches 34;	Indels 0; Gaps 0;
Qy	2	QTDTTLTPEYEAELEAFMADGGTTLMLQDITGDTLEOLYALAFSQYQAGKWEDAHKIFQA	61	
Db	74	QQAATPSDTCQQQALEAFRLRGDTLMLRGSEDTLEOLYALGNQYQAGKWDAAKIFQA	133	
Qy	62	LCMLDHYEPRYFGLGACROAMGEFTAVQSYSGAMLDLKDPRFPFHAGECRLOQGDNL	121	
Db	134	LCMLDHYARYFLGACROSLGLYEQALQSYSGALMDINEPRFPFHAAEHLQGLDLD	193	
Qy	122	GAESGFHSARLLADTPQQADLAASAKVMLEAIRRD	159	
Db	194	GAESGFYSARALAAAPHAHEALAAARAGAMLEAVTARKD	231	

RESULT 2
US-09-543-681A-6578
; Sequence 6578, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A

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; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6578
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6578

Query Match          19.8%; Score 163.5; DB 2; Length 182;
Best Local Similarity 29.8%; Pred. No. 7.7e-12;
Matches 37; Conservative 25; Mismatches 55; Indels 7; Gaps 1;

QY 12 EALE-----AFMADGGTGLAMLQDISGDTLEQLYALAFSQYQAGKWEHAHIFQALCM 64
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 19 EKELDQLANVIVSQNGASIKDESEIPDGFMEGDSFYDFYQKGLDEAEAIKFLCL 78
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 65 LDHYEPYFLGLGACRQAMGEFETAVOSYSGFAMLDLKDPRFPFHAGECRLOQGDNLGAE 124
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 79 YDFYNDYIMGLAAVNQLKKQYQAAIDLVALYNNAKNDYRVPVYAGQCNLISIGEKEKAK 138
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 125 SGFH 128
    ||
Db 139 YCFH 142

RESULT 3
US-09-763-620-19
; Sequence 19, Application US/09763620
; Patent No. 6936425
; GENERAL INFORMATION:
; APPLICANT: Hensel, Michael
; APPLICANT: Guzman, Carlos Alberto
; APPLICANT: Medina, Eva
; APPLICANT: Hueck, Cristoph
; TITLE OF INVENTION: Carrier System for Vaccines
; FILE REFERENCE: 100564-00050
; CURRENT APPLICATION NUMBER: US/09/763,620
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EP 98116827.1
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Salmonella
US-09-763-620-19

Query Match          15.2%; Score 125.5; DB 2; Length 157;
Best Local Similarity 27.0%; Pred. No. 3e-07;
Matches 43; Conservative 28; Mismatches 83; Indels 5; Gaps 4;

QY 1 MQDTDTLTPEYAELEAFNADGGTGLAM-LQDISGDTLEQLYALAFSQYQAGKWEHAHIF 59
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 1 MKKDPTLQOAHDT--MRFFRGSLRMILLDDVTQPTLTYRYATQIMEVKEFAGARLF 58
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 60 QALCMLDHYEPYFLGLGACRQAMGEFETAVOSYSGFAMLDLKDPRFPFHAGECRLOQGD 119
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 59 QLLTIYDAWSFDYWFRLGCCQAQKHGWEAIYAGRAAQIKIDAPQAPWAAAEACYLACDN 118
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 120 LGAESGFHS-ARLLADTDPQADLAASAKVMLEATAIR 157
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 119 VCYAIKALKAVRIGEVSEHQI-LRQRAEKMLQLSDR 156
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 4
US-09-902-540-13633
; Sequence 13633, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
```

```
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13633
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13633

Query Match          14.7%; Score 121.5; DB 2; Length 158;
Best Local Similarity 26.5%; Pred. No. 9.3e-07;
Matches 41; Conservative 26; Mismatches 77; Indels 11; Gaps 4;

QY 9 PEYAELEAFM---ADGGTGLAMLQDISGDTLEQLYALAFSQY---QAGKWEHAHIFQAL 62
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 9 PKDEAKLDTLLQRWADG--KATLRDVRGYSDELYAIKTAITYFFYQGRVSEARTLFOGL 66
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 63 CMLDHYEPYFLGLGACRQAMGEFETAVOSYSGFAMLDLKDPRFPFHAGECRLOQGDNLG 122
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 67 YAVNPTDAYFAKALGVVEWAAGNGOGALAAFDVAAKLTPHDPFSVYVGRAEVKLMAGQ--- 123
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 123 ABSGFHSARLLADTDPQADLAASAKVMLEATAIR 157
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 124 KPQALEDLRRRAAMQPGDDPVVRKAAAMISALSRR 158
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 5
US-09-763-620-21
; Sequence 21, Application US/09763620
; Patent No. 6936425
; GENERAL INFORMATION:
; APPLICANT: Hensel, Michael
; APPLICANT: Guzman, Carlos Alberto
; APPLICANT: Medina, Eva
; APPLICANT: Apfel, Heiko
; APPLICANT: Hueck, Cristoph
; TITLE OF INVENTION: Carrier System for Vaccines
; FILE REFERENCE: 100564-00050
; CURRENT APPLICATION NUMBER: US/09/763,620
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: EP 98116827.1
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Salmonella
US-09-763-620-21

Query Match          14.3%; Score 118; DB 2; Length 144;
Best Local Similarity 24.2%; Pred. No. 2.2e-06;
Matches 32; Conservative 24; Mismatches 68; Indels 8; Gaps 1;

QY 31 ISGDTLEQL-----YALAFSQYQAGKWEHAHIFQALCMLDHYEPYFLGLGACRQA 82
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 11 IPEDILKQLLSVDPETVYASGYASWQEGDSRAVIDFSWLVMAQPSWRAHIALAGTWM 70
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 83 MGEFETAVOSYSGFAMLDLKDPRFPFHAGECRLOQGDNLGASGFHSARLLADTDPQAD 142
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 71 LKEYTTAINFYCHALMLDASHPEPVYQTGVCLKMWGEFGLAREAFQTAKMSYADASWSE 130
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 143 LAASAKVMLEAI 154
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 131 IRQNAQIMVDTL 142
    |||:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
```

RESULT 6
US-09-902-540-16064
; Sequence 16064, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16064
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16064

Query Match 14.1%; Score 116.5; DB 2; Length 154;
Best Local Similarity 26.9%; Pred. No. 3.7e-06;
Matches 35; Conservative 29; Mismatches 61; Indels 5; Gaps 3;

QY 28 LODISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCMLDHYEPRYFLGLGACROAMGEFE 87
DB 14 VKPLSGEMLEATERGENLFDQGRFRESLTLFQSLAAMDPTAEYFQTALGACHLAEDLD 73

QY 88 TAVOSYSFGMLDLKDPFRPF-HAGECRLOQDNLNGAESGFHSAARLADTDPOQADLAAS 146
DB 74 LAESYFNRALEDPD-LTFPVNRGEVHLRGKVHEAARDFNHA---VGLDPGEQDPLSA 129

QY 147 AKVMLEIAI 156
DB 130 RARMLAAAL 139

RESULT 7
US-09-198-452A-869
; Sequence 869, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 869
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-869

Query Match 12.7%; Score 105; DB 2; Length 210;
Best Local Similarity 23.4%; Pred. No. 0.00015;
Matches 33; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

QY 19 MADGGTLMQLDISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCMLDHYEPRYFLGLGA 78
DB 43 LSNGLDLQQLGLSDYLLEIYTVAYTFYSQKYNBAVGLFQLLAAAQPNQYKMYLGLSS 102

QY 79 CROAMGEFETAVOSY--SFGAMLDLKDPRFFPHAGE--CRLOQDNLNGAESGFHSAARL-L 133
DB 103 CYHQLHLYNEAAGFFLAFDAQPD--NPIPPYYIADSLKLQOPE---ESNNFLDVTMDI 157

QY 134 ADTDPQADLAASAKVMLEAI 154

DB 158 CGNPEFKILKERCQIMKQSI 178

RESULT 8
US-09-438-185A-813
; Sequence 813, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 813
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; OTHER INFORMATION: Cpn0811
US-09-438-185A-813

Query Match 12.7%; Score 105; DB 2; Length 242;
Best Local Similarity 23.4%; Pred. No. 0.00018;
Matches 33; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

QY 19 MADGGTLMQLDISGDTLEQLYALAFSQYQAGKWEADAHKIFQALCMLDHYEPRYFLGLGA 78
DB 75 LSNGLDLQQLGLSDYLLEIYTVAYTFYSQKYNBAVGLFQLLAAAQPNQYKMYLGLSS 134

QY 79 CROAMGEFETAVOSY--SFGAMLDLKDPRFFPHAGE--CRLOQDNLNGAESGFHSAARL-L 133
DB 135 CYHQLHLYNEAAGFFLAFDAQPD--NPIPPYYIADSLKLQOPE---ESNNFLDVTMDI 189

QY 134 ADTDPQADLAASAKVMLEAI 154
DB 190 CGNPEFKILKERCQIMKQSI 210

RESULT 9
US-09-198-452A-1095
; Sequence 1095, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1095
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1095

Query Match 12.1%; Score 100; DB 2; Length 191;
Best Local Similarity 22.2%; Pred. No. 0.00054;
Matches 32; Conservative 28; Mismatches 80; Indels 4; Gaps 1;

QY 4 DTTLTPEYAELEAFMADGG----TLAMLQDISGDTLEQLYALAFSQYQAGKWEADAHKIF 59

APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336.618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VPI91-06A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-618-24

Query Match 9.7%; Score 80; DB 1; Length 458;
Best Local Similarity 23.9%; Pred. No. 0.55; Indels 24; Gaps 5;
Matches 38; Conservative 21; Mismatches 76; Indels 24; Gaps 5;
Qy 7 LTPEYAELEAFMADGGTTLMLQDISGDTLEQLYALAFSQY-QAGKWEDAHKIF----- 59
Db 261 MSSEKLEQSAIVKERTGYF-----KEGKYQALLQYKKIVSMLEYESSFSSEVQ 312
Qy 60 --QALCMLDHYEPYFYLGLGACRAMGEFETAVOSYSGFAMLDLKDPRFPFHAGECRLQ 117
Db 313 KAQALRLASH-----LNLAMCHLKLOAFSAAVESCNAKLELDSNNKGLFRGAEHLAV 366
Qy 118 GDLNGAEGGHSFA-RLLADTDPQADLAASAQVWLEAIA 155
Db 367 NDFPLARADFOKVLQLYPSNKAQAQALAVCOORIRKOIA 405

RESULT 14
US-09-585-645A-42
Sequence 42, Application US/09585645A
Patent No. 6838444
GENERAL INFORMATION:
APPLICANT: Zoghbi, Huda
APPLICANT: Bellen, Hugo
APPLICANT: Birmingham, Nessim
APPLICANT: Hassan, Bessam
APPLICANT: Ben-Arie, Nissim

TITLE OF INVENTION: Compositions and Methods for Therapeutic Use of Atonal-associate
TITLE OF INVENTION: for Deafness, Osteoarthritis, and Abnormal Cell Proliferation
FILE REFERENCE: P01899US2
CURRENT APPLICATION NUMBER: US/09/585,645A
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/137,060
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 60/176,993
PRIOR FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 315
TYPE: PRT
ORGANISM: FROG
US-09-585-645A-42

Query Match 9.6%; Score 79; DB 2; Length 315;
Best Local Similarity 27.2%; Pred. No. 0.43; Indels 28; Gaps 4;
Matches 28; Conservative 11; Mismatches 36; Indels 28; Gaps 4;
Qy 8 TPEYAELEAFMADGGTTLMLQDISGDTLEQLYALAFSQYQAGKWEDAHKIFQALCMLDH 67
Db 237 TPYEGALTPLSLGNGFSLKQSSPD-MDKSTAFR-SPYPA----- 276

Qy 68 YEPYFYLGLGACRAMGEFETAVOSYSGFAMLDLKDPRFPFPHA 110
Db 277 -----LGLGSHGHASHFHTSVRYEL--PIDMAYEPYFPHA 311

RESULT 15
US-09-248-796A-18663
Sequence 18663, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18663
LENGTH: 667
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18663

Query Match 9.6%; Score 79; DB 2; Length 667;
Best Local Similarity 19.7%; Pred. No. 1.3; Indels 76; Gaps 10;
Matches 42; Conservative 34; Mismatches 61; Indels 76; Gaps 10;

Qy 11 YEAELEAFMADGGTTLMLQD--ISGDTLEQLYA-----LAFSQ 46
Db 160 YEQALNPHVENGETWGLLGHLYMLDNLQRAYAAYQALFYLENPNVPKLVHGGIGILYDR 219
Qy 47 YQAGKWEDAHKIFQALCMLDHYEPY-----FLGLGACRAMGEFETAVOSYSGFAMLD 100
Db 220 Y--GSLEYAEAFVRVLDD---PNFDKANEIVFRLGIYKHQKLOPALECFQY----I 270
Qy 101 LKDRPFP-----FHAGECRLQOGLNGAESGF-----HSARLL-----ADT 136
Db 271 LNNPPHPLTQPDVWFQIGSVYEQQKNGAKDAYEKVLQINPHHAKVLQQLGCLYSQAES 330

Qy 137 DQ-----QADLAASAQVWLEAIAI 156
Db 331 NPSTPANGAAPPHKPFQODLTIALKYLKQSLV 363

Search completed: June 16, 2006, 19:28:58
Job time : 30.3439 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 16, 2006, 20:12:36 ; Search time 88.9366 Seconds
(without alignments)
828.131 Million cell updates/sec

Title: US-10-813-908A-9
Perfect score: 827
Sequence: 1 MQTDTTTPYEAELEAFMA.....QADLAASAKVMLEAIAIRRD 159

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pbp.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pbp.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pbp.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pbp.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pbp.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	827	100.0	159	5	US-10-813-908-9
2	549	66.4	167	4	US-10-282-122A-66316
3	214	25.9	179	6	US-11-098-686-11402
4	177	21.4	171	4	US-10-282-122A-50249
5	169.5	20.5	172	4	US-10-282-122A-68873
6	166.5	20.1	165	4	US-10-282-122A-73507
7	166.5	20.1	165	4	US-10-282-122A-76036
8	125.5	15.2	157	4	US-10-282-122A-75323
9	125.5	15.2	157	4	US-10-763-883-19
10	118	14.3	144	4	US-10-763-883-21
11	109	13.2	246	3	US-10-282-122A-55326
12	107.5	13.0	163	3	US-09-741-669-329
13	107.5	13.0	163	4	US-10-282-122A-42727
14	105	12.7	210	4	US-10-289-762-869
15	105	12.7	231	4	US-10-282-122A-54986
16	105	12.7	231	5	US-10-503-135-88
17	103.5	12.5	232	5	US-10-503-135-117
18	100	12.1	172	5	US-10-503-135-91
19	100	12.1	191	4	US-10-289-762-1095
20	90	10.9	304	4	US-10-369-493-18939
21	88.5	10.7	280	4	US-10-369-493-11967
22	84.5	10.2	1564	5	US-10-732-923-17031
23	83	10.0	834	4	US-10-156-761-12909
24	80.5	9.7	562	6	US-11-024-959-422
25	80.5	9.7	579	4	US-10-282-122A-48469
26	80.5	9.7	601	6	US-11-079-463-7428
27	80.5	9.7	676	4	US-10-369-493-3268

28	80	9.7	380	4	US-10-425-115-290062	Sequence 290062,
29	80	9.7	458	5	US-10-732-923-9310	Sequence 9310, Ap
30	80	9.7	482	6	US-11-079-463-6494	Sequence 6494, Ap
31	80	9.7	554	4	US-10-425-115-204269	Sequence 204269,
32	79.5	9.6	225	4	US-10-424-599-260796	Sequence 260796,
33	79	9.6	315	4	US-10-004-717-42	Sequence 42, Appl
34	79	9.6	315	5	US-10-860-373-42	Sequence 42, Appl
35	79	9.6	315	5	US-10-860-724-42	Sequence 11914, A
36	79	9.6	574	6	US-11-024-959-300	Sequence 300, App
37	79	9.6	658	4	US-10-369-493-11914	Sequence 11914, A
38	79	9.6	1080	4	US-10-451-467A-466	Sequence 466, App
39	78.5	9.5	240	5	US-10-732-923-9366	Sequence 9366, Ap
40	78.5	9.5	242	5	US-10-732-923-9367	Sequence 9367, Ap
41	78.5	9.5	292	5	US-10-450-763-50531	Sequence 50531, A
42	78	9.4	193	4	US-10-425-114-62615	Sequence 62615, A
43	78	9.4	211	3	US-09-933-767-263	Sequence 263, App
44	78	9.4	211	4	US-10-004-860-263	Sequence 263, App
45	78	9.4	211	4	US-10-023-282-263	Sequence 263, App

ALIGNMENTS

RESULT 1

US-10-813-908-9
; Sequence 9, Application US/10813908
; Publication No. US20050058662A1
; GENERAL INFORMATION:
; APPLICANT: Frey, Joachim Stuber
; TITLE OF INVENTION: Novel Type III Secretion Pathway in Aeromonas Salmonicida, and t
; FILE REFERENCE: MIC01/2315/WO
; CURRENT APPLICATION NUMBER: US/10/813.908
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US/10/416,902
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: PCT/CA01/01589
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Aeromonas salmonicida
; US-10-813-908-9

Query Match	100.0%;	Score 827;	DB 5;	Length 159;
Best Local Similarity	100.0%;	Pred. No. 6.3e-88;		
Matches	159;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MQTDTTTPYEAELEAFMADGGTFLAMLQDISGDTLEQLYALAFSQYQAGKWEAHKIFQ	60	
Db	1	MQTDTTTPYEAELEAFMADGGTFLAMLQDISGDTLEQLYALAFSQYQAGKWEAHKIFQ	60	
Qy	61	ALCMLDHYERYFLGLGACQAMGEFETAVQSYSGFAMLDLKDPFFPHAGECRLQOQDL	120	
Db	61	ALCMLDHYERYFLGLGACQAMGEFETAVQSYSGFAMLDLKDPFFPHAGECRLQOQDL	120	
Qy	121	NGAESGFHARLLADTPQQADLAASAKVMLEAIAIRRD	159	
Db	121	NGAESGFHARLLADTPQQADLAASAKVMLEAIAIRRD	159	

RESULT 2

US-10-282-122A-66316
; Sequence 66316, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith

```
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66316
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-10-282-122A-66316

Query Match      66.4%; Score 549; DB 4; Length 167;
Best Local Similarity 64.8%; Pred. No. 1.8e-55;
Matches 103; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 1 MNOTDTTLTPEYAELEAFMADGGTGLAMLODISGDTLEQLYALAFSQYQAGKWEADHKIFQ 60
Db 1 MNQPTSDTDQQALEAFRLDGGTGLAMRLGSLDTEQLYALGFNGYQAGKWDQAQKIFQ 60

QY 61 ALCMLDHYEPYFLGLGACRQAMGBETAVQSYSGFAMLDLKDPRPPFFHAGECRLQGGDL 120
Db 61 ALCMLDHYDARYFLGLGACRQSLGLYEALQSYSGALMDINEPRPPFFHAAECHLQGLDL 120

QY 121 NGAESGFHSARLLADTDPQOADLAASAKVMLEAIRRD 159
Db 121 DGAESGFYSARALAAQAAPAEALAAAGAMLEAVTARKD 159

RESULT 3
US-11-098-686-11402
; Sequence 11402, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 11402
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
; US-11-098-686-11402

Query Match      25.9%; Score 214; DB 6; Length 179;
Best Local Similarity 33.8%; Pred. No. 2.5e-16;
Matches 54; Conservative 27; Mismatches 69; Indels 10; Gaps 4;

QY 1 MQTDTTLTPEYAELEAFMADGGTGLAMLODISGDTLEQ---LYALAFSQYQAGKWEADHK 57
Db 20 MGTDDNM---ERVEAIMDALSTGSSIGDIIGITQEQMDVLVTIAYGAYQAKNYQDAET 74

QY 58 IPOALCMLDHYEPYFLGLGACRQAMGBETAVQSYSGFAMLDLKDPRPPFFHAGECRLQ 116
Db 75 LFOALCLYQHMDERYWMYGLAGSRQGLENYKGAIEAYEMAGLAGSLGDPPTFLYAGICYMK 134

QY 117 QGDLNGAESGFHSARLLADTDPQOADLAAS-AKVMLEAIA 155
Db 135 FGDKESARVAFULSTEALCOEGNRKHDVLVKERAKAMLEILS 174

RESULT 4
US-10-282-122A-50249
; Sequence 50249, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50249
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Burkholderia mallei
; US-10-282-122A-50249
```

```

Query Match      21.4%; Score 177; DB 4; Length 171;
Best Local Similarity 33.1%; Pred. No. 4.8e-12;
Matches 40; Conservative 17; Mismatches 60; Indels 4; Gaps

```

Qy	2	QDTTTLTPEYEAELAFWAD----	CGTTLAMLDISGDTLLEQLYALAFSQYQAGKWEDAHK	57
Db	3	ORDVNNIDIEAQEMAALLDVAVQNGATIKDLHQVQDLMWDGIIYAFAYRPFYQOGRUDDAEV	62	
Qy	58	IFOALCMLDHYEPYFLGLIGACRQAGMBFETAVQSFGAMLDLKDPRPPFPFHAGECRLOQ	117	
Db	63	FFRFELCIYFNAEYAMGLAAVCQLKKEYARAIIDLYALAYSLSKDDHPRMFHTGQCHLLM	122	
Qy	118	G 118		
Db	123	G 123		

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RESULT 5
US-10-282-122A-68873
; Sequence 68873, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68873
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-10-282-122A-68873

```

```

Query Match      20.5%; Score 169.5; DB 4; Length 172;
Best Local Similarity 29.8%; Pred. No. 3.6e-11;
Matches 37; Conservative 26; Mismatches 54; Indels 7; Gaps 1

```

Qy	12	EAELE-----AFMADGGTTLAMLDISGDTLLEQLYALAFSQYQAGKWEDAHKIFQALCM	64
----	----	---	----

```

Db      9  EKELDQLANYITVSVQNGASIKDESEIPDGFMEGIYSFAYDFYQKGKLDDEABAIKFKFLCL 68
QY      65  LDHYEPRYFLGLGACROAMGEFEFATAVQSYSGFAMCLDLKDPFPFPFHAGECRLQOQDLNGAB 124
DB      69  YDFVNDYIMGLAANVLKKQYQAAIDLYALYNLAKNDYRPFVYAGQCNLSIGEKEKAK 128
QY      125  SGFH 128
DB      129  YCFH 132

RESULT 6
US-10-282-122A-73507
; Sequence 73507, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73507
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-73507

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	Query Match	20.1%; Score 166.5; DB 4; Length 165;
	Best Local Similarity	30.8%; Pred. No. 7.7e-11;
	Matches	48; Conservative 25; Mismatches 76; Indels 7; Gaps 3
Qy	1 MQTTTTTPEYAEEL--EAFWADGGTTAMLQDISGDTLEQLYALAFSQYQAQKWDNAKI 58	. : : : : : : : : : : : : : : : :
Dd	1 MDYQNNVSEERVAEMIWA-VSEGATLKDVGHI PQDMMGLYAHAYEFYNQRLDEAETF 59	: : : : : : : : : : : : : : : :
Qy	59 FOALCMLDHYPYFLGLIGACRQAMGPETAVQSYSFCAMLDLKDPRPFPHAGECRLOQG 118	: : : : : : : : : : : : : : : :
Dd	60 FRFLCIYDFNPDPYTMGLAAVCOLKKQFKQACDLIYAFTLLKNDRYRVFFVTGCQCQLMR 119	: : : : : : : : : : : : : : : :

QY
119 DLNGAEGFHSARLLADTDPPQQADLAASAKVMLEAI 154

Db
120 KAAKARQCFE----LVNRTEDESLRKALVYLEAL 151

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RESULT 7
US-10-282-122A-76036
; Sequence 76036, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

```

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; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-76036

Query Match      20.1%   Score 166.5;   DB 4;   Length 165;
Best Local Similarity 30.8%;   Pred. No. 7.7e-11;
Matches 48; Conservative 25; Mismatches 76; Indels 7; Gaps 3

QY    1  MOTDTTITPEYEAL--EAFNADGCTLMLDLDISGDTLEQLYALASQYCAQGWEDAHI 58
Db                    :|::||::||::||::||::||::||::||::||::||:
QY    1  MDYQNNSSEERVAEMWDA-VSEGATLKDVHGIPQDDMGGLYAHAYEFYNQGRLDEAEFT 59
Db                    :|::||::||::||::||::||::||::||::||::|
QY    59 FOALCMLDHYEPFRLGLGACRQAMGBETAVOSYSFGAMDLDKDRPFPFHAGECRLOQG 118
Db                    :|::||::||::||::||::||::||::||::||::|
QY    60 FRFLCIYDFYNPDYTMGLAAVCQLKKQFOKACDLYAVAFTLLKNKYRPVFFTGQCQLLMR 119
Db                    :|::||::||::||::||::||::||::||::||::|
QY    119 DLNGAESGFHSARLLADTPQQADLAASAKVMLEAI 154
Db                    :|::||::||::||::||::||::||::||::||::|
QY    120 KAAKARQCFE----LVNERTEDESLRKALVYLEAL 151
Db                    :|::||::||::||::||::||::||::||::||::|

```

RESULT 8

```

US-10-282-122A-75323
; Sequence 75323, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75323
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-75323

```

```

Query Match      15.2%; Score 125.5; DB 4; Length 157;
Best Local Similarity 27.0%; Pred. No. 4.4e-06;
Matches 43; Conservative 26; Mismatches 83; Indels 5; Gaps 4

Qy 1 MQTDTTLTPYEAELEAFMADGGTLLM-LODISGDTLEQLYALAFSQYQAGKWEDAHKIF 59
Db 1 MKKDPTLQQAHDT--NRFFRRGSLRMLLDDDDVTQPLNTLYRYATQLMVEKFAAGARLF 58

Qy 60 QALCMLDHYBPYRFLGLGACRQAMGEPETAVSQSYSGFAMLDLDKDPRPFPFHAGECRLQOQD 119
Db 59 QLLTIYDAWSEDFYWRFLGECQCKHGEAIYAGRAAQIKIDAPQAPWAAECYVLACDN 118

Qy 120 LNAESGFHS-ARKLADTFQOQADLAASAKVMLEAIAIR 157
Db 119 VCYAIKALKAVRAICGEVSEHQI-LRQRAEKMQLQLSDR 156

RESULT 9
US-10-763-883-19
; Sequence 19, Application US/10763883
; Publication No. US2004020309A1
; GENERAL INFORMATION:
; APPLICANT: Michael Hensel
; APPLICANT: David William Holden

```

```

; APPLICANT: Jacqueline Elizabeth Shea
; TITLE OF INVENTION: Attenuated Salmonella SPI2 Mutants as Antigen Carriers
; FILE REFERENCE: ICI 104 DIV
; CURRENT APPLICATION NUMBER: US/10/763,883
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 09/763,620
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06514
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: EP 98116827.1
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Salmonella
US-10-763-883-19

Query Match 15.2%; Score 125.5; DB 4; Length 157;
Best Local Similarity 27.0%; Pred. No. 4.4e-06;
Matches 43; Conservative 28; Mismatches 83; Indels 5; Gaps 4;

Qy 1 MQDTTTLTPEYAEAEAPMAGGTILAM-LQDISGDTLEQLYALAFSQYQAGKWEHAHIF 59
Db 1 MKKOPTLQAAHDT--MREFFRGGSRLMLLDDVDTPLNTLYRYATQLMEVKEFAGAARLF 58

Qy 60 QALCMLDHYEPYRFLGLGACQAMGEPETAQVSYSFGAMLDLKDPRPFPFHAGECRLOQGD 119
Db 59 QLLTIYDAWSFDYWRFLGECQAKHWEGLIYAVGRAAQIKIDAPQAPWAAAEYVLACDN 118

Qy 120 LNGAESGFHS-ARLLADTDPQADLAASAKVMLEAIAIR 157
Db 119 VCYAIKALKAVVRIGCEVSEHQI-LRQRAERMLQLSDR 156

RESULT 10
US-10-763-883-21
; Sequence 21, Application US/10763883
; Publication No. US2004020309A1
; GENERAL INFORMATION:
; APPLICANT: Michael Hensel
; APPLICANT: David William Holden
; APPLICANT: Jacqueline Elizabeth Shea
; TITLE OF INVENTION: Attenuated Salmonella SPI2 Mutants as Antigen Carriers
; FILE REFERENCE: ICI 104 DIV
; CURRENT APPLICATION NUMBER: US/10/763,883
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 09/763,620
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/EP99/06514
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: EP 98116827.1
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Salmonella
US-10-763-883-21

Query Match 14.3%; Score 118; DB 4; Length 144;
Best Local Similarity 24.2%; Pred. No. 2.9e-05;
Matches 32; Conservative 24; Mismatches 68; Indels 8; Gaps 1;

Qy 31 ISGDTLEQL-----YALAFSQYQAGKWEHAHIFQALCMLDHYEPYRFLGLGACRQA 82
Db 11 IPEDILKQLLSDVPETVYASGVASQWQEGDYSRAVIDFSWLVMYAPQWRAHIALAGTMM 70

Qy 83 MGEFETAQVSYSFGAMLDLKDPRFPFHAGECRLOQGD LINGAESGFHSARLLADTDPQAD 142
Db 71 LKEYTTAINFYGHALLMDASHPEPVYQTGCVLKWMBPGLAREAFOTAIKMSYADASWSE 130

```

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; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Olesen, Kari L.
; APPLICANT: Zyskind, Judith W.
; TITLE OF INVENTION: Genes identified as required for
; FILE REFERENCE: ELITRA.009A
; CURRENT APPLICATION NUMBER: US/09/741,669
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/173005
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-741-669-329

Query Match      13.0%; Score 107.5; DB 3; Length 163;
Best Local Similarity 22.3%; Pred. No. 0.00058;
Matches 31; Conservative 30; Mismatches 61; Indels 17; Gaps 3;

QY 1 MQTDT----TLTPEYAEAEAFMADGGTLLMLQDISGDTLEQLYALAFSQYQAGKWEDAH 56
Db 1 MSTETIEIFNNSDEWANQLKHALSKGENLALLHGLTPDILDRIYAYAFDYHEKGNITDAE 60

QY 57 KIFQALCMLDHYEPFVLGLGACRQAMGEFETAVQSYSGAMLDLKDPRFP-----FH 109
Db 61 IYKFLCIYAFENHKEYLKDFASVCQPKKYQAYDLYK-----LSYNYFPDYDSVIYR 114

QY 110 AGECLRQOGLNGAESGFH 128
Db 115 MGQCQIGAKNIDNMQCFY 133

RESULT 13
US-10-282-122A-42727
; Sequence 42727, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Olesen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42727
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-282-122A-42727

Query Match      13.0%; Score 107.5; DB 4; Length 163;
Best Local Similarity 22.3%; Pred. No. 0.00058;
Matches 31; Conservative 30; Mismatches 61; Indels 17; Gaps 3;

QY 1 MQTDT----TLTPEYAEAEAFMADGGTLLMLQDISGDTLEQLYALAFSQYQAGKWEDAH 56
Db 1 MSTETIEIFNNSDEWANQLKHALSKGENLALLHGLTPDILDRIYAYAFDYHEKGNITDAE 60

QY 57 KIFQALCMLDHYEPFVLGLGACRQAMGEFETAVQSYSGAMLDLKDPRFP-----FH 109
Db 61 IYKFLCIYAFENHKEYLKDFASVCQPKKYQAYDLYK-----LSYNYFPDYDSVIYR 114

QY 110 AGECLRQOGLNGAESGFH 128
Db 115 MGQCQIGAKNIDNMQCFY 133

RESULT 14
US-10-289-762-869
; Sequence 869, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 869
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; US-10-289-762-869

Query Match      12.7%; Score 105; DB 4; Length 210;
Best Local Similarity 23.4%; Pred. No. 0.0016;
Matches 33; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

QY 19 MADGGTLLMLQDISGDTLEQLYALAFSQYQAGKWEDAHKIFQALCMLDHYEPFVLGLGA 78
Db 43 LSNGLDLQOILGLSYLLEIIVTAVTFYSQKYNKAVGLFOLLAAAQPNQYKYMGLGSS 102

QY 79 CRQAMGEFETAVQSY--SFGAMLDLKDPRFPFHAGE--CRLOOGLNGAESGFHSARL-L 133
Db 103 CYHQLHLHYNEAAGFFLAFDAQPD--NPIPPYYIADSLKLQOPE---BSNNFLDVTMDI 157

QY 134 ADTDPQOADLAASAKVMLEAI 154
Db 158 CGNPFKILKERCQIMKQSI 178

RESULT 15
US-10-282-122A-54986
; Sequence 54986, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguu
; APPLICANT: Zamudio, Carlos

```

```

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54986
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54986
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```

Query Match      12.7%; Score 105; DB 4; Length 231;
Best Local Similarity 23.4%; Pred.No. 0.0018;
Matches 33; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

Qy      19  MADGGTAMQLQDISGDTLEQLYALAFSQYQAGKWEAHKIFQALCMLDHYEPRYFLGLGA 78
Db      64  LSNGLDQQILGLSDYLEEIIYVAYTFYSQGYNEAVGLFQLLAAAQPNKYKMYLGLSS 123

Qy      79  CRQAMGEFETAVQSY--SFGAMLDLKDPRFPFHAGE--CRLQQGDLNGAESGFHSARL-L 133
Db      124  CYHQHLHYNEAAGFFLAFAQPD--NPIPPYYIADSLKLOQPE---ESNNFLDVTMDI 178

Qy      134  ADTDPQQAADLAASAKVMLEAI 154
Db      179  CGNNPEFKILKERCQIMKQSI 199
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Job time : 89.9366 secs

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[illegible]


```
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: {346}..(346)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13122

Query Match      8.1%; Score 67; DB 6; Length 357;
Best Local Similarity 21.6%; Pred. No. 9.9;
Matches 24; Conservative 16; Mismatches 37; Indels 34; Gaps 5;

QY 39 LVYALAFSOYQAGKQWED--AHKIFQALCMLDHYEPRYFLGLGACROAMGEFETAVQSYSGF 96
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 15 LFSLLFTSYATNSAENNFVH-----CLVNHSEPHPIISAAIFTQSSFSVLQAY--- 65
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 97 AMLDLKDPFRF-----PPHAGE-----CRLQOQDNLNGAESGFH 128
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 66 ---IRNLRFNTSTTRKPFLLIVTPPHVSHVQASIVCAKKHLLMKIRSGGH 112
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 14
US-10-953-349-13121
; Sequence 13121, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13121
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: {364}..(364)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13121

Query Match      8.1%; Score 67; DB 6; Length 375;
Best Local Similarity 21.6%; Pred. No. 11;
Matches 24; Conservative 16; Mismatches 37; Indels 34; Gaps 5;

QY 39 LVYALAFSOYQAGKQWED--AHKIFQALCMLDHYEPRYFLGLGACROAMGEFETAVQSYSGF 96
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 33 LFSLLFTSYATNSAENNFVH-----CLVNHSEPHPIISAAIFTQSSFSVLQAY--- 83
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 97 AMLDLKDPFRF-----PPHAGE-----CRLQOQDNLNGAESGFH 128
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 84 ---IRNLRFNTSTTRKPFLLIVTPPHVSHVQASIVCAKKHLLMKIRSGGH 130
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 15
US-10-449-902-54809
; Sequence 54809, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-363870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54809
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54809

Query Match      8.1%; Score 67; DB 6; Length 483;
Best Local Similarity 19.8%; Pred. No. 14;
Matches 25; Conservative 24; Mismatches 71; Indels 6; Gaps 1;

QY 37 EQLYALAFSOYQAGKQWEDAHKIFQALCMLDHYEPRYFLGLGACROAMGEFETAVQSYSGF 96
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 13 EELKLANDAFKANKFSLAIELYQAIELNSSNAVYWANRAFAHTKLEYSAGVQDASKA 72
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 97 AMLDLKDPFRFPFHAGECRLQOQDNLNGAESGFHSLRLIADTDP-----QQADLAASAKVM 150
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 73 IEIDARYSKGYRGRGAAYLANGKPKFALKDFQOVKRISPNDPDATRKLEKEKAVQKIRF 132
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 151 LEAIAI 156
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 133 EEATSV 138
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Job time : 7.85122 secs

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